RevoScaleR User's Guide

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Chapter 1.

Introduction

1.1 Why RevoScaleR?

RevoScaleR™ provides tools for both High Performance Computing (HPC) and High Performance Analytics (HPA) with R. HPC capabilities allow you to distribute the execution of essentially any R function across cores and nodes, and deliver the results back to the user. HPA adds 'big data' to the challenge. This guide focuses on these HPA 'big data' capabilities. [See the *RevoScaleR Distributed Computing Guide* (RevoScaleR_Distributed_Computing.pdf) for information on both HPC and HPA capabilities in a distributed context.]

RevoScaleR provides tools for scalable data management and analysis. These tools can be used with data sets in memory, and applied the same way to huge data sets stored on disk. It includes functionality for:

1) Accessing external data sets (SAS, SPSS, ODBC, Teradata, and delimited and fixed format text) for analysis in R
2) Efficiently storing and retrieving data in a high performance data file
3) Cleaning, exploring, and manipulating data
4) Fast, basic statistical analyses

RevoScaleR also includes an extensible framework for writing your own analyses for big data sets.

With RevoScaleR, you can use R to analyze data sets far larger than can be kept in memory. This is possible because RevoScaleR uses external memory algorithms that allow it to work on one chunk of data at a time (that is, a subset of the rows and perhaps the variables in the data set), update the results, and proceed through all available data.

1.1.1 Accessing External Data Sets

Data can be stored in a wide-variety of formats. Typically, the first step in any RevoScaleR analysis is to make the data accessible. With RevoScaleR's data import capability, you can access data from a SAS file, SPSS file, fixed format or delimited text file, an ODBC connection, or a Teradata data base, bringing it into a data frame in memory, or storing it for fast access in chunks on disk.

1.1.2 Efficiently Storing and Retrieving Data

A key component of RevoScaleR is a data file format (.xdf) that is extremely efficient for both reading and writing data. You can create .xdf files by importing data files or from R data frames, and add rows or variables to an existing .xdf file. Once your data is in this file format you can use it directly with analysis functions provided with RevoScaleR, or quickly extract a subsample and read it into a data frame in memory for use in other R functions.

1.1.3 Data Cleaning, Exploration, and Manipulation

When working with a new data set, the first step is to clean and explore. With RevoScaleR, you can quickly obtain information about your data set (e.g., how many rows and variables) and the variables in your data set (e.g., name, data type, value labels). With RevoScaleR's summary statistics and cube functionality, you can examine summary information about your data and quickly plot histograms or relationships between variables.

RevoScaleR also provides all of the power of R to use in data transformations and manipulations. In RevoScaleR's data step functionality, you can specify R expressions to transform specific variables and have them automatically applied to a single data frame or to each block of data as it is read in from an .xdf file. You can create new variables, recode variables, and set missing values with all the flexibility of the R language.

1.1.4 Statistical Analysis

In addition to descriptive statistics and crosstabs, RevoScaleR provides functions for fitting linear and binary logistic regression models, generalized linear models, k-means models, and decision trees and forests. These functions access .xdf files or other data sources directly or operate on data frames in memory. Because these functions are so efficient and do not require that all of the data be in memory at one time, you can analyze huge data sets without requiring huge computing power. In particular, you can relax assumptions previously required. For example, instead of assuming a linear or polynomial functional form in a model, you can break

independent variables into many categories providing a completely flexible functional form. The many degrees of freedom provided by large data sets, combined with RevoScaleR's efficiency, make this approach feasible.

1.1.5 Writing Your Own Analyses for Large Data Sets

All of the main analysis functions in RevoScaleR use updating or external memory algorithms, that is, they analyze a chunk of data, update the results, then move on to the next chunk of data and repeat the process. When all the data has been processed (sometimes multiple times), final results can be calculated and the analysis is complete. You can write your own functions to process a chunk of data and update results, and use RevoScaleR functionality to provide you with access to your data file chunk by chunk.

1.2 Getting Started

In this initial chapter, we take a quick walk through the five feature areas described above using a sample data set. More detailed information about the functions used is available in the other chapters of this manual. We then briefly describe other sample data available for use with RevoScaleR. Finally, we describe the online help available. For additional introductory material, see the *RevoScaleR Getting Started Guide* (RevoScaleR_Getting_Started.pdf). For information on using RevoScaleR for distributing computations over more than one computer, see the *RevoScaleR Distributed Computing Guide* (RevoScaleR_Distributed_Computing.pdf) and the various Getting Started guides for particular distributed computing platforms:

- *RevoScaleR Hadoop Getting Started Guide* (RevoScaleR_Hadoop_Getting_Started.pdf)
- *RevoScaleR Teradata Getting Started Guide* (RevoScaleR_Teradata_Getting_Started.pdf)

For more information on accessing databases via ODBC, see the *RevoScaleR ODBC Import Guide* (RevoScaleR_ODBC.pdf).

1.2.1 Accessing External Data Sets

The most common way to store data is in a text file. For example, a comma-delimited, text data file containing a subsample of information on airline departures and arrivals in the United States is available in the RevoScaleR sample data directory. (More examples using this data file are available in the *Getting Started Guide* [RevoScaleR_Getting_Started.pdf].) The sample code below will import it using the `rxImport` function. There are a total of 600,000 rows in the data file. By specifying the argument `rowsPerRead`, we read and write the data in 3 blocks of 200,000 rows each.

```
#######################################################
# Chapter 1: Introduction
Ch1Start <- Sys.time()
```

```
inFile <- file.path(rxGetOption("sampleDataDir"), "AirlineDemoSmall.csv")
airData <- rxImport(inData=inFile, outFile = "airExample.xdf",
     stringsAsFactors = TRUE, missingValueString = "M", rowsPerRead = 200000)
```

If the *outFile* argument had been omitted, the returned *airData* object would be a data frame containing the data. Since the imported data is being stored in an .xdf file, *rxImport* returns an .xdf data source object. This object represents the .xdf data file, but doesn't take up much memory. It can be used in many other RevoScaleR objects interchangeably with a data frame.

To get basic information about the data set and variables, we use *rxGetInfo*:

```
rxGetInfo(airData, getVarInfo = TRUE)
```

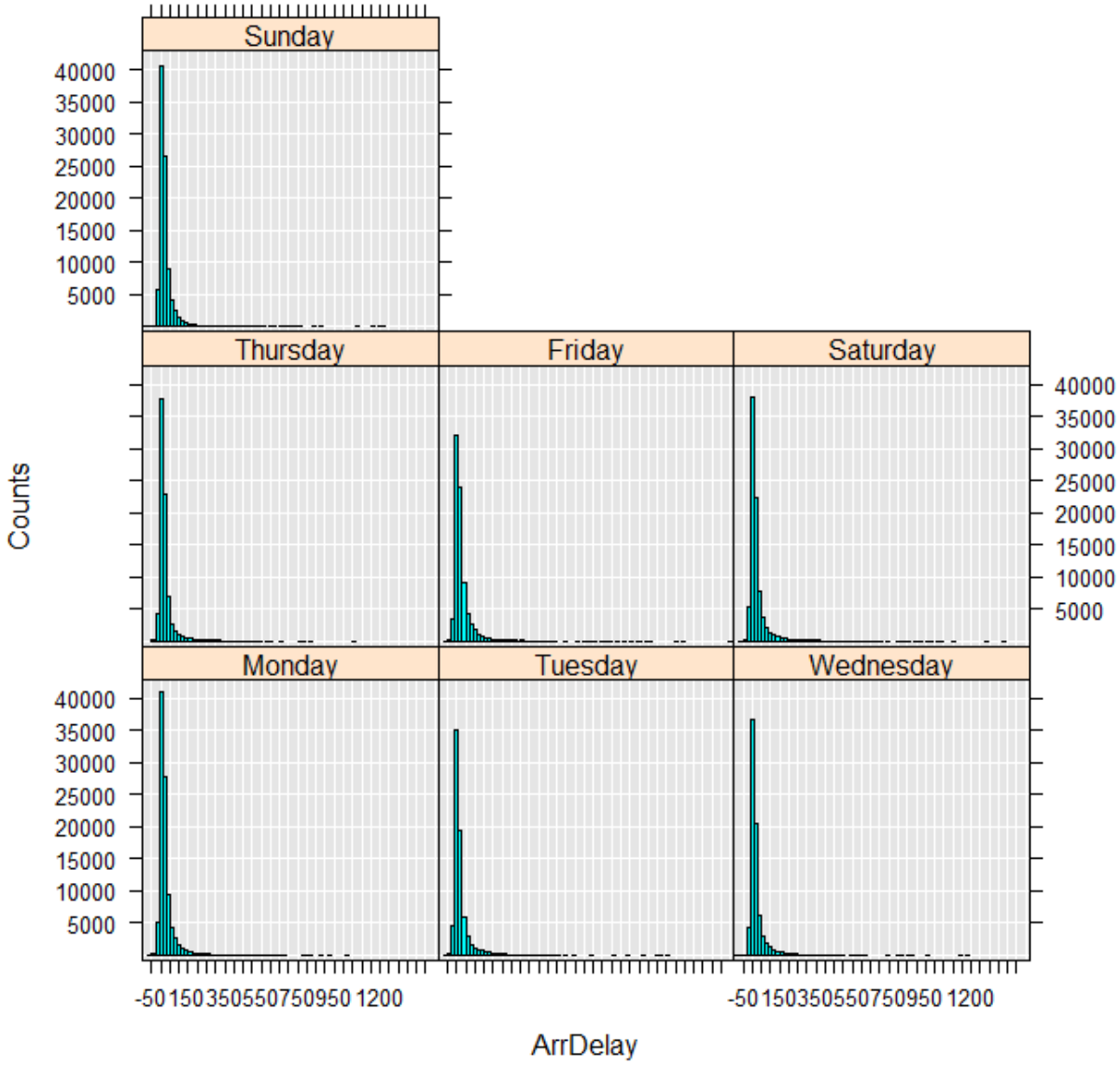
which results in the following output:

```
File name: C:\YourOutputPath\airExample.xdf
Number of observations: 6e+05
Number of variables: 3
Number of blocks: 3
Compression type: zlib
Variable information:
Var 1: ArrDelay, Type: integer, Low/High: (-86, 1490)
Var 2: CRSDepTime, Type: numeric, Storage: float32, Low/High: (0.0167, 23.9833)
Var 3: DayOfWeek
       7 factor levels: Monday Tuesday Wednesday Thursday Friday Saturday
Sunday
```

1.2.2 Data Cleaning, Exploration, and Transformations

Let's take a quick look at the data. We can use the *rxHistogram* function to show the distribution in arrival delay by day of week. It uses the *rxCube* function (described later in this manual) to calculate information for a histogram:

```
rxHistogram(~ArrDelay|DayOfWeek,  data = airData)
```



We can also compute descriptive statistics for the variable:

```
rxSummary(~ ArrDelay, data = airData )

 Call:
 rxSummary(formula = ~ArrDelay, data = airData)

 Summary Statistics Results for: ~ArrDelay
 Data: airData (RxXdfData Data Source)
 File name: airExample.xdf
 Number of valid observations: 6e+05

  Name     Mean     StdDev   Min Max  ValidObs MissingObs
  ArrDelay 11.31794 40.68854 -86 1490 582628   17372
```

Our first look tells us two important things: arrival delay has a long "tail" for every day of the week, with a few flights delayed for well over two hours, and there are quite a few missing values (17,372). Presumably the missing values for arrival delay represent flights that did not arrive, that is, were cancelled.

We can use RevoScaleR's data step functionality to create a new variable, *VeryLate*, that represents flights that were either over two hours late or canceled. Since we have our original data safely stored in a text file, we will simply add this variable to our existing airline.xdf file using the *transforms* argument to *rxDataStep*. The *transforms* argument takes a list of one or more R expressions, typically in the form of assignment statements. In this case, we use the following expression: *list(VeryLate = (ArrDelay > 120 | is.na(ArrDelay))*

The full RevoScaleR data step then consists of the following steps:

1) Read in the *data* a block (200,000 rows) at a time.
2) For each block, pass the *ArrDelay* data to the R interpreter for processing the transformation to create *VeryLate*.
3) Write the data out to the data set a block at a time. The argument *overwrite=TRUE* allows us to overwrite the data file.

```
airData <- rxDataStep(inData = airData, outFile = "airExample.xdf",
    transforms=list(VeryLate = (ArrDelay > 120 | is.na(ArrDelay))),
    overwrite = TRUE)
```

1.2.3 Statistical Analysis

We can perform statistical analysis using a data frame or .xdf file. For example, we can estimate a logistic regression on whether or not a flight is "very late" depending on the day of week using *rxLogit*:

```
logitResults <- rxLogit(VeryLate ~ DayOfWeek, data = airData )
summary(logitResults)
```

```
 Call:
 rxLogit(formula = VeryLate ~ DayOfWeek, data = airData)

 Logistic Regression Results for: VeryLate ~ DayOfWeek
 File name:
     C:\YourOutputPath\airExample.xdf
 Dependent variable(s): VeryLate
 Total independent variables: 8 (Including number dropped: 1)
 Number of valid observations: 6e+05
 Number of missing observations: 0
 -2*LogLikelihood: 251244.7201 (Residual deviance on 599993 degrees of freedom)

 Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
 (Intercept)         -3.29095    0.01745 -188.64 2.22e-16 ***
 DayOfWeek=Monday     0.40086    0.02256   17.77 2.22e-16 ***
 DayOfWeek=Tuesday    0.84018    0.02192   38.33 2.22e-16 ***
 DayOfWeek=Wednesday  0.36982    0.02378   15.55 2.22e-16 ***
```

```
DayOfWeek=Thursday   0.29396    0.02400   12.25 2.22e-16 ***
DayOfWeek=Friday     0.54427    0.02274   23.93 2.22e-16 ***
DayOfWeek=Saturday   0.48319    0.02282   21.18 2.22e-16 ***
DayOfWeek=Sunday     Dropped    Dropped Dropped  Dropped
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Condition number of final variance-covariance matrix: 16.7804
Number of iterations: 3
```

The results show that in this sample, a flight on Tuesday is most likely to be very late or cancelled, followed by flights departing on Friday. In this model, Sunday is the control group, so that coefficient estimates for other days of the week are relative to Sunday. The intercept shown is the same as the coefficient you would get for Sunday if you omitted the intercept term:

```
logitResults2 <- rxLogit(VeryLate ~ DayOfWeek - 1, data = airData )
summary(logitResults2)
```

```
Call:
rxLogit(formula = VeryLate ~ DayOfWeek - 1, data = airData)

Logistic Regression Results for: VeryLate ~ DayOfWeek - 1
File name:
    C:\YourOutputPath\airExample.xdf
Dependent variable(s): VeryLate
Total independent variables: 7
Number of valid observations: 6e+05
Number of missing observations: 0
-2*LogLikelihood: 251244.7201 (Residual deviance on 599993 degrees of freedom)

Coefficients:
                   Estimate Std. Error z value Pr(>|z|)
DayOfWeek=Monday    -2.89008    0.01431  -202.0 2.22e-16 ***
DayOfWeek=Tuesday   -2.45077    0.01327  -184.7 2.22e-16 ***
DayOfWeek=Wednesday -2.92113    0.01617  -180.7 2.22e-16 ***
DayOfWeek=Thursday  -2.99699    0.01648  -181.9 2.22e-16 ***
DayOfWeek=Friday    -2.74668    0.01459  -188.3 2.22e-16 ***
DayOfWeek=Saturday  -2.80776    0.01471  -190.9 2.22e-16 ***
DayOfWeek=Sunday    -3.29095    0.01745  -188.6 2.22e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Condition number of final variance-covariance matrix: 1
Number of iterations: 7
```

1.2.4 Writing Your Own Analyses for Large Data Sets

We can have RevoScaleR provide data to us, one chunk at a time, and perform our own custom analysis. There are four basic steps in the analysis:

1) Initialize results
2) Process data, a chunk at a time
3) Update results, after processing each chunk
4) Final processing of results

For illustrative purposes, suppose that we want to compute the average arrival delay for flights that leave in the morning, afternoon, and evening. For each chunk of data, we need to compute the sum of arrival delay for each of the three time intervals, as well as the counts for each interval. We will accumulate these results in a list of "transformObjects" containing the six values. At the end after processing all the data, we will divide the accumulated totals by the accumulated counts to compute the averages.

Most of the work takes place within a transformation function, which processes the data and updates the results for each chunk of data that is read in. We use the .rxGet and .rxSet functions to store information from one pass of the data to the next. Because we are processing data and not creating newly transformed variables, we return NULL from the function:

```
#  Writing Your Own Analyses for Large Data Sets

ProcessAndUpdateData <- function( data )
{
    # Process Data
    notMissing <- !is.na(data$ArrDelay)
    morning <- data$CRSDepTime >= 6 & data$CRSDepTime < 12 & notMissing
    afternoon <- data$CRSDepTime >= 12 & data$CRSDepTime < 17 & notMissing
    evening <- data$CRSDepTime >= 17 & data$CRSDepTime < 23 & notMissing
    mornArr <- sum(data$ArrDelay[morning], na.rm = TRUE)
    mornCounts <- sum(morning, na.rm = TRUE)
    afterArr <- sum(data$ArrDelay[afternoon], na.rm = TRUE)
    afterCounts <- sum(afternoon, na.rm = TRUE)
    evenArr <- sum(data$ArrDelay[evening], na.rm = TRUE)
    evenCounts <- sum(evening, na.rm = TRUE)


 # Update Results
   .rxSet("toMornArr", mornArr + .rxGet("toMornArr"))
   .rxSet("toMornCounts", mornCounts + .rxGet("toMornCounts"))
   .rxSet("toAfterArr", afterArr + .rxGet("toAfterArr"))
   .rxSet("toAfterCounts", afterCounts + .rxGet("toAfterCounts"))
   .rxSet("toEvenArr", evenArr + .rxGet("toEvenArr"))
   .rxSet("toEvenCounts", evenCounts + .rxGet("toEvenCounts"))

    return( NULL )
}
```

Our transformation object values are initialized in a list passed into rxDataStep. We also use the argument `returnTransformObjects` to indicate that we want updated values of the `transformObjects` returned rather than a transformed data set:

```
totalRes <- rxDataStep( inData = airData , returnTransformObjects = TRUE,
    transformObjects =
        list(toMornArr = 0, toAfterArr = 0, toEvenArr = 0,
        toMornCounts = 0, toAfterCounts = 0, toEvenCounts = 0),
    transformFunc = ProcessAndUpdateData,
    transformVars = c("ArrDelay", "CRSDepTime"))
```

The rxDataStep function will automatically chunk through the data for us. All we need to do is process the final results:

```
FinalizeResults <- function(totalRes)
{
    return(data.frame(
        AveMorningDelay = totalRes$toMornArr / totalRes$toMornCounts,
        AveAfternoonDelay = totalRes$toAfterArr / totalRes$toAfterCounts,
        AveEveningDelay = totalRes$toEvenArr / totalRes$toEvenCounts))
}
FinalizeResults(totalRes)
```

The calculated results are:

```
  AveMorningDelay AveAfternoonDelay AveEveningDelay
1        6.146039          13.66912        16.71271
```

In this case we can check our results by using the *rowSelection* argument in *rxSummary*:

```
rxSummary(~ArrDelay, data = "airExample.xdf",
rowSelection = CRSDepTime >= 6 & CRSDepTime < 12 & !is.na(ArrDelay))
```

```
Call:
rxSummary(formula = ~ArrDelay, data = "airExample.xdf",
       rowSelection = CRSDepTime >= 6 & CRSDepTime < 12 & !is.na(ArrDelay))

Summary Statistics Results for: ~ArrDelay
File name:
    C:\YourOutputPath\airExample.xdf
Number of valid observations: 234403

 Name     Mean     StdDev  Min Max  ValidObs MissingObs
 ArrDelay 6.146039 35.4734 -85 1490 234403   0
```

1.3 Sample Data for Use with RevoScaleR

Sample data is available both within the RevoScaleR package and online. To view the files available within the package, use the following command:

```
#  Sample Data for Use with RevoScaleR

list.files(system.file("SampleData", package = "RevoScaleR"))
```

This should yield the following list:

```
 [1] "AirlineDemo1kNoMissing.csv" "AirlineDemoSmall.csv"
 [3] "AirlineDemoSmall.xdf"       "CensusWorkers.xdf"
 [5] "claims.dat"                 "claims.sas7bdat"
 [7] "claims.sav"                 "claims.sd7"
 [9] "claims.sqlite"              "claims.sts"
[11] "claims.txt"                 "claims.xdf"
[13] "claimsExtra.txt"            "claimsQuote.txt"
[15] "claimsTab.txt"              "CustomerSurvey.xdf"
[17] "DJIAdaily.xdf"              "fourthgraders.xdf"
[19] "Kyphosis.xdf"               "mortDefaultSmall.xdf"
[21] "mortDefaultSmall2000.csv"   "mortDefaultSmall2001.csv"
```

```
 [23] "mortDefaultSmall2002.csv"   "mortDefaultSmall2003.csv"
 [25] "mortDefaultSmall2004.csv"   "mortDefaultSmall2005.csv"
 [27] "mortDefaultSmall2006.csv"   "mortDefaultSmall2007.csv"
 [29] "mortDefaultSmall2008.csv"   "mortDefaultSmall2009.csv" "
```

The location of the sample data directory is stored as an option in RevoScaleR, and you can access it with the following command:

```
rxGetOption("sampleDataDir")
```

Larger data sets containing the full airline, census, and mortgage default data sets are available for download online. We make extensive use of the sample data sets both in this *User's Guide* and the companion documents *RevoScaleR Getting Started Guide* (RevoScaleR_Getting_Started.pdf) and *RevoScaleR Distributed Computing Guide* (RevoScaleR_Distributed_Computing.pdf).

1.4 Managing Threads

A process is an instance of a software program, running under an operating system. RevoScaleR runs in two separate processes, one running R and R-related code, and one running RevoScaleR's underlying compute engine.

In order to perform parallel computations, a process must provide blocks of executable code to the operating system that can be run in parallel.

There are two primary approaches to this problem. One approach is to use threads. Threads can be thought of as sub-programs that are still bound to the original process that creates them. They communicate with the creating process, while still being autonomous enough to allow the operating system to schedule their operation independently, thus allowing parallelization.

By way of contrast, forking a process (a technique only available on Unix-based systems) creates a complete copy of one process that differs only by a flag available within each of the resulting processes.

Unfortunately, these two methods of parallelization are not completely compatible unless steps are taken to ensure that they do not interfere with each other and cause the software to malfunction. Specifically, program failures can be caused by forking a Unix process while the objects used to control communication and synchronization between threads are in use.

In order to optimize performance, RevoScaleR is capable of establishing and maintaining a pool of threads. This way, there is no overhead in creating these threads to parallelize a computation. However, given the above issues, this functionality is, by default, disabled on

Linux (this is not an issue on Windows, as Windows does not use fork; hence, the thread pool is always instantiated and ready for use on Windows).

If you know that you will not be forking your R process (such as spawning it using nohup or creating multiple R processes with the multicore package), or if you know exactly when you might fork a process, you can turn the thread pool on and off. RevoScaleR provides an interface to activate the thread pool:

```
rxSetEnableThreadPool(TRUE)
```

Similarly, the thread pool may be disabled as follows:

```
rxSetEnableThreadPool(FALSE)
```

Enabling the thread pool will improve performance, but should not be done if there is any chance you will fork your R process. If you want to ensure that the thread pool is always enabled, you can add the above command to a `.First` function defined in either your own Rprofile startup file, or the system Rprofile.site file. For example, you can add the following lines after the closing right parenthesis of the existing Rprofile.site file:

```
.First <- function()
{
      .First.sys()
      invisible(rxSetEnableThreadPool(TRUE))
}
```

The `.First.sys` function is normally run after all other initialization is complete, including the evaluation of the `.First` function. We need the call to `rxSetEnableThreadPool` to occur after RevoScaleR is loaded, and that is done by `.First.sys`, so we call `.First.sys` first.

1.5 Generating Random Numbers

R has extensive facilities for managing random number generation, and these are all fully supported in RevoScaleR. In addition, RevoScaleR provides an interface to random number generators supplied by the Vector Statistical Library that is part of Intel's Math Kernel Library. To use one of these generators, call the RevoScaleR function `rxRngNewStream`, specifying the desired generator (the default is a version of the Mersenne-Twister, MT-2203), the desired substream (if applicable), and a seed (if desired). See the help file for a complete list of the available generators and examples of their use.

The VSL random number generators are most useful in a distributed setting, where they allow parallel processes to generate uncorrelated random number streams. See the *RevoScaleR Distributed Computing Guide* (RevoScaleR_Distributed_Computing.pdf) for complete details.

1.6 Using RevoScaleR with Rscript

RevoScaleR depends on a number of packages that are specified as "default packages" in Microsoft R Services. To ensure these packages are loaded when using Rscript, you must include the flag `--default-packages=` (with nothing on the right-hand side), and not use the flag `--vanilla` when invoking Rscript. In particular, the methods package is required for correct operation of RevoScaleR.

1.7 Getting Help

The RevoScaleR package includes comprehensive help for all of its functions and data sets, along with an overview topic describing the package as a whole. To view this overview topic, use the R ? operator at the R prompt as follows:

```
?RevoScaleR
```

To obtain help on a RevoScaleR function, use the R `?` operator at the R prompt together with the function name. For example, the following command displays help about `rxLinMod`:

```
?rxLinMod
```

We will often refer to help topic pages as a function's help file, as in "see the `rxLinMod` help file for details." This always means to type the `?` operator followed by the function name.

Chapter 2.

Importing Data

The main function for importing data is `rxImport`. The `rxImport` function supports delimited text data, fixed-format text data, SAS data, SPSS data, and database data, provided you have a suitable ODBC driver for your database. Note that if you are using rxImport in a distributed compute context, you will be limited by the data types supported within your context. See the *RevoScaleR Distributed Computing Guide* (RevoScaleR_Distributed_Computing.pdf) or the various Getting Started Guides for specific compute contexts for details on which data types are supported on various distributed computing platforms.

Smaller data sets can be imported into data frames in memory. In addition, the RevoScaleR package provides a data file format (.xdf) designed to be very efficient for reading arbitrary rows and columns.

In this chapter, we explain how to import data in various formats, how to create a data frame in memory from a subset of an .xdf file, and how to write an .xdf file to a text file.

2.1 Data Compression in .xdf Files

Newer versions of the .xdf format support data compression via the *xdfCompressionLevel* argument to *rxImport* (and most other RevoScaleR functions that write .xdf files). You specify this as an integer in the range -1 to 9. The value -1 tells *rxImport* to use the current default compression value; the integers 1 through 9 specify increasing levels of compression—higher numbers perform more compression, but take more time. The value 0 specifies no compression.

The .xdf format allows different blocks to have different compression levels (but not within a single call to *rxImport*). This can be useful, for example, when appending to an existing data set of unknown compression level—you can specify the compression for the new data without affecting the compression of the existing data.

You can specify a standard compression level for all future .xdf file writes by setting *xdfCompressionLevel* using *rxOptions*. For example, to specify a compression level of 3, use *rxOptions* as follows:

```
rxOptions(xdfCompressionLevel = 3)
```

The default value of this option is 1.

If you have one or more existing .xdf files and would like to compress them, you can use the function *rxCompressXdf*. You can specify a single file or xdf data source, a character vector of files and data sources, or the path to a directory containing .xdf files. For example, to compress all the .xdf files in the C:\data directory, you would call *rxCompressXdf* as follows:

```
rxCompressXdf("C:/data", xdfCompressionLevel = 1, overwrite = TRUE)
```

2.2 Importing Delimited Text Data

Use the *rxImport* function to convert a text file to a data frame or .xdf file. In the simplest case, just provide the path to the input file. If your text format data set is delimited by commas or tabs, this is all that is required for simple data conversion. For example, the SampleData folder of the RevoScaleR package contains a file claims.txt containing information on car insurance claims. The following sequence of commands imports the data and returns a data frame, which we save as the object *claimsDF*:

```
#######################################################
# Chapter 2: Importing Data
Ch2Start <- Sys.time()

#  Importing Delimited Text Data
readPath <- rxGetOption("sampleDataDir")
infile <- file.path(readPath, "claims.txt")
```

```
claimsDF <- rxImport(infile)
```

The *rxGetInfo* function then shows us a useful summary of what's contained in the data frame. If we include the argument *getVarInfo=TRUE*, this summary includes the names of the variables and their types:

```
rxGetInfo(claimsDF, getVarInfo = TRUE)
```

```
 Data frame: claimsDF
 Number of observations: 128
 Number of variables: 6
 Number of blocks: 1
 Variable information:
 Var 1: RowNum, Type: integer, Low/High: (1, 128)
 Var 2: age, Type: character
 Var 3: car.age, Type: character
 Var 4: type, Type: character
 Var 5: cost, Type: numeric, Storage: float32, Low/High: (11.0000, 850.0000)
 Var 6: number, Type: numeric, Storage: float32, Low/High: (0.0000, 434.0000)
```

If we want just the names of the variables in the data file, we can use the *names* function:

```
names(claimsDF)
```

```
 [1] "RowNum"  "age"     "car.age" "type"    "cost"    "number"
```

If instead of importing the data into a data frame in memory, we want to store the data in an .xdf file, we just specify the path as the *outFile*. By default, the new data set is created in our current working directory:

```
claimsDS <- rxImport(inData = infile, outFile = "claims.xdf")
```

An .xdf file is created, and instead of returning a data frame, the *rxImport* function returns a data source object. This is a small R object that contains information about a data source, in this case the name and path of the .xdf file it represents. This data source object can be used as the input data in most RevoScaleR functions. For example:

```
rxGetInfo( claimsDS, getVarInfo = TRUE)
names( claimsDS )
```

2.2.1 Specifying a Missing Value String

If your text data file uses a string other than NA to identify missing values, you must use the *missingValueString* argument. Only one missing value string is allowed per file. We used this briefly in Chapter 1 when we imported the AirlineDemoSmall data:

```
inFile <- file.path(rxGetOption("sampleDataDir"), "AirlineDemoSmall.csv")
airData <- rxImport(inData = inFile, outFile="airExample.xdf",
     stringsAsFactors = TRUE, missingValueString = "M",
     rowsPerRead = 200000, overwrite = TRUE)
```

2.3 Importing Fixed-Format Data

Fixed-format data is text data in which each variable occupies a fixed-width column in the input data file. The format is completely specified by the width of each column and each column's data type. You can import fixed-format data using the `rxImport` function.

Fixed-format data may be accompanied by a *schema file* with an .sts extension describing the width and type of each column. For complete details on creating a schema file, see page 93 of the Stat/Transfer PDF Manual (http://www.stattransfer.com/stman10.pdf). If you have a schema file, you can create the input data source very simply by specifying the schema file name as the input data file. For example, the RevoScaleR SampleData directory contains a fixed-format version of the claims data as the file claims.dat and a schema file named claims.sts. To import the data using this schema file, we use `RxImport` as follows:

```
#  Importing Fixed Format Data

inFile <- file.path(readPath, "claims.sts")
claimsFF <- rxImport(inData = inFile, outFile = "claimsFF.xdf")
```

You can get information about the file using `rxGetInfo` as usual:

```
rxGetInfo(claimsFF, getVarInfo=TRUE)
```

This gives the following output:

```
File name: C:\YourOutputPath\claims.xdf
Number of observations: 128
Number of variables: 6
Number of blocks: 1
Compression type: zlib
Variable information:
Var 1: RowNum, Type: numeric, Storage: float32, Low/High: (1.0000, 128.0000)
Var 2: age, Type: character
Var 3: car.age, Type: character
Var 4: type, Type: character
Var 5: cost, Type: numeric, Storage: float32, Low/High: (11.0000, 850.0000)
Var 6: number, Type: numeric, Storage: float32, Low/High: (0.0000, 434.0000)
```

To read all string data as factors, set the `stringsAsFactors` argument to `TRUE` in your call to `rxImport`

```
claimsFF2 <- rxImport(inFile, outFile = "claimsFF2.xdf", stringsAsFactors=TRUE)
rxGetInfo(claimsFF2, getVarInfo=TRUE)
```

If you have fixed-format data without a schema file, you can specify the start, width, and type information for each variable using the `colInfo` argument to the `RxTextData` data source constructor, and then read in the data using `rxImport`:

```
inFileNS <- file.path(readPath, "claims.dat")
outFileNS <- "claimsNS.xdf"
```

```
colInfo=list("rownum" = list(start = 1, width = 3, type = "integer"),
             "age" = list(start = 4, width = 5, type = "factor"),
             "car.age" = list(start = 9, width = 3, type = "factor"),
             "type" = list(start = 12, width = 1, type = "factor"),
             "cost" = list(start = 13, width = 6, type = "numeric"),
             "number" = list(start = 19, width = 3, type = "numeric"))
claimsNS <- rxImport(inFileNS, outFile = outFileNS, colInfo = colInfo)
rxGetInfo(claimsNS, getVarInfo=TRUE)
```

If you have a schema file, you can still use the *colInfo* argument to specify type information or factor level information. However, in this case, all the variables will be read according to the schema file, and then the *colInfo* data specifications will be applied. This means that you cannot use your *colInfo* list to omit variables, as you can when there is no schema file.

Fixed-width character data is treated as a special type by RevoScaleR for efficiency purposes. You can use this same type for character data in delimited data by specifying a colInfo argument with a width argument for the character column. (Typically, you will need to find the longest string in the column and specify a width sufficient to include it.)

2.4 Importing SAS Data

The *rxImport* function can also be used to read data from SAS files having a .sas7bdat or .sd7 extension. You do not need to have SAS installed on your computer.

The RevoScaleR SampleData directory contains a SAS version of the claims data as claims.sas7bdat. We can read it into .xdf format most simply as follows:

```
#  Importing SAS Data

inFileSAS <- file.path(rxGetOption("sampleDataDir"), "claims.sas7bdat")
xdfFileSAS <- "claimsSAS.xdf"
claimsSAS <- rxImport(inData = inFileSAS, outFile = xdfFileSAS)
rxGetInfo(claimsSAS, getVarInfo=TRUE)
```

This gives the following output:

```
File name: C:\YourOutputPath\claimsSAS.xdf
Number of observations: 128
Number of variables: 6
Number of blocks: 1
Compression type: zlib
Variable information:
Var 1: RowNum, Type: character
Var 2: age, Type: character
Var 3: car_age, Type: character
Var 4: type, Type: character
Var 5: cost, Type: numeric, Low/High: (11.0000, 850.0000)
Var 6: number, Type: numeric, Low/High: (0.0000, 434.0000)
```

Sometimes, SAS data files on Windows come in two pieces, a *.sas7bdat* file containing the data and a *.sas7bcat* file containing value label information. You can read both the data and

the value label information by specifying the *.sas7bdat* file with the *inData* argument and the *.sas7bcat* file with the *formatFile* argument. To do so, in the following code replace *myfile* with your SAS file name:

```
myData <- rxImport(inData = "myfile.sas7bdat",
     outFile ="myfile.xdf",
     formatFile = "myfile.sas7bcat")
```

2.5 Importing SPSS Data

The *rxImport* function can also be used to read data from SPSS files.

The RevoScaleR SampleData directory contains an SPSS version of the claims data as claims.sav. We can read it into .xdf format as follows:

```
#  Importing SPSS Data

inFileSpss <- file.path(rxGetOption("sampleDataDir"), "claims.sav")
xdfFileSpss <- "claimsSpss.xdf"
claimsSpss <- rxImport(inData = inFileSpss, outFile = xdfFileSpss)
rxGetInfo(claimsSpss, getVarInfo=TRUE)
```

This gives the following output:

```
File name: C:\YourOutputPath\claimsSpss.xdf
Number of observations: 128
Number of variables: 6
Number of blocks: 1
Compression type: zlib
Variable information:
Var 1: RowNum, Type: character
Var 2: age, Type: character
Var 3: car_age, Type: character
Var 4: type, Type: character
Var 5: cost, Type: numeric, Low/High: (11.0000, 850.0000)
Var 6: number, Type: numeric, Low/High: (0.0000, 434.0000)
```

Variables in SPSS data sets often contain value labels with important information about the data. SPSS variables with value labels are typically most usefully imported into R as categorical "factor" data; that is, there is a one-to-one mapping between the values in the data set (e.g., 1, 2, 3) and the labels that apply to them (e.g. TOO LITTLE, ABOUT RIGHT, and TOO MUCH). However, SPSS allows for value labels where this is not the case. For example, a variable with values from 1 to 99 might have value labels of "NOT HOME" for 97, "DIDN'T KNOW" for 98, and "NOT APPLICABLE" for 99. If this variable were converted to a factor in R using the value labels as the factor labels, all of the values from 1 to 96 would be set to missing because they would have no corresponding factor level. Essentially all of the actual data would be thrown away. To prevent this, use the flag *labelsAsLevels=FALSE*. By default, the information from the value labels is retained even if the variables aren't converted to factors. This information can be

returned using *rxGetVarInfo*. If you don't wish to retain the information from the value labels you can specify *labelsAsInfo=FALSE*.

2.6 Specifying Variable Data Types

The *rxImport* function supports three arguments for specifying variable data types: *stringsAsFactors*, *colClasses*, and *colInfo*. For example, consider storing character data. Often data stored in text files as string data actually represents categorical or *factor* data, which can be more compactly represented as a set of integers denoting the distinct *levels* of the factor. This is common enough that users frequently want to transform *all* string data to factors. This can be done using the *stringsAsFactors* argument:

```
#  Specifying Variable Data Types

inFile <- file.path(rxGetOption("sampleDataDir"), "claims.sts")
rxImport(inFile, outFile = "claimsSAF.xdf", stringsAsFactors = TRUE)
rxGetInfo("claimsSAF.xdf", getVarInfo = TRUE)

 File name: C:\YourOutputPath\claimsSAF.xdf
 Number of observations: 128
 Number of variables: 6
 Number of blocks: 1
 Variable information:
 Var 1: RowNum, Type: integer, Low/High: (1, 128)
 Var 2: age
        8 factor levels: 17-20 21-24 25-29 30-34 35-39 40-49 50-59 60+
 Var 3: car.age
        4 factor levels: 0-3 4-7 8-9 10+
 Var 4: type
        4 factor levels: A B C D
 Var 5: cost, Type: numeric, Storage: float32, Low/High: (11.0000, 850.0000)
 Var 6: number, Type: numeric, Storage: float32, Low/High: (0.0000, 434.0000)
```

You can also specify data types for individual variables using the *colClasses* argument, and even more specific instructions for converting each variable using the *colInfo* argument. Here we use the *colClasses* argument to specify that the variable *number* in the claims data be stored as an integer:

```
outfileColClass <- "claimsCCNum.xdf"
rxImport(infile, outFile = outfileColClass, colClasses=c(number = "integer"))
rxGetInfo("claimsCCNum.xdf", getVarInfo = TRUE)

 File name: C:\YourOutputPath\claimsCCNum.xdf
 Number of observations: 128
 Number of variables: 6
 Number of blocks: 1
 Compression type: zlib
 Variable information:
 Var 1: RowNum, Type: integer, Low/High: (1, 128)
 Var 2: age, Type: character
 Var 3: car.age, Type: character
 Var 4: type, Type: character
```

```
Var 5: cost, Type: numeric, Storage: float32, Low/High: (11.0000, 850.0000)
Var 6: number, Type: integer, Low/High: (0, 434)
```

We can use the *colInfo* argument to specify the levels of the *car.age* column. This is particularly useful when reading data in chunks, to assure that factors levels are in the desired order.

```
outfileCAOrdered <- "claimsCAOrdered.xdf"
colInfoList <- list("car.age"= list(type = "factor", levels = c("0-3",
    "4-7", "8-9", "10+")))
rxImport(infile, outFile = outfileCAOrdered, colInfo = colInfoList)
rxGetInfo("claimsCAOrdered.xdf", getVarInfo = TRUE)
```

This gives the following output:

```
File name: C:\YourOutputPath\claimsCAOrdered.xdf
Number of observations: 128
Number of variables: 6
Number of blocks: 1
Compression type: zlib
Variable information:
Var 1: RowNum, Type: integer, Low/High: (1, 128)
Var 2: age, Type: character
Var 3: car.age
       4 factor levels: 0-3 4-7 8-9 10+
Var 4: type, Type: character
Var 5: cost, Type: numeric, Storage: float32, Low/High: (11.0000, 850.0000)
Var 6: number, Type: numeric, Storage: float32, Low/High: (0.0000, 434.0000)
```

These various methods of providing column information can be combined as follows:

```
outfileCAOrdered2 <- "claimsCAOrdered2.xdf"
colInfoList <- list("car.age" = list(type = "factor", levels = c("0-3",
    "4-7", "8-9", "10+")))
claimsOrdered <- rxImport(infile, outfileCAOrdered2,
     colClasses = c(number = "integer"),
     colInfo = colInfoList, stringsAsFactors = TRUE)
rxGetInfo(claimsOrdered, getVarInfo = TRUE)
```

This produces the following output:

```
File name: C:\YourOutputPath\claimsCAOrdered2.xdf
Number of observations: 128
Number of variables: 6
Number of blocks: 1
Compression type: zlib
Variable information:
Var 1: RowNum, Type: integer, Low/High: (1, 128)
Var 2: age
       8 factor levels: 17-20 21-24 25-29 30-34 35-39 40-49 50-59 60+
Var 3: car.age
       4 factor levels: 0-3 4-7 8-9 10+
Var 4: type
       4 factor levels: A B C D
Var 5: cost, Type: numeric, Storage: float32, Low/High: (11.0000, 850.0000)
Var 6: number, Type: integer, Low/High: (0, 434)
```

In general, variable specifications provided by the *colInfo* argument are used in preference to *colClasses*, and those in *colClasses* are used in preference to the *stringsAsFactors* argument.

Also note that the .xdf data format supports a wider variety of data types than R, allowing for efficient storage. For example, by default floating point variables are stored as 32-bit floats in .xdf files. When they are read into R for processing, they are converted to doubles (64-bit floats).

2.7 Specifying Additional Variable Information

If you need to modify the name of a variable or the names of the factor levels, or add a description of a variable, you can do this using the *colInfo* argument. For example, the claims data includes a variable *type* specifying the type of car, but the levels A, B, C, and D give us no particular information. If we knew what the types signified, perhaps "Subcompact", "Compact", "Mid-size", and "Full-size", we could relabel the levels as follows:

```
#  Specifying Additional Variable Information

inFileAddVars <- file.path(rxGetOption("sampleDataDir"), "claims.txt")
outfileTypeRelabeled <- "claimsTypeRelabeled.xdf"
colInfoList <- list("type" = list(type = "factor", levels = c("A",
    "B", "C", "D"), newLevels=c("Subcompact", "Compact", "Mid-size",
    "Full-size"), description="Body Type"))
claimsNew <- rxImport(inFileAddVars, outFile = outfileTypeRelabeled,
     colInfo = colInfoList)
rxGetInfo(claimsNew, getVarInfo = TRUE)
```

This produces the following output:

```
File name: C:\YourOutputPath\claimsTypeRelabeled.xdf
Number of observations: 128
Number of variables: 6
Number of blocks: 1
Compression type: zlib
Variable information:
Var 1: RowNum, Type: integer, Low/High: (1, 128)
Var 2: age, Type: character
Var 3: car.age, Type: character
Var 4: type, Body Type
       4 factor levels: Subcompact Compact Mid-size Full-size
Var 5: cost, Type: numeric, Storage: float32, Low/High: (11.0000, 850.0000)
Var 6: number, Type: numeric, Storage: float32, Low/High: (0.0000, 434.0000)
```

To specify *newLevels*, you must also specify *levels*, and it is important to note that the *newLevels* argument can only be used to rename levels—it cannot be used to fully recode the factor. That is, the number of *levels* and number of *newLevels* must be the same.

2.8 Appending to an Existing File

If you have observations on the same variables in multiple input files, you can use the *append* argument to *rxImport* to combine them into one file. For example, we could append another copy of the claims text data set in a second block to the claimCAOrdered2.xdf file we created in section 2.6:

```
#  Appending to an Existing File

inFile <- file.path(rxGetOption("sampleDataDir"), "claims.txt")
colInfoList <- list("car.age" = list(type = "factor", levels = c("0-3",
    "4-7", "8-9", "10+")))
outfileCAOrdered2 <- "claimsCAOrdered2.xdf"

claimsAppend <- rxImport(inFile, outFile = outfileCAOrdered2,
     colClasses = c(number = "integer"),
     colInfo = colInfoList, stringsAsFactors = TRUE, append = "rows")
rxGetInfo(claimsAppend, getVarInfo=TRUE)
```

```
File name: C:\YourOutputPath\claimsCAOrdered2.xdf
Number of observations: 256
Number of variables: 6
Number of blocks: 2
Compression type: zlib
Variable information:
Var 1: RowNum, Type: integer, Low/High: (1, 128)
Var 2: age
       8 factor levels: 17-20 21-24 25-29 30-34 35-39 40-49 50-59 60+
Var 3: car.age
       4 factor levels: 0-3 4-7 8-9 10+
Var 4: type
       4 factor levels: A B C D
Var 5: cost, Type: numeric, Storage: float32, Low/High: (11.0000, 850.0000)
Var 6: number, Type: integer, Low/High: (0, 434)
```

2.9 Transforming Data on Import

You can use the *transforms* argument to *rxImport* to create new variables or modify existing variables when you initially read the data into .xdf format. For example, we could create a new variable, *logcost*, by taking the log of the existing cost variable as follows:

```
#  Transforming Data on Import

inFile <- file.path(rxGetOption("sampleDataDir"), "claims.txt")
outfile <- "claimsXform.xdf"
claimsDS <-rxImport(inFile, outFile = outfile,
     transforms=list(logcost=log(cost)))
rxGetInfo(claimsDS, getVarInfo=TRUE)
```

This gives the following output, showing the new variable:

```
File name: C:\YourOutputPath\claimsXform.xdf
Number of observations: 128
```

```
Number of variables: 7
Number of blocks: 1
Compression type: zlib
Variable information:
Var 1: RowNum, Type: integer, Low/High: (1, 128)
Var 2: age, Type: character
Var 3: car.age, Type: character
Var 4: type, Type: character
Var 5: cost, Type: numeric, Storage: float32, Low/High: (11.0000, 850.0000)
Var 6: number, Type: numeric, Storage: float32, Low/High: (0.0000, 434.0000)
Var 7: logcost, Type: numeric, Low/High: (2.3979, 6.7452)
```

2.10 Converting Dates Stored As Character Strings

The .xdf format can store dates using the standard R *Date* class. When importing data from other data formats that support dates such as SAS or SPSS, the *rxImport* function will convert dates data automatically. However, some data sets even in those formats include dates as character string data. You can store such data more efficiently by converting it to *Date* data using the *transforms* argument. For example, suppose you have a character variable TransactionDate with a representative date of the form "14 Sep 2010". You can convert this to a *Date* variable using the following *transforms* argument:

```
transforms=list(TransactionDate=as.Date(TransactionDate, format="%d %b %Y"))
```

(The format argument is a character string that may contain conversion specifications, as in the example shown. These conversion specifications are described in the *strptime* help file.)

2.11 Importing Wide Data

Big data mainly comes in two forms, long or wide, each presenting unique challenges. Most of the topics in the guide deal with long data, or data with many observations compared to the number of variables or columns. With wide data, or data sets with a large number of variables, there are specific considerations to take into account during import.

We highly recommend that you import your wide data into the .xdf format using the *rxImport* function whenever you plan to do repeated analyses on your dataset. For wide data with many variables it is especially convenient to store the data in an .xdf file and then read subsets of columns into a data frame in memory for specific analyses. Please see earlier sections of this chapter for specifics on importing different data formats into .xdf.

Section 6 of this chapter mentions multiple ways in which the user can specify variable data types upon import. For wide data that contain many categorical variables, the time to import will be substantially improved by using the *colInfo* argument to define the variable levels. If an import is done using just the *stringsAsFactors* argument or is done without specifying variable levels using *colInfo*, RSR will go through the data and create new levels on a "first-come, first-served" basis for each factor variable. Each time a new level is encountered the

metadata has to be updated. For a wide dataset with many factor variables this takes a considerable amount of time. Using the *colInfo* argument to define the levels first speeds up the import.

For wide data, it is useful to create the *colInfo* as an object prior to using rxImport. The following is an example of defining the colInfo with factor levels for the claims data from an earlier chapter:

```
#  Importing Wide Data

colInfoList <- list("age" = list(type = "factor",
      levels = c("17-20","21-24","25-29","30-34","35-39","40-49","50-59","60+")),
    "car.age" = list(type = "factor",
      levels = c("0-3","4-7","8-9","10+")),
    "type" = list(type = "factor",
      levels = c("A","B","C","D")))
```

The colInfo list can then be used as the *colInfo* argument in the *rxImport* function to get your data into .xdf format:

```
inFileClaims <- file.path(rxGetOption("sampleDataDir"),"claims.txt")
outFileClaims <- "claimsWithColInfo.xdf"
rxImport(inFile, outFile = outFileClaims, colInfo = colInfoList)
```

2.12 Reading Data from an .xdf File into a Data Frame

It is often convenient to store a large amount of data in an .xdf file and then read a subset of columns and rows of the data into a data frame in memory for analysis. The *rxDataStep* function makes this easy. For example, let's consider taking subsamples from the sample data set CensusWorkers.xdf. Using a *rowSelection* expression and list of *varsToKeep*, we can extract the *age*, *perwt*, and *sex* variables for individuals over the age of 40 living in Washington State:

```
#  Reading Data from an .xdf File into a Data Frame

inFile <- file.path(rxGetOption("sampleDataDir"), "CensusWorkers.xdf")
myCensusDF <- rxDataStep(inData=inFile,
  rowSelection = state == "Washington" & age > 40,
  varsToKeep = c("age", "perwt", "sex"))
```

When subsampling rows, we need to be aware that the rowSelection is processed on each chunk of data after it is read in. Consider an example where we want to extract every 10th row of the data set. For each chunk we will create a sequence starting with the start row number in that chunk (provided by the internal variable, .rxStartRow) with a length equal to the number of rows in the data chunk. We will determine that number of rows by using the length of the of

one of the variables that has been read from the data set, age. We will keep only the rows where the remainder after dividing the row number by 10 is 0:

```
myCensusSample <- rxDataStep(inData=inFile,
    rowSelection= (seq(from=.rxStartRow,length.out=.rxNumRows) %% 10) == 0 )
```

We can also create transformed variables while we are reading in the data. For example, create an 10-year *ageGroup* variable, starting with 20 (the minimum age in the data set):

```
myCensusDF2 <- rxDataStep(inData=inFile,
  varsToKeep = c("age", "perwt", "sex"),
  transforms=list(ageGroup = cut(age, seq(from=20, to=70, by=10))))
```

2.13 Splitting Data Files

RevoScaleR makes it possible to analyze huge data sets easily and efficiently, and for most purposes the most efficient computations are done on a single .xdf file. However, there are many circumstances when you will want to work with only a portion of your data. For example, you may want to distribute your data over the nodes of a cluster; in such a case, RevoScaleR's analysis functions will process each node's data separately, combining all the results for the final return value. You might also want to split your data into training and test data so that you can fit a model using the training data and validate it using the test data.

Use the function *rxSplit* to split your data. For example, to split variables of interest in the large 2000 U.S. Census data into five files for distribution on a five node cluster, you could use *rxSplit* as follows (change the location of the bigDataDir to the location of your downloaded file):

```
#  Splitting Data Files
rxSetComputeContext("local")

bigDataDir <- "C:/MRS/Data"
bigCensusData <- file.path(bigDataDir, "Census5PCT2000.xdf")
splitFiles <- rxSplit(bigCensusData, numOutFiles = 5, splitBy = "blocks",
     varsToKeep = c("age",  "incearn", "incwelfr", "educrec", "metro", "perwt"))
names(splitFiles)
```

By default, *rxSplit* simply appends a number in the sequence from 1 to *numOutFiles* to the base file name to create the new file names, and in this case the resulting file names, for example, "Census5PCT20001.xdf", are a bit confusing. You can exercise greater control over the output file names by using the *outFilesBase* and *outFilesSuffixes* arguments. With *outFilesBase*, you can specify either a single character string to be used for all files or a character vector the same length as the desired number of files. The latter option is useful, for example, if you would like to create four files with the same file name, but different paths:

```
nodePaths <- paste("compute", 10:13, sep="")
baseNames <- file.path("C:", nodePaths, "DistCensusData")
splitFiles2 <- rxSplit(bigCensusData, splitBy = "blocks",
     outFilesBase = baseNames,
     varsToKeep = c("age", "incearn", "incwelfr", "educrec", "metro", "perwt"))
names(splitFiles2)
```

This creates the four directories C:/compute10, etc., and creates a file named "DistCensusData.xdf" in each directory. You will want to do something like this when using distributed data with the standard RevoScaleR analysis functions such as *rxLinMod* and *rxLogit* in an RxHpcServer compute context.

You can supply the *outFilesSuffixes* arguments to exercise greater control over what is appended to the end of each file. Returning to our first example, we can add a hyphen between our base file name and the sequence 1 to 5 using *outFilesSuffixes* as follows:

```
splitFiles3 <- rxSplit(bigCensusData, splitBy = "blocks",
     outFileSuffixes=paste("-", 1:5, sep=""),
     varsToKeep = c("age", "incearn", "incwelfr", "educrec", "metro", "perwt"))
names(splitFiles3)
```

The *splitBy* argument specifies whether to split your data file row-by-row or block-by-block. The default is *splitBy="rows"*, which distributes data from each block into different files. The examples above use the faster split by blocks instead. The *splitBy* argument is ignored if you also specify the *splitByFactor* argument as a character string representing a valid factor variable. In this case, one file is created per level of the factor variable.

You can use the *splitByFactor* argument and a transforms argument to easily create test and training data sets from an .xdf file. Note that this will take longer than the previous examples because each block of data is being processed:

```
splitFiles4 <- rxSplit(inData = bigCensusData,
     outFilesBase="censusData",
     splitByFactor="testSplitVar",
     varsToKeep = c("age", "incearn", "incwelfr", "educrec", "metro", "perwt"),
     transforms=list(testSplitVar = factor(
        sample(0:1,  size=.rxNumRows, replace=TRUE, prob=c(.10, .9)),
        levels=0:1, labels = c("Test", "Train"))))
names(splitFiles4)
rxSummary(~age, data = splitFiles4[[1]], reportProgress = 0)
rxSummary(~age, data = splitFiles4[[2]], reportProgress = 0)
```

This takes approximately 10% of the data as a test data set, with the remainder going into the training data.

If your .xdf file is relatively small, you may want to set *outFilesBase = ""* so that a list of data frames is returned instead of having files created. You can also use *rxSplit* to split data frames; see the *rxSplit* help file for details.

2.14 Importing Data as Composite Xdf Files

The .xdf file format has been modified for analyses on Hadoop to store data on HDFS in a composite set of files rather than a single file. The composite set consists of a named directory with two subdirectories, 'data' and 'metadata', containing split '.xdfd' files and a metadata '.xdfm' files respectively. Data is split into individual '.xdfd' files such that each file remains within a single HDFS block. (The HDFS block size varies from installation to installation but is typically either 64MB or 128MB). The '.xdfm' file contains the metadata for all of the .xdfd files. For more in depth information about the composite XDF format and its use within a Hadoop

compute context see the *RevoScaleR Hadoop Getting Started Guide* (RevoScaleR_Hadoop_Getting_Started.pdf).

In most cases, a single .xdf file will be the most efficient way to store and analyze your data in a local compute context, unless you are using data from HDFS as input .(discussed in the next section). However, you can still read, write and analyze a set of composite XDF files in a local compute context.

`rxImport` is used to read in a .csv file or directory of .csv files into the composite XDF format described above. When the compute context is `RxHadoopMR`, a composite set of XDF is always created. However, while working in a local compute context you must specify the option `createCompositeSet=TRUE` within the `RxXdfData` data source object being used as the `outFile` argument for `rxImport`.

In the following example we demonstrate creating a composite set of .xdf files within the native file system in a local compute context. Using `rxImport`, you specify an `RxTextData` data source, in this case a directory containing the mortDefaultSmall .csv files, as the `inData` and an `RxXdfData` source object as the `outFile` argument. We define our data source objects as follows (assuming you've copied the 10 mortDefaultSmall .csv files into a separate directory from the SampleData folder of the RevoScaleR package):

```
mortDefaultCsvDir <- "C:/MRS/Data/mortDefaultCsv"
mortDefaultCsv <- RxTextData(mortDefaultCsvDir)
mortDefaultCompXdfDir <- "C:/MRS/Data/mortDefaultXdf"
mortDefaultCompXdf <- RxXdfData(mortDefaultCompXdfDir, createCompositeSet=TRUE)
```

We then import the data using `rxImport`:

```
rxImport(inData=mortDefaultCsv, outFile=mortDefaultCompXdf)
```

This creates a directory named 'mortDefaultXdf' and subdirectories 'data' and 'metadata' containing the split '.xdfd' files and a metadata '.xdfm' file respectively as shown below.

```
list.files(mortDefaultCompXdfDir, recursive=TRUE, full.names=TRUE)

 [1] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_1.xdfd"
 [2] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_10.xdfd"
 [3] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_2.xdfd"
 [4] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_3.xdfd"
 [5] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_4.xdfd"
 [6] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_5.xdfd"
 [7] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_6.xdfd"
 [8] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_7.xdfd"
 [9] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_8.xdfd"
[10] "C:/MRS/Data/mortDefaultXdf/data/mortDefaultXdf_9.xdfd"
[11] "C:/MRS/Data/mortDefaultXdf/metadata/mortDefaultXdf.xdfm"
```

Note that the composite XDF can then be referenced in future analyses using the data source object that was used as the `outFile` for `rxImport`. See the help file for `RxXdfData` for more

information regarding how the numbers of blocks in each '.xdfd' file is determined depending on the compute context.

2.15 Using Data from the Hadoop Distributed File System

If you are using RevoScaleR on a Linux system that is part of a Hadoop cluster, you can store and access text or xdf data files on your system's native file system or the Hadoop Distributed File System (HDFS). By default, data is expected to be found on the native file system. If all your data is on HDFS, you can use `rxSetFileSystem` to specify this as a global option.. You can then specify your global option as follows:

```
rxSetFileSystem(RxHdfsFileSystem())
```

If only some files are on HDFS, you can use `RxTextData` or `RxXdfData` data sources to specify these as files on HDFS. For example,

```
hdfsFS <- RxHdfsFileSystem()
txtSource <- RxTextData("/test/HdfsData/AirlineCSV/CSVs/1987.csv",
    fileSystem=hdfsFS)
xdfSource <- RxXdfData("/test/HdfsData/AirlineData1987",
    fileSystem=hdfsFS)
```

The `RxHdfsFileSystem` function is used to create a file system object for the HDFS file system; the `RxNativeFileSystem` function does the same thing for the native file system.

If you are using a local compute context, you can currently use data files on HDFS as input files only; output must be written to the native file system.

As a more complete example, consider again the mortgage default example from *section 2.13*. If the mortgage default composite XDF resides in the HDFS file system, we can run the example as follows:

```
rxSetFileSystem(RxHdfsFileSystem())
mortDS <- RxXdfData("/share/SampleData/mortDefaultXdf")
rxGetInfo(mortDS, numRows = 5)
rxSummary(~., data = mortDS, blocksPerRead = 2)
logitObj <- rxLogit(default~F(year) + creditScore + yearsEmploy + ccDebt,
                data = mortDS, blocksPerRead = 2,  reportProgress = 1)
summary(logitObj)
```

Note that in this example we set the file system to HDFS globally so we did not need to specify the file system within the data source constructors.

2.15.1 Note on Using RevoScaleR with rhdfs

If you are using both RevoScaleR and the RHadoop connector package rhdfs, you need to ensure that the two do not interfere with each other. The rhdfs package depends upon the rJava package, which will prevent access to HDFS by RevoScaleR if it is called before RevoScaleR

makes its connection to HDFS. To prevent this interaction, use the function rxHdfsConnect to establish a connection between RevoScaleR and HDFS. An install-time option on Linux can be used to trigger such a call from the Rprofile.site startup file. If the install-time option is not chosen, you can add it later by setting the REVOHADOOPHOST and REVOHADOOPPORT environment variables with the host name of your Hadoop name node and the name node's port number, respectively. You can also call rxHdfsConnect interactively within a session, provided you have not yet attempted any other rJava or rhdfs commands. For example, the following call will fix a connection between the Hadoop host sandbox-01 and RevoScaleR; if you make a subsequent call to rhdfs, RevoScaleR can continue to use the previously established connection. Note, however, that once rhdfs (or any other rJava call) has been invoked, you cannot change the host or port you use to connect to RevoScaleR:

```
rxHdfsConnect(hostName = "sandbox-01", port = 8020)
```

Chapter 3.

Data Sources

A *data source* in RevoScaleR can be thought of as a small R object representing a data set. We have already encountered them as the return objects of `rxImport` and `rxDataStep`. The data itself may be on disk, but the data source is an in-memory object that allows us to treat data from disparate sources in a consistent manner within RevoScaleR. Behind the scenes, `rxImport` often creates data sources "on the fly" to facilitate data import. You can create your own data sources to give you finer control over how data is imported. In this chapter, we describe how to create a variety of data sources and use them with RevoScaleR High Performance Analytics functions (discussed in more detail in later chapters). For occasional analysis of external data, running the analysis on the original data source can save you some time. However, when you will be performing repeated analysis of a single data set, it will almost always be faster for you to import the data into the .xdf format and run your analyses on the .xdf data source. This chapter also describes how to use .xdf data sources to easily access your .xdf file in blocks so that you can write your own "chunking" algorithms.

3.1 Data Source Constructors

To create data sources directly, use the constructors listed in the following table:

Source Data	Data Source Constructor
Text (fixed-format or delimited)	RxTextData
SAS	RxSasData
SPSS	RxSpssData
Database (must have appropriate ODBC driver installed)	RxOdbcData
Teradata Database	RxTeradata
.xdf data files	RxXdfData

For simple data import, you do not need to create a data source—you can simply specify a file of the appropriate type and RevoScaleR will read it using the default settings. However, if you need to provide additional options specific to that data source type, you will want to refer to the data source's documentation; in this case creating a data source will be useful. (For more information on accessing databases via ODBC, see the *RevoScaleR ODBC Import Guide* (RevoScaleR_ODBC.pdf).)

3.2 Specifying Delimiters

As a simple example, RevoScaleR includes a sample text data file hyphens.txt that is not separated by commas or tabs, but by hyphens, with the following contents:

```
Name-Rank-SerialNumber
Smith-Sgt-02912
Johnson-Cpl-90210
Michaels-Pvt-02931
Brown-Pvt-11311
```

The `RxImport` function does not include a parameter for specifying a delimiter; in this case, you must create an `RxTextData` data source and specify the delimiter using the `delimiter` argument:

```
#  Chapter 3: Data Sources
Ch3Start <- Sys.time()
readPath <- rxGetOption("sampleDataDir")
infile <- file.path(readPath, "hyphens.txt")
hyphensTxt <- RxTextData(infile, delimiter="-")
hyphensDF <- rxImport(hyphensTxt)
```

```
hyphensDF
```

```
      Name Rank SerialNumber
1    Smith  Sgt         2912
2  Johnson  Cpl        90210
3 Michaels  Pvt         2931
4    Brown  Pvt        11311
```

In normal usage, the `delimiter` argument is a single character, such as `delimiter="\t"` for tab-delimited data or `delimiter=","` for comma-delimited data. However, each column may be delimited by a different character; all the delimiters must be concatenated together into a single character string. For example, if you have one column delimited by a comma, a second by a plus sign, and a third by a tab, you would use the argument `delimiter=",+\t"`.

3.3 Compute Contexts and Data Sources

In the local compute context, all of RevoScaleR's supported data sources are available to you. In a distributed context, however your choice of data sources may be severely limited. The most extreme case is the RxInTeradata compute context, which supports only the RxTeradata data source – this makes sense, as the computations are being performed on data inside the Teradata database. Please refer to the table below to see which data sources are available for each compute context (x indicates available).

Compute Context → Data Source↓	RxLocalSeq	RxHadoopMR	RxInTeradata
Delimited Text (RxTextData)	x	x	
Fixed-Format Text (RxTextData)	x		
.xdf data files (RxXdfData)	x	x	
SAS data files (RxSasData)	x		
SPSS data files (RxSpssData)	x		
ODBC data (RxOdbcData)	x		
Teradata database (RxTeradata)	x		x

Beyond the compute context, there may also be differences in availability within a single data source type depending on the file system. For example, the composite .xdf files that we discussed in section 2.13 created on the Hadoop File System are somewhat different from .xdf created in a non-distributed file system. Similarly, as discussed in Section 2.12, you may need to split and distribute your data across the available nodes of your cluster.

3.4 Methods for Looking at Data Sources

A number of standard R methods for looking at data have been provided for RevoScaleR data sources. We've already seen the use of *names* to view the variable names and *head* to view the first few rows. Returning to the *claimsDS* data source created in the previous section Importing Delimited Text Data, we can obtain the dimensions of our claims data using the *dim* function:

```
#  Data Sources

readPath <- rxGetOption("sampleDataDir")
infile <- file.path(readPath, "claims.txt")
claimsDS <- rxImport(inData = infile, outFile = "claims.xdf",
     overwrite = TRUE)
dim(claimsDS)
```

```
 [1] 128   6
```

Similarly, an alternative method of obtaining the variable names is to use the *colnames* or *dimnames* functions, but notice that for .xdf file data sources, *dimnames* returns only column names; row names are not provided, because .xdf files do not contain row names:

```
colnames(claimsDS)
```

```
 [1] "RowNum"  "age"     "car.age" "type"    "cost"    "number"
```

```
dimnames(claimsDS)
```

```
 [[1]]
 NULL

 [[2]]
 [1] "RowNum"  "age"     "car.age" "type"    "cost"    "number"
```

You can obtain the number of variables using the *length* function:

```
length(claimsDS)
```

```
 [1] 6
```

If you want to see just the top few rows of data, you can use the *head* function:

```
head(claimsDS)
```

```
   RowNum   age car.age type cost number
```

```
1       1 17-20     0-3    A  289       8
2       2 17-20     4-7    A  282       8
3       3 17-20     8-9    A  133       4
4       4 17-20     10+    A  160       1
5       5 17-20     0-3    B  372      10
6       6 17-20     4-7    B  249      28
```

You can view the *last* rows of a data source using the `tail` function:

```
tail(claimsDS)
```

```
     RowNum age car.age type cost number
123     123 60+      8-9    C  227     20
124     124 60+      10+    C  119      6
125     125 60+      0-3    D  385     62
126     126 60+      4-7    D  324     22
127     127 60+      8-9    D  192      6
128     128 60+      10+    D  123      6
```

3.5 Using Data Sources

Suppose, for example, that you would like to perform a linear regression on the data in the SAS file claims.sas7bdat. You would first create an RxSasData data source as follows:

```
inFileSAS <- file.path(rxGetOption("sampleDataDir"), "claims.sas7bdat")
sourceDataSAS <- RxSasData(inFileSAS, stringsAsFactors=TRUE)
```

Once we have the data source, we can remind ourselves of the variables in the data by calling the names function:

```
names(sourceDataSAS)
```

```
 [1] "RowNum"  "age"     "car_age" "type"    "cost"    "number"
```

We can now compute our desired regression using our data source as the data argument to `rxLinMod` (more on this method in Chapter 8):

```
rxLinMod(cost ~ age + car_age, data = sourceDataSAS)
```

```
 Rows Read: 128, Total Rows Processed: 128, Total Chunk Time: 0.003 seconds
 Computation time: 0.014 seconds.
 Call:
 rxLinMod(formula = cost ~ age + car_age, data = sourceDataSAS)

 Linear Regression Results for: cost ~ age + car_age
 Data: sourceDataSAS (RxSasData Data Source)
 File name:
     C:/Program Files/Microsoft/MRO-for-RRE/8.0/R-
 3.2.2/library/RevoScaleR/SampleData/claims.sas7bdat
 Dependent variable(s): cost
 Total independent variables: 13 (Including number dropped: 2)
 Number of valid observations: 123
 Number of missing observations: 5

 Coefficients:
                   cost
 (Intercept) 117.38544
 age=17-20    88.15174
```

```
 age=21-24     34.15903
 age=25-29     54.68750
 age=30-34      2.93750
 age=35-39    -20.77430
 age=40-49      1.68750
 age=50-59     63.12500
 age=60+        Dropped
 car_age=0-3 159.30531
```

Similarly, you could use the SPSS version of the claims data as follows:

```
inFileSpss <- file.path(rxGetOption("sampleDataDir"), "claims.sav")
sourceDataSpss <- RxSpssData(inFileSpss, stringsAsFactors=TRUE)
rxLinMod(cost ~ age + car_age, data=sourceDataSpss)
```

3.6 Working with an Xdf Data Source

To create an .xdf data source for reading, you can use the *RxXdfData* function. For example, the following creates a data source from the built-in claims.xdf data set:

```
#  Working with an Xdf Data Source

claimsPath <-  file.path(rxGetOption("sampleDataDir"), "claims.xdf")
claimsDs <- RxXdfData(claimsPath)
```

Use the open method *rxOpen* to open the data source:

```
rxOpen(claimsDs)
```

Use the method *rxReadNext* to read the next block of data from the data source:

```
claims <- rxReadNext(claimsDs)
```

Use the *rxClose* method to close the data source:

```
rxClose(claimsDs)
```

3.7 Using an Xdf Data Source with biglm

Since data sources for xdf files read data in chunks, it is a good match for the CRAN package *biglm*. The *biglm* package does a linear regression on an initial chunk of data, then updates the results with subsequent chunks. Below is a function that loops through an xdf file object and creates and updates the *biglm* results.

```
#  Using an Xdf Data Source with biglm

if ("biglm" %in% .packages()){
require(biglm)
biglmxdf <- function(dataSource, formula)
{
      moreData <- TRUE
      df <- rxReadNext(dataSource)
      biglmRes <- biglm(formula, df)
```

```
        while (moreData)
        {
           df <- rxReadNext(dataSource)
           if (length(df) != 0)
           {
                  biglmRes <- update(biglmRes, df)
           }
           else
           {
                  moreData <- FALSE
           }
        }
        return(biglmRes)
}
```

To use the function, we first open the data file. For example, we can again use the large airline data set AirOnTime87to12.xdf (if you have downloaded the data set, modify the first line below to reflect your local path):

```
bigDataDir <- "C:/MRS/Data"
bigAirData <- file.path(bigDataDir, "AirOnTime87to12/AirOnTime87to12.xdf")
dataSource <- RxXdfData(bigAirData,
      varsToKeep = c("DayOfWeek", "DepDelay","ArrDelay"), blocksPerRead = 15)
rxOpen(dataSource)
```

Then we will time the computation, doing the regression for all the rows— 148,619,655 if you are using the full data set. (Note that in this case it will take at least 5 minutes, even on a very fast machine.)

```
system.time(bigLmRes <- biglmxdf(dataSource, ArrDelay~DayOfWeek))
rxClose(dataSource)
```

We can see the coefficients by looking at a summary of the object returned:

```
summary(bigLmRes)

} # End of use of biglm
```

It is, of course, much faster to compute a linear model using the `rxLinMod` function, but the `biglm` package provides alternative methods of computation.

Chapter 4.

Transforming and Subsetting Data

RevoScaleR provides a full set of functions for modifying, transforming, and subsetting data stored in memory in a data frame or in an .xdf file on disk:

- `rxDataStep` is used to subset rows and/or variables and to create new variables by transforming existing variables. It also allows for easy conversion between data in data frames and .xdf files.
- `rxSetVarInfo` is used to change variable information such as the name or description of a variable in an .xdf file or data frame. `rxSetInfo` is used to add or change a data set description.
- `rxFactors` is used to create or modify factors (categorical variables) based on existing variables.
- `rxSort` is used to sort a data set by one or more key variables.
- `rxMerge` is used to merge two data sets by one or more key variables.

4.1 Creating a Subset of Rows and Columns

A common use of *rxDataStep* is to create a new data set with a subset of rows and variables. The following simple example uses a data frame as the input data set. The call to rxDataStep uses the *rowSelection* argument to select only the rows where the variable *y* is greater than .5, and the *varsToKeep* argument to keeps only the variables *y* and *z*. The *rowSelection* argument is an R expression that evaluates to *TRUE* if the observation should be kept. The *varsToKeep* argument contains a list of variable names to read in from the original data set. Because no *outFile* is specified, a data frame is returned:

```
#########################################################
# Chapter 4: Transforming and Subsetting Data
Ch4Start <- Sys.time()


# Create a data frame
set.seed(59)
myData <- data.frame(
x = rnorm(100),
y = runif(100),
z = rep(1:20, times = 5))

# Subset observations and variables
myNewData <- rxDataStep( inData = myData,
     rowSelection = y > .5,
     varsToKeep = c("y", "z"))

# Get information about the new data frame
rxGetInfo(data = myNewData, getVarInfo = TRUE)
```

```
Data frame: myNewData
Number of observations: 52
Number of variables: 2
Variable information:
Var 1: y, Type: numeric, Low/High: (0.5516, 0.9941)
Var 2: z, Type: integer, Low/High: (1, 20)
```

Subsetting is particularly useful if your original data set contains millions of rows or hundreds of thousands of variables. As a smaller example, the CensusWorkers.xdf sample data file has six variables and 351,121 rows. To create a subset containing only workers who have worked less than 30 weeks in the year and five variables, we can again use *rxDataStep* with the *rowSelection* and *varsToKeep* arguments. Since the resulting data set will clearly fit in memory, we omit the *outFile* argument and assign the result of the data step, then use *rxGetInfo* to see our results as usual:

```
readPath <- rxGetOption("sampleDataDir")
censusWorkers <- file.path(readPath, "CensusWorkers.xdf")
partWorkers <- rxDataStep(inData = censusWorkers, rowSelection = wkswork1 < 30,
               varsToKeep = c("age", "sex", "wkswork1", "incwage", "perwt"))
rxGetInfo(partWorkers, getVarInfo = TRUE)
```

The result is a data set with 14,317 rows:

```
Data frame: partWorkers
Number of observations: 14317
Number of variables: 5
Variable information:
Var 1: age, Age
       Type: integer, Low/High: (20, 65)
Var 2: sex, Sex
       2 factor levels: Male Female
Var 3: wkswork1, Weeks worked last year
       Type: integer, Low/High: (21, 29)
Var 4: incwage, Wage and salary income
       Type: integer, Low/High: (0, 354000)
Var 5: perwt, Type: integer, Low/High: (2, 163)
```

Alternatively, and in this case more easily, you can use *varsToDrop* to prevent variables from being read in from the original data set. This time we'll specify an *outFile*; use the *overwrite* argument to allow the output file to be replaced.

```
partWorkersDS <- rxDataStep(inData = censusWorkers,
        outFile = "partWorkers.xdf",
        rowSelection = wkswork1 < 30,
        varsToDrop = c("state"), overwrite = TRUE)
```

As noted above, if you omit the *outFile* argument to *rxDataStep,* then the results will be returned in a data frame in memory. This is true whether or not the input data is a data frame or an .xdf file (assuming the resulting data is small enough to reside in memory). If an *outFile* is specified, a data source object representing the new .xdf file is returned, which can be used in subsequent RevoScaleR function calls.

```
rxGetVarInfo( partWorkersDS )
```

4.2 Transforming Data with rxDataStep

A crucial step in many analyses is transforming the data into the form best suited for the chosen analysis. For example, variations in scale between variables can sometimes make it convenient to take a log or a power of the original variable before fitting a linear model. In RevoScaleR, transforming data is an important issue because we are typically reading and processing data from disk, so we want to be as efficient as possible, minimizing the passes through the data. To provide maximum flexibility, RevoScaleR allows you to perform data transformations in virtually all of its functions, from the *rxImport* function discussed in the previous chapter, to the *rxDataStep* function that is the primary focus here, to the analysis functions *rxSummary*, *rxLinMod*, *rxLogit*, *rxGlm*, *rxCrossTabs*, *rxCube*, *rxCovCor*, and *rxKmeans* discussed in subsequent chapters. In all these cases, the basic procedures for transforming the data are the same.

The heart of the RevoScaleR data step is a list of *transforms*, each of which specifies an R expression to be evaluated and typically is an assignment either creating a new variable or modifying an existing variable from the original data set.

4.2.1 Creating and Transforming Variables

To create or modify variables, we use the `transforms` argument to `rxDataStep`. The `transforms` argument is specified as a list of expressions. Any R expression that operates row-by-row (that is, the computed value of the new variable for an observation is only dependent on values of other variables for that observation) can be used. Let's begin with a simple data frame containing a small sample of transaction data:

```
#  Transforming Data with rxDataStep

expData <- data.frame(
   BuyDate = c("2011/10/1", "2011/10/1", "2011/10/1",
    "2011/10/2", "2011/10/2", "2011/10/2", "2011/10/2",
    "2011/10/3", "2011/10/4", "2011/10/4"),
   Food =      c( 32, 102,  34,  5,   0, 175,  15, 76, 23, 14),
   Wine =      c( 0,  212,   0,  0, 425,  22,   0, 12,  0, 56),
   Garden =    c( 0,   46,   0,  0,   0,  45, 223,  0,  0, 0),
   House = c( 22,  72,  56,  3,   0,  0,    0, 37, 48, 23),
   Sex =   factor(c("F", "F", "M", "M", "M", "F", "F", "F", "M", "F")),
   Age =          c( 20,  51,  32,  16,  61, 42,  35, 99, 29, 55),
   stringsAsFactors = FALSE)
```

Now we would like to perform a series of data transformations:

- Compute the total expenditures for each store visit
- Compute the average category expenditure for each store visit
- Set the variable `Age` to missing if the value is 99
- Create a new logical variable `UnderAge` if the purchaser is under 21
- Find the day of week the purchase was made using R's `as.POSIXlt` function, then convert it to a factor. [Note that when creating factors in a transform, you must specify the levels or you may get unpredictable results. Alternatively use `rxFactors`.]
- Create a factor variable for categories of expenditure levels
- Create a logical variable for expenditures of $50 or more on either Food or Wine
- Remove the variable BuyDate from the data set

The following call to rxDataStep will accomplish all of the above, returning a new data frame with the transformed variables:

```
            newExpData = rxDataStep( inData = expData,
  transforms = list(
      Total      = Food + Wine + Garden + House,
      AveCat     = Total/4,
      Age        = ifelse(Age == 99, NA, Age),
      UnderAge   = Age < 21,
```

```
        Day        = (as.POSIXlt(BuyDate))$wday,
        Day        = factor(Day, levels = 0:6,
                            labels = c("Su","M","Tu", "W", "Th","F", "Sa")),
        SpendCat   = cut(Total, breaks=c(0, 75, 250, 10000),
                            labels=c("low", "medium", "high"), right=FALSE),
        FoodWine = ifelse( Food > 50, TRUE, FALSE),
        FoodWine = ifelse( Wine > 50, TRUE, FoodWine),
        BuyDate  = NULL))
newExpData
```

The new data frame shows all of the transformed data:

```
   Food Wine Garden House Sex Age Total AveCat UnderAge Day SpendCat FoodWine
1    32    0      0    22   F  20    54  13.50     TRUE  Sa      low    FALSE
2   102  212     46    72   F  51   432 108.00    FALSE  Sa     high     TRUE
3    34    0      0    56   M  32    90  22.50    FALSE  Sa   medium    FALSE
4     5    0      0     3   M  16     8   2.00     TRUE  Su      low    FALSE
5     0  425      0     0   M  61   425 106.25    FALSE  Su     high     TRUE
6   175   22     45     0   F  42   242  60.50    FALSE  Su   medium     TRUE
7    15    0    223     0   F  35   238  59.50    FALSE  Su   medium    FALSE
8    76   12      0    37   F  NA   125  31.25       NA   M   medium     TRUE
9    23    0      0    48   M  29    71  17.75    FALSE  Tu      low    FALSE
10   14   56      0    23   F  55    93  23.25    FALSE  Tu   medium     TRUE
```

If we had a large data set containing expenditure data in an .xdf file, we could use exactly the same transformation code; the only changes in the call to *rxDataStep* would be the *inData* and specifying an *outFile* for the newly created data set.

Sometimes it is useful to use computed values as part of a transformation. For example, you might want to impute missing values, replacing any missings with the variable mean. Let's look at a simple data frame example; again the same basic code could be used for a huge data set. First create a data set with missing values:

```
# Create a data frame with missing values
set.seed(59)
myData1 <- data.frame(x = rnorm(100), y = runif(100))

xmiss <- seq.int(from = 5, to = 100, by = 5)
ymiss <- seq.int(from = 2, to = 100, by = 5)
myData1$x[xmiss] <- NA
myData1$y[ymiss] <- NA
rxGetInfo(myData1, numRows = 5)
```

The call to *rxGetInfo* shows the following:

```
Data frame: myData1
Number of observations: 100
Number of variables: 2
Data (5 rows starting with row 1):
           x          y
1 -1.8621337 0.06206201
2  1.1398069         NA
3  0.3176267 0.84132161
4  1.3998593 0.26298559
5         NA 0.97069679
```

Now use *rxSummary* (discussed in detail in a later chapter) to compute summary statistics, putting the computed means into a named vector:

```
# Compute the summary statistics and extract
# the means in a named vector
sumStats <- rxResultsDF(rxSummary(~., myData1))
sumStats
meanVals <- sumStats$Mean
names(meanVals) <- row.names(sumStats)
```

The computed statistics are:

```
         Mean    StdDev         Min       Max ValidObs MissingObs
x 0.07431126 0.9350711 -1.94160646 1.9933814       80         20
y 0.54622241 0.3003457  0.04997869 0.9930338       80         20
```

Next we pass the computed means into a *rxDataStep* using the *transformObjects* argument:

```
# Use rxDataStep to replace missings with imputed mean values
myData2 <- rxDataStep(inData = myData1, transforms = list(
    x = ifelse(is.na(x), meanVals["x"], x),
    y = ifelse(is.na(y), meanVals["y"], y)),
    transformObjects = list(meanVals = meanVals))
rxGetInfo(myData2, numRows = 5)
```

The resulting data set information is:

```
Data frame: myData2
Number of observations: 100
Number of variables: 2
Data (5 rows starting with row 1):
           x          y
1 -1.86213372 0.06206201
2  1.13980693 0.54622241
3  0.31762673 0.84132161
4  1.39985928 0.26298559
5  0.07431126 0.97069679
```

4.2.2 Subsetting and Transforming Variables

Returning to our earlier example with CensusWorkers, we will now combine subsetting and transformations in one data step operation. Suppose we want to extract the same five variables as before from the CensusWorkers data set, but also add a factor variable based on the integer variable *age*. For example, to create our factor variable, we can use the following *transforms* argument:

```
transforms = list(ageFactor = cut(age, breaks=seq(from = 20, to = 70,
                                  by = 5), right = FALSE))
```

In doing a data step operation, RevoScaleR reads in a chunk of data read from the original data set, including only the variables indicated in *varsToKeep*, or omitting variables specified in *varsToDrop*. It then passes the variables needed for data transformations back to R for manipulation:

```
rxDataStep (inData = censusWorkers, outFile = "newCensusWorkers",
varsToDrop = c("state"), transforms = list(
     ageFactor = cut(age, breaks=seq(from = 20, to = 70, by = 5),
    right = FALSE)))
```

The *rxGetInfo* function reveals the added variable:

```
rxGetInfo("newCensusWorkers", getVarInfo = TRUE)

 File name: C:\YourOutputPath\newCensusWorkers.xdf
 Number of observations: 351121
 Number of variables: 6
 Number of blocks: 6
 Compression type: zlib
 Variable information:
 Var 1: age, Age
        Type: integer, Low/High: (20, 65)
 Var 2: incwage, Wage and salary income
        Type: integer, Low/High: (0, 354000)
 Var 3: perwt, Type: integer, Low/High: (2, 168)
 Var 4: sex, Sex
        2 factor levels: Male Female
 Var 5: wkswork1, Weeks worked last year
        Type: integer, Low/High: (21, 52)
 Var 6: ageFactor
        10 factor levels: [20,25) [25,30) [30,35) [35,40) [40,45) [45,50)
 [50,55) [55,60) [60,65) [65,70)
```

We can combine the *transforms* argument with the *transformObjects* argument to create new variables from objects in your global environment (or other environments in your current search path).

For example, suppose you would like to estimate a linear model using wage income as the dependent variable, and want to include state-level of per capita expenditure on education as one of the independent variables. We can define a named vector to contain this state-level data as follows:

```
educExp <- c(Connecticut=1795.57, Washington=1170.46, Indiana = 1289.66)
```

We can then use *rxDataStep* to add the per capita education expenditure as a new variable using the *transforms* argument, passing *educExp* to the *transformObjects* argument as a named list:

```
censusWorkers <- file.path(rxGetOption("sampleDataDir"), "CensusWorkers.xdf")
rxDataStep(inData = censusWorkers, outFile = "censusWorkersWithEduc",
     transforms = list(
         stateEducExpPC = educExp[match(state, names(educExp))] ),
     transformObjects= list(educExp=educExp))
```

The *rxGetInfo* function reveals the added variable:

```
rxGetInfo("censusWorkersWithEduc.xdf",getVarInfo=TRUE)

 File name: C:\YourOutputPath\censusWorkersWithEduc.xdf
 Number of observations: 351121
```

```
Number of variables: 7
Number of blocks: 6
Compression type: zlib
Variable information:
Var 1: age, Age
       Type: integer, Low/High: (20, 65)
Var 2: incwage, Wage and salary income
       Type: integer, Low/High: (0, 354000)
Var 3: perwt, Type: integer, Low/High: (2, 168)
Var 4: sex, Sex
       2 factor levels: Male Female
Var 5: wkswork1, Weeks worked last year
       Type: integer, Low/High: (21, 52)
Var 6: state
       3 factor levels: Connecticut Indiana Washington
Var 7: stateEducExpPC, Type: numeric, Low/High: (1170.4600, 1795.5700)
```

4.3 Using the Data Step to Create an .xdf File from a Data Frame

You can use all of the functionality provided by the *rxDataStep* function to create an .xdf file from a data frame for further use. For example, create a simple data frame:

```
#  Using the Data Step to Create an .xdf File from a Data Frame

set.seed(39)
myData <- data.frame(x1 = rnorm(10000), x2 = runif(10000))
```

Now create an .xdf file, using a row selection and creating a new variable. The *rowsPerRead* argument will specify how many rows of the original data frame to process at a time before writing out a block of the new .xdf file.

```
rxDataStep(inData = myData, outFile = "testFile.xdf",
    rowSelection = x2 > .1,
    transforms = list( x3 = x1 + x2 ),
    rowsPerRead = 5000 )
rxGetInfo("testFile.xdf")

 File name: C:\Users\...\testFile.xdf
 Number of observations: 8970
 Number of variables: 3
 Number of blocks: 2
```

4.4 Converting .xdf Files to Text

If you need to share data with others not using .xdf data files, you can export your .xdf files to text format using the *rxDataStep* function. For example, we can write the claims.xdf file we created earlier to text format as follows:

```
#  Converting .xdf Files to Text
claimsCsv <- RxTextData(file="claims.csv")
claimsXdf <- RxXdfData(file="claims.xdf")

rxDataStep(inData=claimsXdf, outFile=claimsCsv)
```

By default, the text file created is comma-delimited, but you can change this by specifying a different delimiter with the *delimiter* argument to the RxTextData function:

```
claimsTxt <- RxTextData(file="claims.txt", delimiter="\t")
rxDataStep(inData=claimsXdf, outFile=claimsTxt)
```

If you have a large number of variables, you can choose to write out only a subsample by using the *VarsToKeep* or *VarsToDrop* argument. Here we write out the claims data, omitting the *number* variable:

```
rxDataStep(inData=claimsXdf, outFile=claimsTxt, varsToDrop="number",
           overwrite=TRUE)
```

4.5 Re-Blocking an .xdf File

After a series of data import or row selection steps, you may find that you have an .xdf file with very uneven block sizes. This may make it difficult to efficiently perform computations by "chunk." To find the sizes of the blocks in your .xdf file, use *rxGetInfo* with the *getBlockSizes* argument set to TRUE. For example, let's look at the block sizes for the sample CensusWorkers.xdf file:

```
#  Re-Blocking an .xdf File

fileName <- file.path(rxGetOption("sampleDataDir"), "CensusWorkers.xdf")
rxGetInfo(fileName, getBlockSizes = TRUE)
```

The following information is provided:

```
File name: C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-3.2.2\
library\RevoScaleR\SampleData\CensusWorkers.xdf
Number of observations: 351121
Number of variables: 6
Number of blocks: 6
Compression type: zlib
Rows per block: 95420 42503 1799 131234 34726 45439
```

We see that, in fact, the number of rows per block varies from a low of 1799 to a high of 131,234. To create a new file with more even-sized blocks, use the rowsPerRead argument in rxDataStep:

```
newFile <- "censusWorkersEvenBlocks.xdf"
rxDataStep(inData = fileName, outFile = newFile, rowsPerRead = 60000)
rxGetInfo(newFile, getBlockSizes = TRUE)
```

The new file has blocks sizes of 60,000 for all but the last slightly smaller block:

```
File name: C:\Users\...\censusWorkersEvenBlocks.xdf
Number of observations: 351121
Number of variables: 6
Number of blocks: 6
```

```
Compression type: zlib
Rows per block: 60000 60000 60000 60000 60000 51121
```

4.6 Modifying Variable Information

To change variable information (rather than the data values themselves), use the function *rxSetVarInfo*. For example, using the data file created above, we can change the names of two variables and add descriptions:

```
#  Modifying Variable Information

newVarInfo <- list(
    incwage = list(newName = "WageIncome"),
    state   = list(newName = "State", description = "State of Residence"),
    stateEducExpPC = list(description = "State Per Capita Educ Exp"))
fileName <- "censusWorkersWithEduc.xdf"
rxSetVarInfo(varInfo = newVarInfo, data = fileName)
rxGetVarInfo( fileName )
```

```
 Var 1: age, Age
        Type: integer, Low/High: (20, 65)
 Var 2: WageIncome, Wage and salary income
        Type: integer, Low/High: (0, 354000)
 Var 3: perwt, Type: integer, Low/High: (2, 168)
 Var 4: sex, Sex
        2 factor levels: Male Female
 Var 5: wkswork1, Weeks worked last year
        Type: integer, Low/High: (21, 52)
 Var 6: State, State of Residence
        3 factor levels: Connecticut Indiana Washington
 Var 7: stateEducExpPC, State Per Capita Educ Exp
        Type: numeric, Low/High: (1170.4600, 1795.5700)
```

4.7 Sorting Data

Many analysis and plotting algorithms require as a first step that the data be sorted. Sorting a massive data set is both memory-intensive and time-consuming, but the *rxSort* function provides an efficient solution. The *rxSort* function allows you to sort by one or many keys. A *stable* sorting routine is used, so that, in the case of ties, remaining columns are left in the same order as they were in the original data set.

As a simple example, we can sort the census worker data by *age* and *incwage*. We will sort first by *age*, using the default increasing sort, and then by *incwage*, which we will sort in decreasing order:

```
#  Sorting Data

censusWorkers <- file.path(rxGetOption("sampleDataDir"), "CensusWorkers.xdf")
outXDF <- "censusWorkersSorted.xdf"
rxSort(inData = censusWorkers, outFile = outXDF, sortByVars=c("age",
```

```
        "incwage"), decreasing=c(FALSE, TRUE))
```

The first few lines of the sorted file can be viewed as follows:

```
rxGetInfo(outXDF, numRows=10)

 File name: C:\YourOutputPath\censusWorkersSorted.xdf
 Number of observations: 351121
 Number of variables: 6
 Number of blocks: 6
 Compression type: zlib
 Data (10 rows starting with row 1):
    age incwage perwt    sex wkswork1      state
 1   20  336000     3   Male       40 Washington
 2   20  336000    23   Male       46 Washington
 3   20  336000    11   Male       52 Washington
 4   20  314000    33   Male       52    Indiana
 5   20  168000    13   Male       24    Indiana
 6   20  163000    16   Male       26 Washington
 7   20  144000    27 Female       24    Indiana
 8   20   96000    21   Male       48 Washington
 9   20   93000    24   Male       24    Indiana
 10  20   90000     6   Male       52 Washington
```

If the sort keys contain missing values, you can use the *missingsLow* flag to specify whether they are sorted as low values (*missingsLow=TRUE*, the default) or high values (*missingsLow=FALSE*).

4.7.1 Removing Duplicates While Sorting

In many situations, you are sorting a large data set by a particular key, for example, userID, but are looking for a sorted list of unique userIDs. The *removeDupKeys* argument to rxSort allows you to remove the duplicate entries from a sorted list. This argument is supported only for *type="auto"* and *type="mergeSort"*; it is ignored for *type="varByVar"*. When you use *removeDupKeys=TRUE*, the first record containing a unique combination of the *sortByVars* is retained; subsequent matching records are omitted from the sorted results, but, if desired, a count of the matching records is maintained in a new *dupFreqVar* output column. For example, the following artificial data set simulates a small amount of transaction data, with a user name, a state, and a transaction amount. When we sort by the variables *users* and *state* and specify *removeDupKeys=TRUE*, the *transAmt* shown for duplicate entries is the transaction amount for the *first* transaction encountered:

```
set.seed(17)
users <- sample(c("Aiden", "Ella", "Jayden", "Ava", "Max", "Grace", "Riley",
                  "Lolita", "Liam", "Emma", "Ethan", "Elizabeth", "Jack",
                  "Genevieve", "Avery", "Aurora", "Dylan", "Isabella",
                  "Caleb", "Bella"), 100, replace=TRUE)
state <- sample(c("Washington", "California", "Texas", "North Carolina",
                  "New York", "Massachusetts"), 100, replace=TRUE)
transAmt <- round(runif(100)*100, digits=3)
df <- data.frame(users=users, state=state, transAmt=transAmt)

rxSort(df, sortByVars=c("users", "state"), removeDupKeys=TRUE,
    dupFreqVar = "DUP_COUNT")
```

```
Number of rows written to file: 66, Variable(s): users, state, transAmt,
DUP_COUNT, Total number of rows in file: 66
Time to sort data file: 0.100 seconds
       users          state transAmt DUP_COUNT
1      Aiden       New York   11.010         1
2      Aiden North Carolina   73.307         1
3      Aiden          Texas    8.037         2
4     Aurora     California    8.787         1
5     Aurora  Massachusetts   55.187         1
6     Aurora       New York   91.648         1
7     Aurora          Texas   30.566         1
8     Aurora     Washington   27.374         1
9        Ava     California   70.638         2
10       Ava  Massachusetts   82.916         2
11       Ava       New York   45.683         2
12       Ava North Carolina   51.748         1
13       Ava          Texas   52.674         1
14     Avery     California    9.756         4
15     Avery  Massachusetts   63.715         1
16     Avery       New York   93.430         1
17     Avery North Carolina    1.889         2
18     Bella     California   60.258         2
19     Bella          Texas   32.684         1
20     Bella     Washington   60.230         2
21     Caleb  Massachusetts   94.527         1
22     Caleb North Carolina   89.259         2
23     Dylan     California   73.665         1
24     Dylan North Carolina   98.384         1
25     Dylan          Texas   27.067         1
26     Dylan     Washington   82.141         3
27 Elizabeth     California   95.497         2
28 Elizabeth       New York   35.546         3
29 Elizabeth North Carolina   18.892         2
30      Ella     California   11.644         1
31      Ella North Carolina   72.289         1
32      Ella     Washington   66.453         2
33      Emma  Massachusetts   28.502         1
34      Emma North Carolina   63.067         1
35     Ethan  Massachusetts   31.480         1
36     Ethan       New York   95.639         1
37     Ethan North Carolina    6.561         1
38     Ethan          Texas   29.963         1
39     Ethan     Washington   44.187         2
40 Genevieve  Massachusetts   90.783         1
41     Grace       New York   18.232         1
42     Grace North Carolina    5.355         2
43     Grace     Washington   91.084         1
44  Isabella       New York    4.115         1
45  Isabella North Carolina   12.942         2
46  Isabella          Texas    2.227         2
47      Jack     California   40.905         1
48      Jack  Massachusetts   98.080         2
49      Jack       New York    8.071         2
50      Jack North Carolina   11.304         3
51      Jack          Texas   18.795         2
52    Jayden  Massachusetts   83.949         1
53    Jayden North Carolina   67.769         1
54    Jayden     Washington    4.360         1
55      Liam     California    3.300         1
56      Liam  Massachusetts   87.585         1
57      Liam       New York   96.599         1
58      Liam North Carolina   32.997         1
59    Lolita     California   18.102         1
```

```
60    Lolita     Washington   30.649         2
61       Max  Massachusetts   21.683         2
62       Max       New York   14.852         2
63       Max North Carolina   79.982         2
64       Max          Texas   66.749         2
65       Max     Washington   67.326         2
66     Riley       New York   20.527         2
```

Removing duplicates can be a useful way to reduce the size of a data set without losing information of interest. For example, consider an analysis of using data from the sample *AirlineDemoSmall* xdf file. It has 600,000 observations and contains the variables *DayOfWeek*, *CRSDepTime*, and *ArrDelay*. We can create a smaller data set reducing the number of observations, and adding a variable that contains the frequency of the duplicated observation.

```
sampleDataDir <- rxGetOption("sampleDataDir")
airDemo <- file.path(sampleDataDir, "AirlineDemoSmall.xdf")
airDedup <- file.path(tempdir(), "rxAirDedup.xdf")
rxSort(inData = airDemo, outFile = airDedup,
     sortByVars =  c("DayOfWeek", "CRSDepTime", "ArrDelay"),
     removeDupKeys = TRUE, dupFreqVar = "FreqWt")
rxGetInfo(airDedup)
```

The new data file contains about 1/3 of the observations and one additional variable:

```
File name: C:\YourTempDir\rxAirDedup.xdf
Number of observations: 232451
Number of variables: 4
Number of blocks: 2
Compression type: zlib
```

By using the frequency weights argument, we can use many of the RevoScaleR analysis functions on this smaller data set and get same results as we would using the full data set. For example, a linear model for Arrival Delay can be specified as follows, using the *fweights* argument:

```
linModObj <- rxLinMod(ArrDelay~CRSDepTime + DayOfWeek, data = airDedup,
     fweights = "FreqWt")
summary(linModObj)
```

```
Call:
rxLinMod(formula = ArrDelay ~ CRSDepTime + DayOfWeek, data = airDedup,
    fweights = "FreqWt")

Linear Regression Results for: ArrDelay ~ CRSDepTime + DayOfWeek
File name: C:\YourTempDir\rxAirDedup.xdf
Frequency weights: FreqWt
Dependent variable(s): ArrDelay
Total independent variables: 9 (Including number dropped: 1)
Sum of weights of valid observations: 582628
Number of missing observations: 3503

Coefficients: (1 not defined because of singularities)
                    Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept)         -3.19458    0.20413 -15.650 2.22e-16 ***
CRSDepTime           0.97862    0.01126  86.948 2.22e-16 ***
DayOfWeek=Monday     2.08100    0.18602  11.187 2.22e-16 ***
DayOfWeek=Tuesday    1.34015    0.19881   6.741 1.58e-11 ***
DayOfWeek=Wednesday  0.15155    0.19679   0.770    0.441
DayOfWeek=Thursday  -1.32301    0.19518  -6.778 1.22e-11 ***
DayOfWeek=Friday     4.80042    0.19452  24.679 2.22e-16 ***
DayOfWeek=Saturday   2.18965    0.19229  11.387 2.22e-16 ***
DayOfWeek=Sunday     Dropped    Dropped Dropped  Dropped
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 40.39 on 582620 degrees of freedom
Multiple R-squared: 0.01465
Adjusted R-squared: 0.01464
F-statistic:  1238 on 7 and 582620 DF,  p-value: < 2.2e-16
Condition number: 10.6542
```

Using the full data set, we get the following results:

```
linModObjBig <- rxLinMod(ArrDelay~CRSDepTime + DayOfWeek, data = airDemo)
summary(linModObjBig)
```

```
Call:
rxLinMod(formula = ArrDelay ~ CRSDepTime + DayOfWeek, data = airDemo)

Linear Regression Results for: ArrDelay ~ CRSDepTime + DayOfWeek
File name:    C:\YourSampleDir\AirlineDemoSmall.xdf
Dependent variable(s): ArrDelay
Total independent variables: 9 (Including number dropped: 1)
Number of valid observations: 582628
Number of missing observations: 17372

Coefficients: (1 not defined because of singularities)
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)         -3.19458    0.20413 -15.650 2.22e-16 ***
CRSDepTime           0.97862    0.01126  86.948 2.22e-16 ***
DayOfWeek=Monday     2.08100    0.18602  11.187 2.22e-16 ***
DayOfWeek=Tuesday    1.34015    0.19881   6.741 1.58e-11 ***
DayOfWeek=Wednesday  0.15155    0.19679   0.770    0.441
DayOfWeek=Thursday  -1.32301    0.19518  -6.778 1.22e-11 ***
DayOfWeek=Friday     4.80042    0.19452  24.679 2.22e-16 ***
DayOfWeek=Saturday   2.18965    0.19229  11.387 2.22e-16 ***
DayOfWeek=Sunday     Dropped    Dropped Dropped  Dropped
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 40.39 on 582620 degrees of freedom
Multiple R-squared: 0.01465
Adjusted R-squared: 0.01464
F-statistic:  1238 on 7 and 582620 DF,  p-value: < 2.2e-16
Condition number: 10.6542
```

4.7.2 The rxQuantile Function and the Five-Number Summary

Sorting data is, in the general case, a prerequisite to finding exact quantiles, including medians. However, it is possible to compute approximate quantiles by counting binned data then computing a linear interpolation of the empirical cdf. If the data are integers, or can be

converted to integers by exact multiplication, and integral bins are used, the computation is exact. The RevoScaleR function rxQuantile does this computation, and by default returns an approximate five-number summary:

```
#  The rxQuantile Function and the Five-Number Summary

readPath <- rxGetOption("sampleDataDir")
AirlinePath <- file.path(readPath, "AirlineDemoSmall.xdf")
rxQuantile("ArrDelay", AirlinePath)
```

```
Rows Processed: 600000
  0%  25%  50%  75% 100%
 -86   -9    0   16 1490
```

4.8 Merging Data

Merging allows you to combine the information from two data sets into a third data set that can be used for subsequent analysis. One example is merging account information such as account number and billing address with transaction data such as account number and purchase details to create invoices. In this case, the two files are merged on the common information, that is, the account number.

In RevoScaleR, you merge .xdf files and/or data frames with the rxMerge function. This function supports a number of types of merge that are best illustrated by example. The available types are as follows:

- Inner
- Outer: left, right, and full
- One-to-One
- Union

We describe each of these types in the following sections.

4.8.1 Inner Merge

In the default inner merge type, one or more merge key columns is specified, and only those observations for which the specified key columns match exactly are combined to create new observations in the merged data set.

Suppose we have the following data from a dentist's office:

```
AccountNo    Billee       Patient
     0538    Rich C             1
     0538    Rich C             2
     0538    Rich C             3
     0763     Tom D             1
     1534    Kath P             1
```

We can create a data frame with this information:

```
#  Merging Data

acct <- c(0538, 0538, 0538, 0763, 1534)
billee <- c("Rich C", "Rich C", "Rich C", "Tom D", "Kath P")
patient <- c(1, 2, 3, 1, 1)
acctDF<- data.frame( acct=acct, billee= billee, patient=patient)
```

Suppose further we have the following information about procedures performed:

```
  AccountNo    Patient       Procedure
       0538          3      OffVisit
       0538          2      AdultPro
       0538          2      OffVisit
       0538          3      2SurfCom
       0763          1      OffVisit
       0763          1      AdultPro
       0763          2      OffVisit
```

This data is put into another data frame:

```
acct <- c(0538, 0538, 0538, 0538, 0763, 0763, 0763)
patient <- c(3, 2, 2, 3, 1, 1, 2)
type <- c("OffVisit", "AdultPro", "OffVisit", "2SurfCom", "OffVisit", "AdultPro",
"OffVisit")
procedureDF <- data.frame(acct=acct, patient=patient, type=type)
```

Then we use rxMerge to create an inner merge matching on the columns *acct* and *patient:*

```
rxMerge(inData1 = acctDF, inData2 = procedureDF, type = "inner",
     matchVars=c("acct", "patient"))
```

```
     acct billee patient     type
1   538 Rich C       2 AdultPro
2   538 Rich C       2 OffVisit
3   538 Rich C       3 OffVisit
4   538 Rich C       3 2SurfCom
5   763  Tom D       1 OffVisit
6   763  Tom D       1 AdultPro
```

Because the patient 1 in account 538 and patient 1 in account 1534 had no visits, they are omitted from the merged file. Similarly, patient 2 in account 763 had a visit, but does not have any information in the accounts file, so it too is omitted from the merged data set. Also, note that the two input data files are automatically sorted on the merge keys before merging.

4.8.2 Outer Merge

There are three types of outer merge: left, right, and full. In a left outer merge, all the lines from the first file are present in the merged file, either matched with lines from the second file that match on the key columns, or if no match, filled out with missing values. A right outer

merge is similar, except all the lines from the second file are present, either matched with matching lines from the first file or filled out with missings. A full outer merge includes all lines in both files, either matched or filled out with missings. We can use the same dentist data to illustrate the various types of outer merge:

```
rxMerge(inData1 = acctDF, inData2 = procedureDF, type = "left",
     matchVars=c("acct", "patient"))
```

```
   acct billee patient     type
1   538 Rich C       1     <NA>
2   538 Rich C       2 AdultPro
3   538 Rich C       2 OffVisit
4   538 Rich C       3 OffVisit
5   538 Rich C       3 2SurfCom
6   763  Tom D       1 OffVisit
7   763  Tom D       1 AdultPro
8  1534 Kath P       1     <NA>
```

```
rxMerge(inData1 = acctDF, inData2 = procedureDF, type = "right",
     matchVars=c("acct", "patient"))
```

```
   acct billee patient     type
1   538 Rich C       2 AdultPro
2   538 Rich C       2 OffVisit
3   538 Rich C       3 OffVisit
4   538 Rich C       3 2SurfCom
5   763  Tom D       1 OffVisit
6   763  Tom D       1 AdultPro
7   763   <NA>       2 OffVisit
```

```
rxMerge(inData1 = acctDF, inData2 = procedureDF, type = "full",
     matchVars=c("acct", "patient"))
```

```
   acct billee patient     type
1   538 Rich C       1     <NA>
2   538 Rich C       2 AdultPro
3   538 Rich C       2 OffVisit
4   538 Rich C       3 OffVisit
5   538 Rich C       3 2SurfCom
6   763  Tom D       1 OffVisit
7   763  Tom D       1 AdultPro
8   763   <NA>       2 OffVisit
9  1534 Kath P       1     <NA>
```

4.8.3 One-to-one Merge

In the one-to-one merge type, the first observation in the first data set is paired with the first observation in the second data set to create the first observation in the merged data set, the second observation is paired with the second observation to create the second observation in the merged data set, and so on. The data sets must have the same number of rows. It is equivalent to using *append*="*cols*" in a data step.

For example, suppose our first data set contains three observations as follows:

```
1 a x
2 b y
3 c z
```

Create a data frame with this data:

```
myData1 <- data.frame( x1 = 1:3, y1 = c("a", "b", "c"), z1 = c("x", "y", "z"))
```

Suppose our second data set contains three different variables:

```
101 d u
102 e v
103 f w
```

Create a data frame with this data:

```
myData2 <- data.frame( x2 = 101:103, y2 = c("d", "e", "f"),
          z2 = c("u", "v", "w"))
```

A one-to-one merge of these two data sets combines the columns from the two data sets into one data set:

```
rxMerge(inData1 = myData1, inData2 = myData2, type = "oneToOne")
```

```
  x1 y1 z1  x2 y2 z2
1  1  a  x 101  d  u
2  2  b  y 102  e  v
3  3  c  z 103  f  w
```

4.8.4 Union Merge

A union merge is simply the concatenation of two files with the same set of variables. It is equivalent to using `append="rows"` in a data step.

Using the example from one-to-one merge, we rename the variables in the second data frame to be the same as in the first:

```
names(myData2) <- c("x1", "x2", "x3")
```

Then use a union merge:

```
rxMerge(inData1 = myData1, inData2 = myData2, type = "union")
```

```
   x1 y1 z1
1   1  a  x
2   2  b  y
3   3  c  z
4 101  d  u
5 102  e  v
6 103  f  w
```

4.8.5 Using rxMerge with .xdf files

You can use *rxMerge* with a combination of .xdf files and/or data frames. For example, you specify the two the paths for two input .xdf files as the *inData1* and *inData2* arguments, and the path to an output file as the *outFile* argument. As a simple example, we can stack two copies of the claims data using the union merge type as follows:

```
claimsXdf <- file.path(rxGetOption("sampleDataDir"), "claims.xdf")

rxMerge(inData1 = claimsXdf, inData2 = claimsXdf, outFile = "claimsTwice.xdf",
     type = "union")
```

A new .xdf file is created containing twice the number of rows of the original claims file.

You can also merge an .xdf file and data frame into a new .xdf file. For example, suppose that you would like to add a variable on state expenditure on education into each observation in the censusWorkers sample .xdf file. First, take a quick look at the state variable in the .xdf file:

```
censusWorkers <- file.path(rxGetOption("sampleDataDir"), "CensusWorkers.xdf")
rxGetVarInfo(censusWorkers, varsToKeep = "state")
```

```
 Var 1: state
        3 factor levels: Connecticut Indiana Washington
```

We can create a data frame with per capita educational expenditures for the same three states. (Note that because R alphabetizes factor levels by default, the factor levels in the data frame will be in the same order as those in the .xdf file).

```
educExp <- data.frame(state=c("Connecticut", "Washington", "Indiana"),
     EducExp = c(1795.57,1170.46,1289.66 ))
```

Now use rxMerge, matching by the variable *state:*

```
rxMerge(inData1 = censusWorkers, inData2 = educExp,
     outFile="censusWorkersEd.xdf", matchVars = "state", overwrite=TRUE)
```

The new .xdf file has an additional variable, EducExp:

```
rxGetVarInfo("censusWorkersEd.xdf")
```

```
 Var 1: age, Age
        Type: integer, Low/High: (20, 65)
 Var 2: incwage, Wage and salary income
        Type: integer, Low/High: (0, 354000)
 Var 3: perwt, Type: integer, Low/High: (2, 168)
 Var 4: sex, Sex
        2 factor levels: Male Female
 Var 5: wkswork1, Weeks worked last year
        Type: integer, Low/High: (21, 52)
 Var 6: state
```

```
        3 factor levels: Connecticut Indiana Washington
Var 7: EducExp, Type: numeric, Low/High: (1170.4600, 1795.5700)
```

4.9 Creating and Recoding Factors

Factors are variables that represent categories. An example is “sex”, which has the categories “Male” and “Female”. There are two parts to a factor variable:

1. A vector of integer indexes with values in the range of 1:K, where K is the number of categories. For example, “sex” has two categories with indexes 1 and 2. The length of the vector corresponds to the number of observations.
2. A vector of K character strings that are used when the factor is displayed. In R, these are normally printed without quote marks, to indicate that the variable is a factor instead of a character string.

If you have character data in an .xdf file or data frame, you can use the *rxFactors* function to convert it to a factor. Let’s create a simple data frame with character data. Note that by default, *data.frame* converts character data to factor data. That is, the *stringsAsFactors* argument defaults to *TRUE*. In RevoScaleR’s *rxImport* function, *stringsAsFactors* has a default of *FALSE*.

```
# Creating factors from character data

myData <- data.frame(
  id = 1:10,
  sex = c("M","F", "M", "F", "F", "M", "F", "F", "M", "M"),
  state = c(rep(c("WA", "CA"), each = 5)),
  stringsAsFactors = FALSE)
rxGetVarInfo(myData)

 Var 1: id, Type: integer, Low/High: (1, 10)
 Var 2: sex, Type: character
 Var 3: state, Type: character
```

Now we can use *rxFactors* to convert the character data to factors. We can just specify a vector of variable names to convert as the *factorInfo*:

```
myNewData <- rxFactors(inData = myData, factorInfo = c("sex", "state"))
rxGetVarInfo(myNewData)

 Var 1: id, Type: integer, Low/High: (1, 10)
 Var 2: sex
        2 factor levels: M F
 Var 3: state
        2 factor levels: WA CA
```

Note that by default, the factor levels are in the order in which they are encountered. If you would like to have them sorted alphabetically, specify *sortLevels* to be *TRUE*.

```
myNewData <- rxFactors(inData = myData, factorInfo = c("sex", "state"),
```

```
    sortLevels = TRUE)
rxGetVarInfo(myNewData)

 Var 1: id, Type: integer, Low/High: (1, 10)
 Var 2: sex
        2 factor levels: F M
 Var 3: state
        2 factor levels: CA WA
```

If you have variables that are already factors, you may want change the order of the levels, the names of the levels, and/or how they are grouped. Typically recoding a factor means changing from one set of indexes to another. For example, if the levels of "sex" are currently arranged in the order "M", "F" and you want to change that to "F", "M", you need to change the index for every observation.

You can use the rxFactors function to recode factors in RevoScaleR. For example, suppose we have some test scores for a set of male and female subjects. We can generate such data randomly as follows:

```
#  Recoding Factors

set.seed(100)
sex <- factor(sample(c("M","F"), size = 10, replace = TRUE),
              levels = c("M", "F"))
DF <- data.frame(sex = sex, score = rnorm(10))
```

If we look at just the sex variable, we see the levels M or F for each observation:

```
DF[["sex"]]

 [1] M M F M M M F M F M
 Levels: M F
```

To recode this factor so that "Female" is the first level and "Male" the second, we can use rxFactors as follows:

```
newDF <- rxFactors(inData = DF, overwrite = TRUE,
          factorInfo = list(Gender = list(newLevels = c(Female = "F",
                                                        Male = "M"),
                                          varName = "sex")))
```

Looking at the new Gender variable, we see how the levels have changed:

```
newDF$Gender

 [1] Male   Male   Female Male   Male   Male   Female Male   Female Male
 Levels: Female Male
```

As mentioned earlier, by default, RevoScaleR codes factor levels in the order in which they are encountered in the input file(s). This could lead you to have a State variable ordered as "Maine", "Vermont", "New Hampshire", "Massachusetts", "Connecticut", etc. Usually, you would prefer to have the levels of such a variable sorted in alphabetical order. You can do this

with rxFactors using the sortLevels flag. It is most useful to specify this flag as part of the factorInfo list for each variable, although if you have a large number of factors and want most of them to be sorted, you can also set the flag to TRUE globally and then specify sortLevels=FALSE for those variables you want to order in a different way.

When using the sortLevels flag, it is useful to keep in mind that it is the *levels* that are being sorted, not the data itself, and that the levels are always character data. If you are using the individual values of a continuous variable as factor levels, you may be surprised by the sorted order of the levels: for example, the levels 1, 3, 20 are sorted as "1", "20", "3".

Another common use of factor recoding is in analyzing survey data gathered using Likert items with five or seven level responses. For example, suppose a customer satisfaction survey offered the following seven-level responses to each of four questions:

1. Completely satisfied
2. Mostly satisfied
3. Somewhat satisfied
4. Neither satisfied nor dissatisfied
5. Somewhat dissatisfied
6. Mostly dissatisfied
7. Completely dissatisfied

In analyzing this data, the survey analyst may recode the factors to focus on those who were largely satisfied (combining levels 1 and 2), largely dissatisfied (combining levels 6 and 7) and somewhere in-between (combining levels 3, 4, and 5). The CustomerSurvey.xdf file in the SampleData directory contains 25 responses to each of the four survey questions. We can read it into a data frame as follows:

```
# Combining factor levels

surveyDF <- rxDataStep(inData =
     file.path(rxGetOption("sampleDataDir"),"CustomerSurvey.xdf"))
```

To recode each question as desired, we can use rxFactors as follows:

```
sl <- levels(surveyDF[[1]])
quarterList <-  list(newLevels = list(
                          "Largely Satisfied" = sl[1:2],
                          "Neither Satisfied Nor Dissatisfied" = sl[3:5],
                          "Largely Dissatisfied" = sl[6:7]))
surveyDF <- rxFactors(inData = surveyDF,
            factorInfo <- list(
                  Q1 = quarterList,
                  Q2 = quarterList,
                  Q3 = quarterList,
                  Q4 = quarterList))
```

Looking at just Q1, we see the recoded factor:

```
surveyDF[["Q1"]]
```

```
 [1] Neither Satisfied Nor Dissatisfied Largely Satisfied
 [3] Neither Satisfied Nor Dissatisfied Largely Satisfied
 [5] Neither Satisfied Nor Dissatisfied Neither Satisfied Nor Dissatisfied
 [7] Largely Dissatisfied               Neither Satisfied Nor Dissatisfied
 [9] Neither Satisfied Nor Dissatisfied Largely Satisfied
[11] Neither Satisfied Nor Dissatisfied Largely Dissatisfied
[13] Largely Satisfied                  Neither Satisfied Nor Dissatisfied
[15] Largely Dissatisfied               Neither Satisfied Nor Dissatisfied
[17] Largely Satisfied                  Neither Satisfied Nor Dissatisfied
[19] Neither Satisfied Nor Dissatisfied Neither Satisfied Nor Dissatisfied
[21] Neither Satisfied Nor Dissatisfied Neither Satisfied Nor Dissatisfied
[23] Neither Satisfied Nor Dissatisfied Largely Dissatisfied
[25] Neither Satisfied Nor Dissatisfied
3 Levels: Largely Satisfied ... Largely Dissatisfied
```

4.9.1 Recoding Factors to Ensure Variable Compatibility

One important use of factor recoding in RevoScaleR is to ensure that the factor variables in two files are compatible, that is, have the same levels with the same coding. This use comes up in a variety of contexts, including prediction, merging, and distributed computing. For example, suppose you are creating a logistic regression model of whether a given airline flight will be late, and are using the first fifteen years of the airline data as a training set. You then want to test the model on the remaining years of the airline data. You need to ensure that the two files, the training set and the test set, have compatible factor variables. You can generally do this easily using rxGetInfo (with getVarInfo=TRUE) together with rxFactors. Use rxGetInfo to find all the levels in all the files, then use rxFactors to recode each file so that every factor variable contains all the levels found in any of the files.

The rxMerge function automatically checks for factor variable compatibility and recodes on the fly if necessary.

Chapter 5.

Models in RevoScaleR

Specifying a model with RevoScaleR is similar to specifying a model with the standard R statistical modeling functions, but there are some significant differences. Understanding these differences can help you make better use of RevoScaleR. The purpose of this chapter is to explain these differences at a high level so that when we begin fitting models in the next chapter, the terminology does not seem too foreign.

5.1 External Memory Algorithms

The first thing to know about RevoScaleR's statistical algorithms is that they are *external memory* algorithms that work on one chunk of data at time. All of RevoScaleR's algorithms share a basic underlying structure:

- An *initialization* step, in which data structures are created and given initial values, a data source is identified and opened for reading, and any other initial conditions are satisfied.
- A *process data* step, in which a chunk of data is read, some calculations are performed, and the result is passed back to the master process.
- An *update results* step, in which the results of the process data step are merged with previous results.
- A *finalize results* step, in which any final processing is performed and a result is returned.

An important consideration in using external memory algorithms is deciding how big a *chunk* of data is. You want to use a chunk size that's as large as possible while still allowing the process data step to complete without swapping. All of the RevoScaleR modeling functions allow you to specify a `blocksPerRead` argument. To make effective use of this, you need to know how many blocks your data file contains and how large the data file is. The number of blocks can be obtained using the `rxGetInfo` function.

5.2 Formulas in RevoScaleR

RevoScaleR uses a variant of the Wilkinson-Rogers formula notation (Wilkinson & Rogers, 1973) that is similar to, but not exactly the same as, that used in the standard R modeling functions. The response, or dependent, variables are separated from the predictor, or independent, variables by a tilde (~). In most of the modeling functions, multiple response variables are permitted, specified using the `cbind` function to combine them.

Independent variables (*predictors*) are separated by plus signs (+). Interaction terms can be created by joining two or more variables with a colon (:). Interactions between two categorical variables add one coefficient to the model for every combination of levels of the two variables. For example, if we have the categorical variables sex with two levels and education with four levels, the interaction of sex and education will add eight coefficients to the fitted model. Interactions between a continuous variable and a categorical variable add one coefficient to the model representing the continuous variable for each level of the categorical variable. (However, in RevoScaleR, such interactions cannot be used with the `rxCube` or `rxCrossTabs` functions.) The interaction of two continuous variables is the same as multiplying the two variables.

An asterisk (*) between two variables adds all subsets of interactions to the model. Thus, sex*education is equivalent to sex + education + sex:education.

The special function syntax `F(x)` can be used to have RevoScaleR treat a numeric variable `x` as a categorical variable (factor) for the purposes of the analysis. You can include additional arguments `low` and `high` to specify the minimum and maximum values to be included in the factor variable; RevoScaleR creates a bin for each integer value from the low to high values. You can use the logical flag `exclude` to specify whether values outside that range are omitted from the model (`exclude=TRUE`) or included as a separate level (`exclude=FALSE`).

Similarly, the special function syntax `N(x)` can be used to have RevoScaleR treat `x` as a continuous numeric variable. (This syntax is provided for completeness, but is not recommended. In general, if you want to recover numeric data from a factor, you will want to do so from the *levels* of the factor. We give several examples of this in Chapter 6, 7, and 11.)

In RevoScaleR, formulas in which the first independent variable is categorical may be handled specially, as *cubes*. See the following section for more details.

5.3 Letting the Data Speak For Itself

Classical statistics is largely concerned with fitting predictive models to limited observations. Data analysts and statisticians use exploratory techniques to visualize the data and then make informed guesses as to the appropriate form for a predictive model. Large data analysis, on the other hand, provides the opportunity to let the data speak for itself—with millions of observations in hand, we don't have to guess about the form of relationships between variables: they become clear. We will give several examples of this in the chapters that follow, but here's a general idea of how to find the relationship between two numeric variables x and y. First, bin the x values. Then, for each bin, plot the mean of the y values contained in that bin. As the bins become narrower and narrower, the resulting plot becomes a plot of E(y|x) for each value of x.

5.4 Cubes and Cube Regression

In RevoScaleR, a *cube* is a type of multi-dimensional array. It may have any number of dimensions, thus making it a hypercube, and each dimension consists of categorical data. The most common operation on a cube is simple cross-tabulation, computing the cell counts for every combination of levels within the cube; this is done using the `rxCube` function. But cubes can also be passed as the first independent variable in a linear or logistic regression, in which case the regression can be computed in a special way. Because the cube consists of categorical data, one part of the moment matrix is diagonal. This makes it possible to compute the regression using a partitioned inverse method, which may be faster and may use less memory than the usual regression method. When a linear or logistic regression is fitted with the argument `cube=TRUE` (and a categorical variable as the first predictor), the partitioned inverse method is used and the model is fitted without an intercept term. Because the first term in the regression is categorical, it is equivalent to a complete set of dummy variables and thus is collinear with a constant term. By dropping the intercept term, the collinearity is resolved and a coefficient can be computed for each level of the categorical predictor. The R-squared, however, is computed as if an intercept were included.

Chapter 6.

Data Summaries

In previous chapters, we've used the rxGetVarInfo and rxSummary functions to view summary information about data files and the data itself. In this chapter we explore the use of these functions in more detail, and also take a look at the rxLorenz function as a way of visually summarizing cumulative distributions of variables.

6.1 Using Variable Information

The rxGetVarInfo function returns a list containing information about each variable in a .xdf file. For numeric data, this information includes Low/High values. These Low/High values do not necessarily indicate the minimum and maximum of a numeric or integer variable. Rather, they indicate the values RevoScaleR uses to establish the lowest and highest factor levels when treating the variable as a factor. For practical purposes, this is what you will want—for example, if you want to create histograms or hexbin plots, you want to treat the numerical data as categorical, with levels corresponding to the plotting bins. It is often convenient to cut off the highest and lowest data points, and the Low/High information allows you to do this.

For example, consider again the census data we manipulated in Chapter 3.

```
#######################################################
# Chapter 6: Data Summaries
#  Using Variable Information
Ch6Start <- Sys.time()
```

```
readPath <- rxGetOption("sampleDataDir")
censusWorkers <- file.path(readPath, "CensusWorkers.xdf")
censusWorkerInfo <- rxGetVarInfo(censusWorkers)
names(censusWorkerInfo)
```

This returns the following:

```
[1] "age"      "incwage"  "perwt"    "sex"      "wkswork1" "state"
```

We then drill down to examine the age component:

```
names(censusWorkerInfo$age)
```

```
[1] "description" "varType"     "storage"     "low"         "high"
```

We obtain the High value as follows:

```
censusWorkerInfo$age$high
```

```
[1] 65
```

Similarly, the Low value is obtained as follows:

```
censusWorkerInfo$age$low
```

```
[1] 20
```

If we are interested in workers between the ages of 30 and 50, we could create a copy of the data file in the working directory, set the High/Low fields as follows and then treat age as a factor in our subsequent analysis:

```
outputDir <- rxGetOption("outDataPath")
tempCensusWorkers <- file.path(outputDir, "tempCensusWorkers.xdf")
file.copy(from = censusWorkers, to = tempCensusWorkers)
censusWorkerInfo$age$low <- 35
censusWorkerInfo$age$high <- 50
rxSetVarInfo(censusWorkerInfo, tempCensusWorkers)
rxSummary(~F(age), data = tempCensusWorkers)
```

The resulting output is restricted to the 35 to 50 age range:

```
Call:
rxSummary(formula = ~F(age), data = tempCensusWorkers)

Summary Statistics Results for: ~F(age)
File name:
    C:\YourOutDir\tempCensusWorkers.xdf
Number of valid observations: 351121


Category Counts for F_age
Number of categories: 16
Number of valid observations: 158309
Number of missing observations: 192812

 F_age Counts
```

```
35     9743
36     9888
37     9860
38    10211
39    10378
40    10756
41    10503
42    10511
43    10296
44    10122
45    10074
46     9703
47     9527
48     9093
49     8776
50     8868
```

To reset the low and high values, we use the same process with the original values:

```
censusWorkerInfo$age$low <- 20
censusWorkerInfo$age$high <- 65
rxSetVarInfo(censusWorkerInfo, "tempCensusWorkers.xdf")
```

6.2 Formulas for rxSummary

The *rxSummary* function provides descriptive statistics using a *formula* argument similar to that used in R's modeling functions. With one exception, the formula given to *rxSummary* may not contain a response variable, so that *rxSummary* is generally given a formula of the form "~ predictors." For example, returning to the CensusWorkers data file we used in Chapter 4, we can obtain a data summary of that file as follows:

```
# Formulas in rxSummary

readPath <- rxGetOption("sampleDataDir")
censusWorkers <- file.path(readPath, "CensusWorkers.xdf")
rxSummary(~ age + incwage + perwt + sex + wkswork1, data = censusWorkers)
```

This gives the following output:

```
Call:
rxSummary(formula = ~age + incwage + perwt + sex + wkswork1,
    data = censusWorkers)

Summary Statistics Results for: ~age + incwage + perwt + sex + wkswork1
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Number of valid observations: 351121

 Name     Mean         StdDev       Min Max    ValidObs MissingObs
 age         40.42814    11.385017 20      65 351121   0
 incwage  35333.83894 40444.544084  0  354000 351121   0
 perwt       20.34423     9.633100  2     168 351121   0
 wkswork1    48.62566     6.953843 21      52 351121   0

Category Counts for sex
Number of valid observations: 351121
Number of missing observations: 0
```

```
sex    Counts
Male   189344
Female 161777
```

For each term in the formula, the mean, standard deviation, minimum, maximum, and number of valid observations is shown. If *byTerm=FALSE*, observations (rows) containing missing values for any of the specified variables are omitted in calculating the summary. Cell counts for categorical variables are included.

6.3 Computation of Summary Statistics by Group Using Interactions

If you specify an interaction between a numeric variable and a factor variable, you obtain a summary of the numeric variable for each level of the factor. For example, using the sample data set AirlineDemoSmall.xdf, we can use the following command to ask for a summary of arrival delay by day of week:

```
rxSummary(~ ArrDelay:DayOfWeek, data = file.path(readPath,
    "AirlineDemoSmall.xdf"))
```

The request produces the following output:

```
Call:
rxSummary(formula = ~ArrDelay:DayOfWeek, data = file.path(readPath,
    "AirlineDemoSmall.xdf"))

Summary Statistics Results for: ~ArrDelay:DayOfWeek
File name: C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-3.2.2\library\
RevoScaleR\SampleData\AirlineDemoSmall.xdf
Number of valid observations: 6e+05

 Name               Mean     StdDev   Min Max  ValidObs MissingObs
 ArrDelay:DayOfWeek 11.31794 40.68854 -86 1490 582628   17372

Statistics by category (7 categories):

 Category                      DayOfWeek   Means     StdDev   Min Max  ValidObs
 ArrDelay for DayOfWeek=Monday    Monday    12.025604 40.02463 -76 1017 95298
 ArrDelay for DayOfWeek=Tuesday   Tuesday   11.293808 43.66269 -70 1143 74011
 ArrDelay for DayOfWeek=Wednesday Wednesday 10.156539 39.58803 -81 1166 76786
 ArrDelay for DayOfWeek=Thursday  Thursday   8.658007 36.74724 -58 1053 79145
 ArrDelay for DayOfWeek=Friday    Friday    14.804335 41.79260 -78 1490 80142
 ArrDelay for DayOfWeek=Saturday  Saturday  11.875326 45.24540 -73 1370 83851
 ArrDelay for DayOfWeek=Sunday    Sunday    10.331806 37.33348 -86 1202 93395
```

Interactions provide the one exception to the “responseless” formula mentioned above. If you want to obtain the interaction of a continuous variable with one or more factors, you can use a formula of the form y ~ x:z, where y is the continuous variable and x and z are factors. This has precisely the same effect as specifying the formula as ~y:x:z, but is more suggestive of the result—that is, summary statistics for y at every combination of levels of x and z.

6.4 On-the-Fly Factors in Formulas

You can force RevoScaleR to treat a variable as a factor (with a level for each integer value from the low to high value) by wrapping it with the function call syntax `F()`. Returning to the CensusWorkers.xdf file, in the following example a factor level will temporarily be created for each age from 20 through 65:

```
rxSummary(~ incwage:F(age), data = censusWorkers)
```

The results provide us not only summary statistics for wage income in the overall data set, but summary statistics on wage income for each age:

```
Call:
rxSummary(formula = ~incwage:F(age), data = censusWorkers)

Summary Statistics Results for: ~incwage:F(age)
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Number of valid observations: 351121

 Name           Mean     StdDev   Min Max    ValidObs MissingObs
 incwage:F(age) 35333.84 40444.54 0   354000 351121   0

Statistics by category (46 categories):

 Category              F_age Means    StdDev   Min Max    ValidObs
 incwage for F(age)=20 20    12669.94 12396.99 0   336000  6500
 incwage for F(age)=21 21    14114.23 12107.81 0   336000  6479
 incwage for F(age)=22 22    15982.00 12374.14 0   336000  6676
 incwage for F(age)=23 23    18503.92 15093.53 0   336000  6884
 incwage for F(age)=24 24    20672.06 14315.67 0   354000  6931
 incwage for F(age)=25 25    23856.25 17319.42 0   336000  7273
 incwage for F(age)=26 26    25938.17 20707.39 0   354000  7116
 incwage for F(age)=27 27    26902.97 20608.09 0   354000  7584
 incwage for F(age)=28 28    28531.59 24185.48 0   354000  8184
 incwage for F(age)=29 29    30153.10 25715.94 0   354000  8889
 incwage for F(age)=30 30    30691.10 26955.27 0   354000  9055
 incwage for F(age)=31 31    31647.06 27331.38 0   354000  8670
 incwage for F(age)=32 32    33459.31 33405.36 0   354000  8459
 incwage for F(age)=33 33    34208.33 33497.33 0   354000  8574
 incwage for F(age)=34 34    34364.06 33874.67 0   354000  9058
 incwage for F(age)=35 35    35739.92 36549.20 0   354000  9743
 incwage for F(age)=36 36    36945.24 40035.96 0   354000  9888
 incwage for F(age)=37 37    36970.63 39981.26 0   354000  9860
 incwage for F(age)=38 38    37331.39 39574.54 0   354000 10211
 incwage for F(age)=39 39    38899.67 44190.88 0   354000 10378
 incwage for F(age)=40 40    38279.34 42388.61 0   354000 10756
 incwage for F(age)=41 41    39678.52 45528.92 0   354000 10503
 incwage for F(age)=42 42    40748.10 46685.33 0   354000 10511
 incwage for F(age)=43 43    39910.90 45446.32 0   354000 10296
 incwage for F(age)=44 44    40524.19 46282.94 0   354000 10122
 incwage for F(age)=45 45    41450.27 47370.00 0   354000 10074
 incwage for F(age)=46 46    40521.07 44746.48 0   354000  9703
 incwage for F(age)=47 47    41371.40 45954.91 0   354000  9527
 incwage for F(age)=48 48    42061.04 47094.85 0   354000  9093
 incwage for F(age)=49 49    41618.36 45835.39 0   354000  8776
 incwage for F(age)=50 50    42789.36 48414.56 0   354000  8868
```

```
 incwage for F(age)=51 51    41912.11 46185.42 0   354000  8506
 incwage for F(age)=52 52    43169.23 49483.34 0   354000  8690
 incwage for F(age)=53 53    41864.13 46522.74 0   354000  8362
 incwage for F(age)=54 54    42920.45 50279.99 0   354000  6275
 incwage for F(age)=55 55    42939.81 50010.80 0   354000  6171
 incwage for F(age)=56 56    41157.10 48345.51 0   354000  5915
 incwage for F(age)=57 57    40984.69 48426.82 0   354000  5881
 incwage for F(age)=58 58    40553.04 50305.92 0   354000  5047
 incwage for F(age)=59 59    38738.45 46745.03 0   354000  4512
 incwage for F(age)=60 60    37200.02 46858.16 0   354000  3775
 incwage for F(age)=61 61    35978.18 44335.98 0   354000  3704
 incwage for F(age)=62 62    35000.53 46405.31 0   354000  3206
 incwage for F(age)=63 63    34098.00 45353.94 0   354000  2563
 incwage for F(age)=64 64    32964.57 46318.27 0   354000  2248
 incwage for F(age)=65 65    31698.98 51777.97 0   354000  1625
```

If you include an interaction between two factors, the summary provides cell counts for all combinations of levels of the factors. Since the census data has probability weights, we can use the *pweights* argument to get weighted counts:

```
rxSummary(~ sex:state, pweights = "perwt", data = censusWorkers)

 Call:
 rxSummary(formula = ~sex:state, data = censusWorkers, pweights = "perwt")

 Summary Statistics Results for: ~sex:state
 File name:
     C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
 3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
 Probability weights: perwt
 Number of valid observations: 351121


 Category Counts for sex
 Number of categories: 6

  sex    state       Counts
  Male   Connecticut  843736
  Female Connecticut  755843
  Male   Indiana     1517966
  Female Indiana     1289412
  Male   Washington  1504840
  Female Washington  1231489
```

It is also possible to perform on-the-fly row selections. In the example below, we restrict the analysis to people ages 30 to 39. We can use the *low* and *high* arguments of the *F* function to restrict the creation of on-the-fly factor levels to the same range (the fourth argument to *F*, *exclude*, defaults to TRUE; this is reflected in the T that appears in the output variable name):

```
rxSummary(~ sex:F(age, low = 30, high = 39), data = censusWorkers,
      pweights="perwt", rowSelection = age >= 30 & age < 40)

 Call:
 rxSummary(formula = ~sex:F(age, low = 30, high = 39), data = censusWorkers,
     pweights = "perwt", rowSelection = age >= 30 & age < 40)

 Summary Statistics Results for: ~sex:F(age, low = 30, high = 39)
 File name:
```

```
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Probability weights: perwt
Number of valid observations: 93896


Category Counts for sex
Number of categories: 20

 sex    F_age_30_39_T Counts
 Male   30            103242
 Female 30             84209
 Male   31            100234
 Female 31             77947
 Male   32             96325
 Female 32             75469
 Male   33             97734
 Female 33             77133
 Male   34            103380
 Female 34             81812
 Male   35            110358
 Female 35             89681
 Male   36            113444
 Female 36             91394
 Male   37            110828
 Female 37             91563
 Male   38            113838
 Female 38             95988
 Male   39            115552
 Female 39             97209
```

6.5 Writing By-Group Summary Statistics to an .xdf File

By-group statistics are often computed for further analysis or plotting. It can be convenient to store these results in an .xdf file, especially if there are a large number of groups. For example, let's compute the mean and standard deviation of wage income and number of weeks work for each year of age for both men and women using the CensusWorkers.xdf file with data from three states:

```
# Writing By-Group Summary Statistics to an .xdf File

readPath <- rxGetOption("sampleDataDir")
censusWorkers <- file.path(readPath, "CensusWorkers.xdf")
rxSummary(~ incwage:F(age):sex + wkswork1:F(age):sex, data = censusWorkers,
     byGroupOutFile = "ByAge.xdf",
     summaryStats = c("Mean", "StdDev", "SumOfWeights"),
     pweights = "perwt", overwrite = TRUE)
```

```
Call:
rxSummary(formula = ~incwage:F(age):sex + wkswork1:F(age):sex,
    data = censusWorkers, byGroupOutFile = "ByAge.xdf", summaryStats =
c("Mean",
        "StdDev", "SumOfWeights"), pweights = "perwt", overwrite = TRUE)

Summary Statistics Results for: ~incwage:F(age):sex +
    wkswork1:F(age):sex
File name:
```

```
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Probability weights: perwt
Number of valid observations: 351121

 Name               Mean       StdDev      SumOfWeights
 incwage:F_age:sex  35788.4675 40605.12565 7143286
 wkswork1:F_age:sex    48.6373     6.94423 7143286

By-group statistics for incwage:F(age):sex contained in C:\YourDir\ByAge.xdf
By-group statistics for wkswork1:F(age):sex contained in C:\YourDir\ByAge.xdf
```

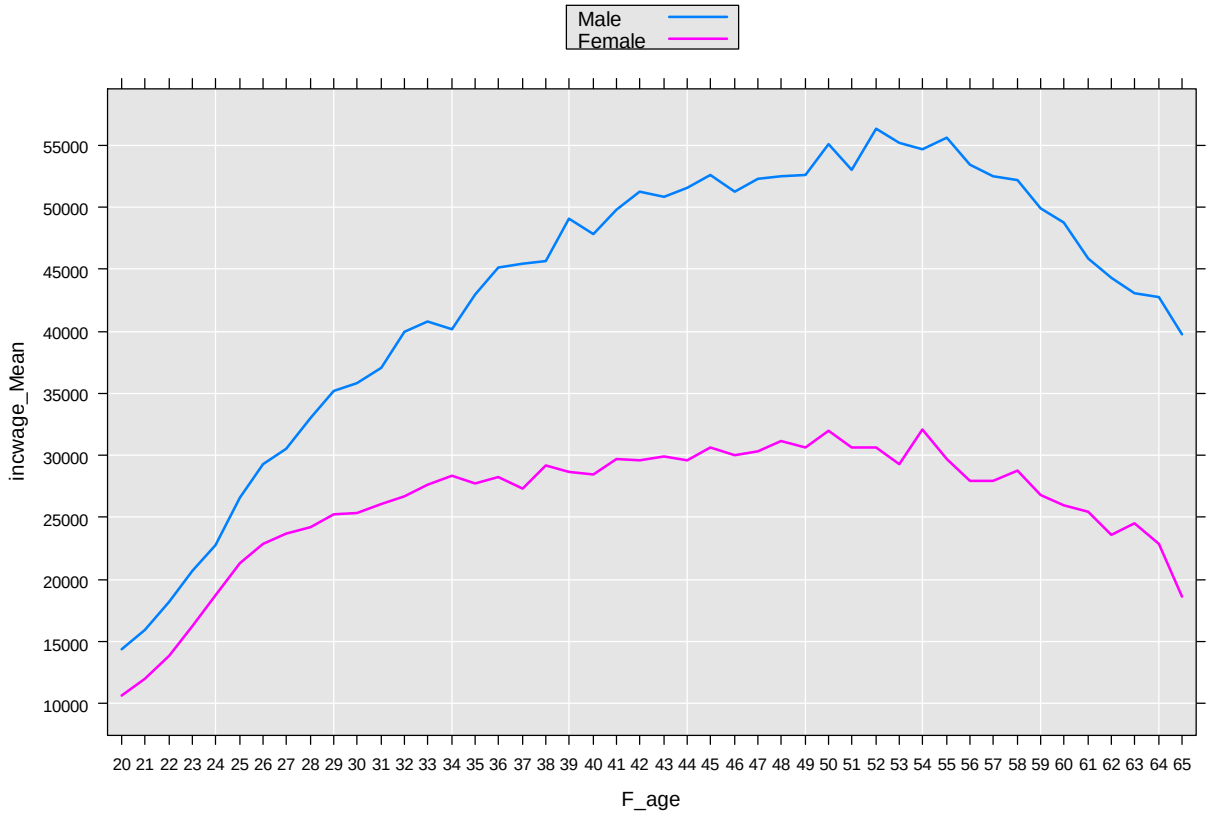
We can take a quick look at the first five rows in the data set to see that the first variables are the two factor variables determining the groups: F_age and sex. The remaining variables are the computed by-group statistics.

```
rxGetInfo("ByAge.xdf", numRows = 5)
```

```
File name: C:\YourDir\ByAge.xdf
Number of observations: 92
Number of variables: 8
Number of blocks: 1
Compression type: zlib
Data (5 rows starting with row 1):
  F_age  sex incwage_Mean incwage_StdDev incwage_SumOfWeights wkswork1_Mean
1    20 Male     14437.68       14118.49                71089      44.29758
2    21 Male     15981.48       13191.73                71150      45.27770
3    22 Male     18258.04       13919.44                75979      46.07166
4    23 Male     20739.91       16511.88                79663      46.75025
5    24 Male     22737.17       15345.41                81412      47.51487
  wkswork1_StdDev wkswork1_SumOfWeights
1        9.755092                 71089
2        9.110743                 71150
3        8.903617                 75979
4        8.451298                 79663
5        7.942226                 81412
```

We can plot directly from the .xdf file to visualize our results:

```
rxLinePlot(incwage_Mean~F_age, groups = sex, data = "ByAge.xdf")
```



6.6 Transforming Data in rxSummary

You can use the *transforms* argument to modify your data set on the fly before computing a summary. When used in this way, the original data is unmodified and no permanent copy of the modified data is written to disk. The data summaries returned, however, reflect the modified data.

You can also transform data in the formula itself, by specifying simple functions of the original variables. For example, you can get a summary based on the natural logarithm of a variable as follows :

```
#Transforming data in rxSummary

rxSummary(~ log(incwage), data = censusWorkers)
```

This gives the following output:

```
Call:
rxSummary(formula = ~log(incwage), data = censusWorkers)

Summary Statistics Results for: ~log(incwage)
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Number of valid observations: 351121
```

```
Name         Mean     StdDev    Min      Max      ValidObs MissingObs
log(incwage) 10.19694 0.8387598 1.386294 12.77705 331625   19496
```

6.7 Using rxGetVarInfo and rxSummary with Wide Data

The functions *rxGetVarInfo* and *rxSummary* provide useful information for summarizing your data set, but these two functions may need to be used differently when the data contain many variables. You will find that building a better understanding of the distribution of each variable and the relationships between variables will allow you to make better decisions during the modeling phase. This is especially important for wide data that may contain hundreds if not thousands of variables. The main goal for your data exploration should be to find any outliers or influential data points, identify redundant variables or correlated variables and transform or combine any variables that seem appropriate.

Once you have your data imported to .xdf, the data type information can easily be accessed using the *rxGetVarInfo* function. However, since wide data has so many variables, printed output can be hard to read. As an alternative, try saving your variable information to an object that can serve as in informal data dictionary. We demonstrate this using the claims data from Chapter 2:

```
# Using rxGetVarInfo and rxSummary with Wide Data

claimsWithColInfo <- "claimsWithColInfo.xdf"
claimsDataDictionary <- rxGetVarInfo(claimsWithColInfo)
```

We can then obtain the information for an individual variable as follows:

```
claimsDataDictionary$age
```

```
 [1] 8 factor levels: 17-20 21-24 25-29 30-34 35-39 40-49 50-59 60+
```

The rxSummary function is a great way to look at the distribution of individual variables and identify outliers. With wide data you will want to store the results of this function into an object. This object will then contain a data frame with the results of the numeric variables, “sDataFrame”, and a list of data frames with the counts for each categorical variable,”categorical”:

```
readPath <- rxGetOption("sampleDataDir")
censusWorkers <- file.path(readPath, "CensusWorkers.xdf")
censusSummary <- rxSummary(~ age + incwage + perwt + sex + wkswork1,
    data = censusWorkers)
names(censusSummary)
```

```
 [1] "nobs.valid"       "nobs.missing"     "sDataFrame"       "categorical"
 [5] "params"           "formula"          "call"             "categorical.type"
```

Printing the rxSummary results to the console wouldn't be very useful with so many variables. Saving the results in an object allows us to not only access the summary results programmatically, but also to view the results separately for numeric and categorical variables. We access the sDataFrame (printed to show structure) as follows:

```
censusSummary$sDataFrame
```

```
       Name         Mean        StdDev Min    Max ValidObs MissingObs
1       age     40.42814     11.385017  20     65   351121          0
2   incwage 35333.83894 40444.544084   0 354000   351121          0
3     perwt     20.34423      9.633100   2    168   351121          0
4       sex           NA            NA  NA     NA   351121          0
5 wkswork1     48.62566      6.953843  21     52   351121          0
```

To view the categorical variables, we access the categorical component:

```
censusSummary$categorical
```

```
[[1]]
     sex Counts
1   Male 189344
2 Female 161777
```

Another key piece of data exploration for wide data is looking at the relationships between variables to find variables that are measuring the same information or variables that are correlated. With variables that are measuring the same information perhaps one stands out as being representative of the group. During data exploration, you will want to use your domain knowledge to group variables into related sets or prioritize variables that are important based on the field or industry. Paring the data set down to related sets will allow you to look more closely at redundancy and relatedness within each set. When looking for correlation between variables the function *rxCrosstabs* is extremely useful. In Chapter 7 you will see how to use rxCrosstabs and rxLinePlot to graph the relationship between two variables. Graphs allow for a really quick view of the relationship between two variables, which may come in handy when you have many variables to consider.

6.8 Computing and Plotting Lorenz Curves

The Lorenz curves was originally developed to illustrate income inequality. For example, it can show us what percentage of total income is attributed to the lowest earning 10% of the population. The rxLorenz function provides a 'big data' version, using approximate quantiles to quickly compute the cumulative distribution by quantile in a single pass through the data.

The rxLorenz function requires an *orderVarName*, the name of the variable used to compute the quantiles. A separate *valueVarName* can also be specified. This is the name of the variable used to compute the mean values by quantile. By default, the same variable is used for both.

We can continue to use the Census Workers data set as an example, computing a Lorenz curve for the distribution of income:

```
lorenzOut <- rxLorenz(orderVarName = "incwage", data = censusWorkers,
     pweights = "perwt")
head(lorenzOut)
```

```
      cumVals  percents
 1 0.0000000  0.000000
 2 0.3642878  9.126934
 3 0.4005827  9.363072
 4 0.5368416 10.181295
 5 0.5666976 10.353428
 6 0.6241598 10.667766
```

The returned object contains the cumulative values and the percentages. Using the plot method for rxLorenz, we can get a visual representation of the income distribution and compare it with the horizontal line representing perfect equality:

```
plot(lorenzOut)
```

The Gini coefficient is often used as a summary statistic for Lorenz curves. It is computed by estimating the ratio of the area between the line of equality and the Lorenz curve to the total area under the line of equality (using trapezoidal integration). The Gini coefficient can range from 0 to 1, with 0 representing perfect equality. We can compute it from using the output from rxLorenz:

```
giniCoef <- rxGini(lorenzOut)
giniCoef
```

```
  [1] 0.4491421
```

Chapter 7.

Crosstabs

Crosstabs, also known as *contingency tables* or *crosstabulations*, are a convenient way to summarize cross-classified categorical data—that is, data that can be tabulated according to multiple levels of two or more factors. If only two factors are involved, the table is sometimes called a *two-way table*. If three factors are involved, the table is sometimes called a *three-way table*.

For large data sets, cross-tabulations of binned numeric data, that is, data which has been converted to a factor where the levels represent ranges of values, can be a very fast way to get insight into the relationships among variables. In RevoScaleR, the `rxCube` function is the primary tool to create contingency tables.

For example, the built-in data set `UCBAdmissions` includes information on admissions by gender to various departments at the University of California at Berkeley. We can look at the contingency table as follows:

```
#########################################################
# Chapter 7: Crosstabs
Ch7Start <- Sys.time()
```

```
UCBADF <- as.data.frame(UCBAdmissions)
z <- rxCube(Freq ~ Gender:Admit, data = UCBADF)
```

(Because cross-tabulations are explicitly about exploring interactions between variables, multiple predictors must always be specified using the interaction operator `":"`, and not the terms operator `"+"`.)

Typing `z` yields the following:

```
Call:
rxCube(formula = Freq ~ Gender:Admit, data = UCBADF)

Cube Results for: Freq ~ Gender:Admit
Data: UCBADF
Dependent variable(s): Freq
Number of valid observations: 24
Number of missing observations: 0
Statistic: Freq means

  Gender    Admit      Freq Counts
1   Male Admitted 199.66667      6
2 Female Admitted  92.83333      6
3   Male Rejected 248.83333      6
4 Female Rejected 213.00000      6
```

This data set is widely used in statistics texts because it illustrates Simpson's paradox, which is that in some cases a comparison that holds true in a number of groups is reversed when those groups are aggregated to form a single group. From the above table, in which admissions data is aggregated across all departments, it would appear that males are admitted at a higher rate than women. However, if we look at the more granular analysis by department, we find that in four of the six departments, women are admitted at a higher rate than men:

```
z2 <- rxCube(Freq ~ Gender:Admit:Dept, data = UCBADF)
z2
```

This yields the following output:

```
Call:
rxCube(formula = Freq ~ Gender:Admit:Dept, data = UCBADF)

Cube Results for: Freq ~ Gender:Admit:Dept
Data: UCBADF
Dependent variable(s): Freq
Number of valid observations: 24
Number of missing observations: 0
Statistic: Freq means

   Gender    Admit Dept Freq Counts
1    Male Admitted    A  512      1
2  Female Admitted    A   89      1
3    Male Rejected    A  313      1
4  Female Rejected    A   19      1
5    Male Admitted    B  353      1
6  Female Admitted    B   17      1
```

```
7    Male Rejected    B  207      1
8  Female Rejected    B    8      1
9    Male Admitted    C  120      1
10 Female Admitted    C  202      1
11   Male Rejected    C  205      1
12 Female Rejected    C  391      1
13   Male Admitted    D  138      1
14 Female Admitted    D  131      1
15   Male Rejected    D  279      1
16 Female Rejected    D  244      1
17   Male Admitted    E   53      1
18 Female Admitted    E   94      1
19   Male Rejected    E  138      1
20 Female Rejected    E  299      1
21   Male Admitted    F   22      1
22 Female Admitted    F   24      1
23   Male Rejected    F  351      1
24 Female Rejected    F  317      1
```

7.1 Letting the Data Speak Example 1: Analyzing U.S. 2000 Census Data

The CensusWorkers.xdf data set contains a subset of the U.S. 2000 5% Census for individuals aged 20 to 65 who worked at least 20 weeks during the year from three states. Let's examine the relationship between wage income (represented in the data set by the variable *incwage*) and age.

As we mentioned in Chapter 4, a useful way to observe the relationship between numeric variables is to bin the predictor variable (in our case, age), and then plot the mean of the response for each bin. The simplest way to bin age is to use the F() wrapper within our initial formula; it creates a separate bin for each distinct value of age. (More precisely, it creates a bin of length one from the low value of age to the high value of age—if some ages are missing in the original data set, bins are created for them anyway.)

We create our original model as follows:

```
#  Letting the data speak: Example 1

readPath <- rxGetOption("sampleDataDir")
censusWorkers <- file.path(readPath, "CensusWorkers.xdf")
censusWorkersCube <- rxCube(incwage ~ F(age), data=censusWorkers)
```

We first look at the results in tabular form by typing the returned object name, *censusWorkersCube*, which yields the following:

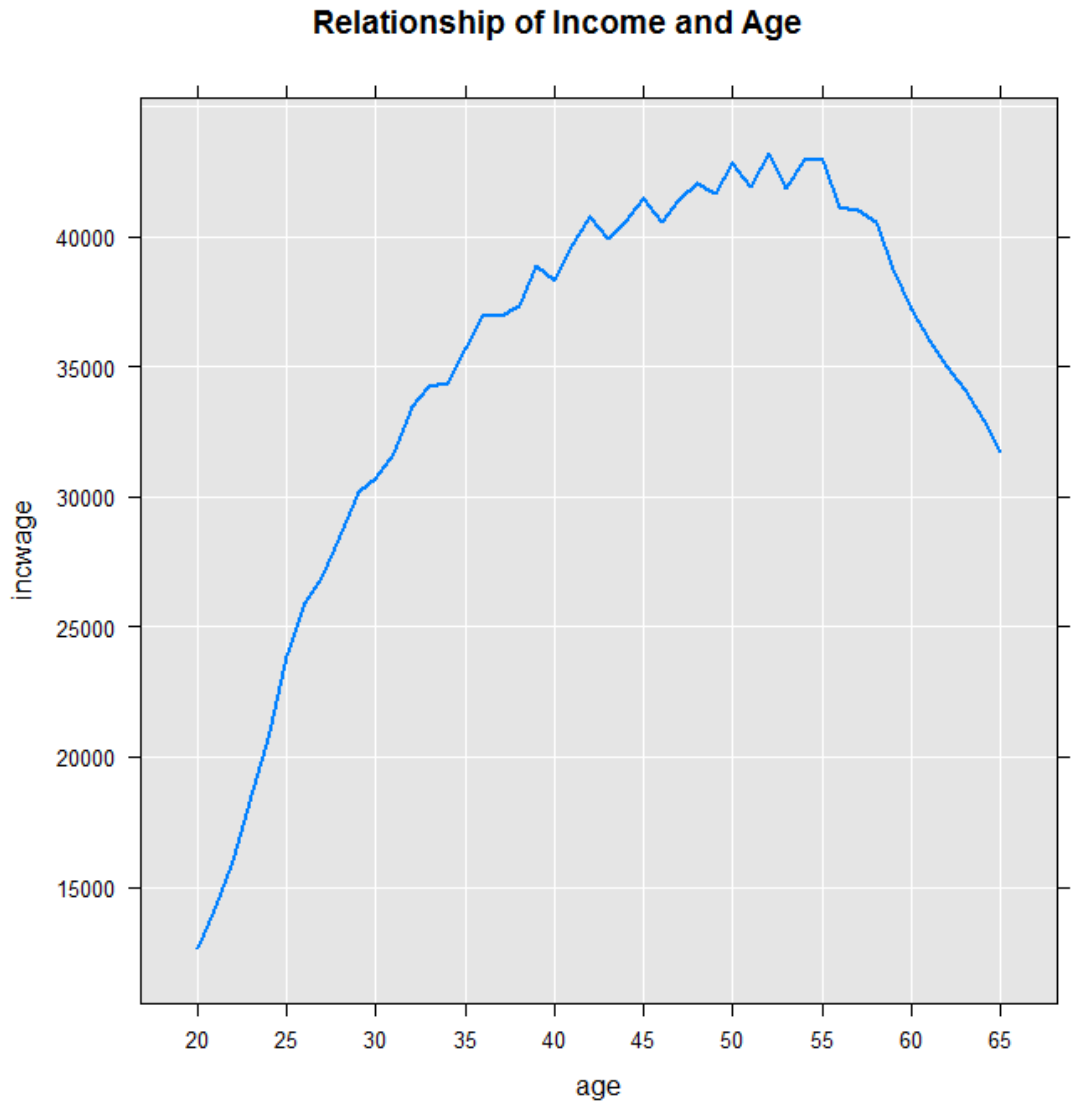
```
Call:
rxCube(formula = incwage ~ F(age), data = censusWorkers)

Cube Results for: incwage ~ F(age)
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Dependent variable(s): incwage
Number of valid observations: 351121
```

```
Number of missing observations: 0
Statistic: incwage means

   F_age incwage  Counts
1     20 12669.94   6500
2     21 14114.23   6479
3     22 15982.00   6676
4     23 18503.92   6884
5     24 20672.06   6931
6     25 23856.25   7273
7     26 25938.17   7116
8     27 26902.97   7584
9     28 28531.59   8184
10    29 30153.10   8889
11    30 30691.10   9055
12    31 31647.06   8670
13    32 33459.31   8459
14    33 34208.33   8574
15    34 34364.06   9058
16    35 35739.92   9743
17    36 36945.24   9888
18    37 36970.63   9860
19    38 37331.39  10211
20    39 38899.67  10378
21    40 38279.34  10756
22    41 39678.52  10503
23    42 40748.10  10511
24    43 39910.90  10296
25    44 40524.19  10122
26    45 41450.27  10074
27    46 40521.07   9703
28    47 41371.40   9527
29    48 42061.04   9093
30    49 41618.36   8776
31    50 42789.36   8868
32    51 41912.11   8506
33    52 43169.23   8690
34    53 41864.13   8362
35    54 42920.45   6275
36    55 42939.81   6171
37    56 41157.10   5915
38    57 40984.69   5881
39    58 40553.04   5047
40    59 38738.45   4512
41    60 37200.02   3775
42    61 35978.18   3704
43    62 35000.53   3206
44    63 34098.00   2563
45    64 32964.57   2248
46    65 31698.98   1625
```

As we wanted, the table contains average values of *incwage* for each level of *age*. If we want to create a plot of the results, we can use the *rxResultsDF* function to conveniently convert the output into a data frame. The *F_age* factor variable will automatically be converted back to an integer *age* variable. Then we can plot the data using *rxLinePlot*:

```
censusWorkersCubeDF <- rxResultsDF(censusWorkersCube)
rxLinePlot(incwage ~ age, data=censusWorkersCubeDF,
    title="Relationship of Income and Age")
```

The resulting plot shows clearly the relationship of income on age:



7.2 Transforming Data

Because crosstabs require categorical data for the predictors, you have to do some work to crosstabulate continuous data. In the previous section, we saw that the F() wrapper can do a simple transformation within a formula. The *transforms* argument to *rxCrossTabs* can be used to give you greater control over such transformations.

For example, the *kyphosis* data from the *rpart* package consists of one categorical variable, *Kyphosis*, and three continuous variables *Age*, *Number*, and *Start*. The *Start* variable indicates the topmost vertebra involved in a certain type of spinal surgery, and has a range of 1

to 18. Since there are 7 cervical vertebrae and 12 thoracic vertebrae, we can specify a transform that classifies the start variable as either cervical or thoracic as follows:

```
#  Transforming Data

cut(Start, breaks=c(0, 7.5, 19.5), labels=c("cervical", "thoracic"))
```

Similarly, we can create a factorized Age variable as follows (in the original data, age is given in months; with our set of breaks, we cut the data into ranges of years):

```
cut(Age, breaks=c(0, 12, 60, 119, 180, 220), labels=c("<1", "1-4",
    "5-9", "10-15", ">15"))
```

We can now crosstabulate the data using the above transforms and it is instructive to start by looking at the three two-way tables formed by tabulating Kyphosis with the three predictor variables:

```
library(rpart)
rxCube(~ Kyphosis:Age, data = kyphosis,
    transforms=list(Age = cut(Age, breaks=c(0, 12, 60, 119,
    180, 220), labels=c("<1", "1-4", "5-9", "10-15", ">15"))))
```

```
 Call:
 rxCube(formula = ~Kyphosis:Age, data = kyphosis, transforms = list(Age =
 cut(Age,
     breaks = c(0, 12, 60, 119, 180, 220), labels = c("<1", "1-4",
         "5-9", "10-15", ">15"))))

 Cube Results for: ~Kyphosis:Age
 Data: kyphosis
 Number of valid observations: 81
 Number of missing observations: 0

    Kyphosis   Age Counts
 1    absent    <1     13
 2   present    <1      0
 3    absent   1-4     13
 4   present   1-4      4
 5    absent   5-9     17
 6   present   5-9      6
 7    absent 10-15     19
 8   present 10-15      7
 9    absent   >15      2
 10  present   >15      0
```

```
rxCube(~ Kyphosis:F(Number), data = kyphosis)
```

```
 Call:
 rxCube(formula = ~Kyphosis:F(Number), data = kyphosis)

 Cube Results for: ~Kyphosis:F(Number)
 Data: kyphosis
 Number of valid observations: 81
 Number of missing observations: 0

    Kyphosis F_Number Counts
 1    absent        2     12
 2   present        2      0
```

```
 3    absent         3     19
 4   present         3      4
 5    absent         4     16
 6   present         4      2
 7    absent         5     12
 8   present         5      5
 9    absent         6      2
10   present         6      2
11    absent         7      2
12   present         7      3
13    absent         8      0
14   present         8      0
15    absent         9      1
16   present         9      0
17    absent        10      0
18   present        10      1
```

```
rxCube(~ Kyphosis:Start, data = kyphosis,
    transforms=list(Start = cut(Start, breaks=c(0, 7.5, 19.5),
    labels=c("cervical", "thoracic"))))
```

```
 Call:
 rxCube(formula = ~Kyphosis:Start, data = kyphosis, transforms = list(Start =
 cut(Start,
     breaks = c(0, 7.5, 19.5), labels = c("cervical", "thoracic"))))

 Cube Results for: ~Kyphosis:Start
 Data: kyphosis
 Number of valid observations: 81
 Number of missing observations: 0

   Kyphosis    Start Counts
 1   absent cervical      8
 2  present cervical      9
 3   absent thoracic     56
 4  present thoracic      8
```

From these, we see that the probability of the post-operative complication Kyphosis seems to be greater if the *Start* is a cervical vertebra and as more vertebrae are involved in the surgery. Similarly, it appears that the dependence on age is non-linear: it first increases with age, peaks in the range 5-9, and then decreases again.

7.3 Cross-Tabulation with rxCrossTabs

The *rxCrossTabs* function is an alternative to the *rxCube* function, which performs the same calculations, but displays its results in format similar to the standard R *xtabs* function. For some purposes, this format can be more informative than the matrix-like display of *rxCube*, and in some situations can be more compact as well.

As an example, consider again the admission data example:

```
#  Cross-Tabulation with rxCrossTabs

z3 <- rxCrossTabs(Freq ~ Gender:Admit:Dept, data = UCBADF)
```

```
z3

 Call:
 rxCrossTabs(formula = Freq ~ Gender:Admit:Dept, data = UCBADF)

 Cross Tabulation Results for: Freq ~ Gender:Admit:Dept
 Data: UCBADF
 Dependent variable(s): Freq
 Number of valid observations: 24
 Number of missing observations: 0
 Statistic: sums

 Freq, Dept = A (sums):
         Admit
 Gender   Admitted Rejected
   Male        512      313
   Female       89       19

 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

 Freq, Dept = B (sums):
         Admit
 Gender   Admitted Rejected
   Male        353      207
   Female       17        8

 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

 Freq, Dept = C (sums):
         Admit
 Gender   Admitted Rejected
   Male        120      205
   Female      202      391

 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

 Freq, Dept = D (sums):
         Admit
 Gender   Admitted Rejected
   Male        138      279
   Female      131      244

 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

 Freq, Dept = E (sums):
         Admit
 Gender   Admitted Rejected
   Male         53      138
   Female       94      299

 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

 Freq, Dept = F (sums):
         Admit
 Gender   Admitted Rejected
   Male         22      351
   Female       24      317
```

You can see the row, column, and total percentages by calling the summary function on the *rxCrossTabs* object:

```
summary(z3)
```

```
Call:
rxCrossTabs(formula = Freq ~ Gender:Admit:Dept, data = UCBADF)

Cross Tabulation Results for: Freq ~ Gender:Admit:Dept
Data: UCBADF
Dependent variable(s): Freq
Number of valid observations: 24
Number of missing observations: 0
Statistic: sums

Freq, Dept = A (sums):
             Admitted   Rejected Row Total
Male        512.000000 313.000000 825.00000
   Row%      62.060606  37.939394
   Col%      85.191348  94.277108
   Tot%      54.876742  33.547696  88.42444
Female       89.000000  19.000000 108.00000
   Row%      82.407407  17.592593
   Col%      14.808652   5.722892
   Tot%       9.539121   2.036442  11.57556
Col Total   601.000000 332.000000
Grand Total 933.000000

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Freq, Dept = B (sums):
             Admitted   Rejected  Row Total
Male        353.000000 207.000000 560.000000
   Row%      63.035714  36.964286
   Col%      95.405405  96.279070
   Tot%      60.341880  35.384615  95.726496
Female       17.000000   8.000000  25.000000
   Row%      68.000000  32.000000
   Col%       4.594595   3.720930
   Tot%       2.905983   1.367521   4.273504
Col Total   370.000000 215.000000
Grand Total 585.000000

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Freq, Dept = C (sums):
             Admitted  Rejected Row Total
Male        120.00000 205.00000 325.00000
   Row%      36.92308  63.07692
   Col%      37.26708  34.39597
   Tot%      13.07190  22.33115  35.40305
Female      202.00000 391.00000 593.00000
   Row%      34.06408  65.93592
   Col%      62.73292  65.60403
   Tot%      22.00436  42.59259  64.59695
Col Total   322.00000 596.00000
Grand Total 918.00000

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Freq, Dept = D (sums):
             Admitted  Rejected Row Total
Male        138.00000 279.00000 417.00000
   Row%      33.09353  66.90647
   Col%      51.30112  53.34608
   Tot%      17.42424  35.22727  52.65152
Female      131.00000 244.00000 375.00000
   Row%      34.93333  65.06667
```

```
   Col%       48.69888  46.65392
   Tot%       16.54040  30.80808  47.34848
Col Total    269.00000 523.00000
Grand Total  792.00000

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Freq, Dept = E (sums):
              Admitted  Rejected Row Total
Male          53.000000 138.00000 191.00000
   Row%       27.748691  72.25131
   Col%       36.054422  31.57895
   Tot%        9.075342  23.63014  32.70548
Female        94.000000 299.00000 393.00000
   Row%       23.918575  76.08142
   Col%       63.945578  68.42105
   Tot%       16.095890  51.19863  67.29452
Col Total    147.000000 437.00000
Grand Total  584.000000

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Freq, Dept = F (sums):
              Admitted  Rejected Row Total
Male          22.000000 351.00000  373.0000
   Row%        5.898123  94.10188
   Col%       47.826087  52.54491
   Tot%        3.081232  49.15966   52.2409
Female        24.000000 317.00000  341.0000
   Row%        7.038123  92.96188
   Col%       52.173913  47.45509
   Tot%        3.361345  44.39776   47.7591
Col Total     46.000000 668.00000
Grand Total  714.000000
```

You can see, for example, that in Department A, 62 percent of male applicants are admitted, but 82 percent of female applicants are admitted, and in Department B, 63 percent of male applicants are admitted, while 68 percent of female applicants are admitted.

7.4 A Large Data Example

The power of *rxCrossTabs* is most evident when you need to tabulate a data set that won't fit into memory. For example, in the large airline data set AirOnTime87to12.xdf, you can obtain the mean arrival delay by carrier and day of week as follows (if you have downloaded the data set, modify the first line below to reflect your local path):

```
#  A Large Data Example


bigDataDir <- "C:/MRS/Data"
bigAirData <- file.path(bigDataDir, "AirOnTime87to12/AirOnTime87to12.xdf")
arrDelayXT <- rxCrossTabs(ArrDelay ~ UniqueCarrier:DayOfWeek,
    data = bigAirData, blocksPerRead = 30)
print(arrDelayXT)
```

This gives the following output:

```
Call:
rxCrossTabs(formula = ArrDelay ~ UniqueCarrier:DayOfWeek, data = bigAirData,
    blocksPerRead = 30)

Cross Tabulation Results for: ArrDelay ~ UniqueCarrier:DayOfWeek
File name: C:\MRS\Data\AirOnTime87to12\AirOnTime87to12.xdf
Dependent variable(s): ArrDelay
Number of valid observations: 145576737
Number of missing observations: 3042918
Statistic: sums

ArrDelay (sums):
             DayOfWeek
UniqueCarrier      Mon     Tues      Wed     Thur      Fri      Sat      Sun
       AA     15956852 13367087 16498840 20554660 20714146  9359729 14577582
       US     11797366 11688903 14065606 17379113 19541862  5865427 10264583
       AS      3144578  2677858  3182356  3980209  4415144  2433581  3039129
       CO      8464507  7966834  9537366 11901028 11749616  3553719  6562487
       DL     18146092 15962559 19474389 24077435 24933864 10483280 16414060
       EA       782103   832332   796811  1152825  1405399   638911   670924
       HP      3577460  3170343  3700890  4734543  5015896  2864314  3985741
       NW      7750970  7818040  9256994 11199718 10294116  3726129  6504924
       PA (1)   191137   235924   225260   290844   345238   174284   229677
       PI      1164688  1391526  1456173  1515403  1568266   939820   986642
       PS        88144   111282   122520   133567   173422    44362    88891
       TW      3356944  3459185  4060151  5027427  5267750  1669048  2377671
       UA     15941096 14731587 17801128 21060697 20920843  9174567 13688577
       WN     12438738  8978339 12215989 21556781 26787623  4972506 15973176
       ML (1)    20735    50927    55881    75030    62855    44549    18173
       KH        20744   -26425   -24265    30078    98529    33595    43026
       MQ      7065052  5152746  5893882  7136735  8087443  2947023  5540099
       B6      1886261  1340744  1736450  2373151  2930423  1012698  1969546
       DH       795614   527649   708129   801968   986930   227907   504644
       EV      5733212  3684210  4005374  5262924  5874647  1753361  4418290
       FL      2666677  1694294  1810548  2928247  3068538   819827  2188420
       OO      4717107  3106319  3438056  4725854  5481441  2797745  4764041
       XE      4870453  3904752  4532069  5349375  5315818  1636826  3531446
       TZ       228508   147963   197371   224693   275340    39722   148940
       HA       -72468   -92714   -66578     4840   153830    -2082   -22196
       OH      2276399  1567510  1830571  2336032  2702519   922531  1659708
       F9       551932   484426   566122   858027   729273   337695   526887
       YV      1959906  1419073  1463954  1930992  2152270  1270104  1830749
       9E       787776   579608   590038   709161   869358   304151   586378
       VX        10208    37079    12956    42661    73457     2943    39987
```

7.5 Using Sparse Cubes

An additional tool that may be useful when using *rxCube* and *rxCrossTabs* with large data is the *useSparseCube* parameter. Compiling cross-tabulations of categorical data can sometimes result in a large number of cells with zero counts, yielding at its core a "sparse matrix". In the usual case, memory is allocated for every cell in the cube, but for large cubes this may overwhelm memory resources. If we instead allocate space only for cells with positive counts, such operations may often proceed successfully.

As an example, let's look at the airline data again and construct a case where the cross-tabulation yields many zero entries. As the overwhelming number of flights in the data set were not cancelled, by appending the *Cancelled* predictor in the formula, we would expect a

large number of categorical predictor combinations to have zero observations. Note that because the *Cancelled* predictor is a logical rather than a factor variable, we need to use the *F(.)* function to convert it.

```
bigDataDir <- "C:/MRS/Data"
bigAirData <- file.path(bigDataDir, "AirOnTime87to12/AirOnTime87to12.xdf")

arrDelaySparse <- rxCube(ArrDelay ~ UniqueCarrier:DayOfWeek:F(Cancelled),
                         data = bigAirData, blocksPerRead = 30, useSparseCube = TRUE)
print(arrDelaySparse)
```

This gives the following output. Note that we get 210 rows with F_Cancelled = 0. By default, if *useSparseCube=TRUE*, rows with zero counts are removed from the result.

```
Call:
rxCube(formula = ArrDelay ~ UniqueCarrier:DayOfWeek:F(Cancelled),
   data = bigAirData, useSparseCube = TRUE, blocksPerRead = 30)

Cube Results for: ArrDelay ~ UniqueCarrier:DayOfWeek:F(Cancelled)
File name: C:/data/AirOnTime87to12/AirOnTime87to12.xdf
Dependent variable(s): ArrDelay
Number of valid observations: 145576737
Number of missing observations: 3042918
Statistic: ArrDelay means
   UniqueCarrier DayOfWeek F_Cancelled ArrDelay    Counts
1   AA            Mon       0            6.54609466 2437614
2   US            Mon       0            5.20151371 2268064
3   AS            Mon       0            6.37231471  493475
4   CO            Mon       0            6.49381077 1303473
5   DL            Mon       0            6.63422763 2735223
6   EA            Mon       0            6.13500730  127482
7   HP            Mon       0            6.85447467  521916
8   NW            Mon       0            5.09910096 1520066
9   PA (1)        Mon       0            4.24550765   45021
10  PI            Mon       0            9.32556128  124892
11  PS            Mon       0            7.11355016   12391
12  TW            Mon       0            6.21971889  539726
13  UA            Mon       0            7.51524443 2121168
14  WN            Mon       0            4.11051602 3026077
15  ML (1)        Mon       0            2.05724774   10079
… [rows omitted] …
201 FL            Sun       0            6.91461396  316492
202 OO            Sun       0            6.30954516  755053
203 XE            Sun       0            7.72464706  457166
204 TZ            Sun       0            5.19715263   28658
205 HA            Sun       0           -0.28030915   79184
206 OH            Sun       0            7.12036827  233093
207 F9            Sun       0            5.61844996   93778
208 YV            Sun       0            8.35988986  218992
209 9E            Sun       0            4.18506623  140112
210 VX            Sun       0            5.06036446    7902
```

While this particular example will likely run successfully to completion even on a minimally equipped modern computer without setting the *useSparseCube* flag to *TRUE*, it illustrates how one can quickly start to see the number of zero entries accumulate in an *rxCube*

computation. With larger data sets and a larger number of categorical variable combinations, however, this setting may allow computations of cubes that would not otherwise fit in memory.

For the *rxCrossTabs* function, the *useSparseCube* option works exactly the same internally. However, because *rxCrossTabs* always returns a table, it may require more memory to format its result than *rxCube*. If you have an extremely large contingency table, we recommend *rxCube* with *useSparseCube=TRUE* for the greatest chance of completing the computation. The *useSparseCube* flag may also be used with *rxSummary*.

7.6 Tests of Independence on Cross-Tabulated Data

One common use of contingency tables is to test whether the tabulated variables are independent. RevoScaleR includes several tests of independence, all of which expect data in the standard R *xtabs* format. You can get data in this format from the *rxCrossTabs* function by using the argument *returnXtabs=TRUE*:

```
#  Tests of Independence on Cross-Tabulated Data


bigDataDir <- "C:/MRS/Data"
bigAirData <- file.path(bigDataDir, "AirOnTime87to12/AirOnTime87to12.xdf")
arrDelayXTab <- rxCrossTabs(ArrDel15~ UniqueCarrier:DayOfWeek,
    data = bigAirData, blocksPerRead = 30, returnXtabs=TRUE)
```

You can then use this as input to any of the following functions:

- *rxChiSquaredTest*: performs Pearson's chi-squared test of independence.
- *rxFisherTest*: performs Fisher's exact test of independence.
- *rxKendallCor*: performs a Kendall tau test of independence. There are three flavors of test, a, b, and c; by default, the b flavor, which accounts for ties, is used.

(In fact, regular *rxCrossTabs* or *rxCube* output can be used as input to these functions, but they will be converted to *xtabs* format first, so it is generally somewhat more efficient to have *rxCrossTabs* return the *xtabs* format directly.)

Here we use the *arrDelayXTab* data created above and perform a Pearson's chi-squared test of independence on it:

```
rxChiSquaredTest(arrDelayXTab)
```

This gives the following output:

```
Chi-squared test of independence between UniqueCarrier and DayOfWeek
 X-squared  df p-value
  105645.8 174       0
```

For large contingency tables such as this one, the chi-squared test is the tool of choice. For smaller tables, particularly those with cells with expected counts fewer than five, Fisher's exact test is useful. On a large table, however, Fisher's exact test may not be an option. For example, if we try it on our airline table, it returns an error:

```
rxFisherTest(arrDelayXTab)
```

```
 Error in FUN(tbl[, , i], ...) : FEXACT error 40.
 Out of workspace.
```

To show the Fisher test, we return to the admissions data from the beginning of the chapter. This time we use *rxCrossTabs* to return an *xtabs* object:

```
UCBADF <- as.data.frame(UCBAdmissions)
admissCTabs <- rxCrossTabs(Freq ~ Gender:Admit, data = UCBADF,
    returnXtabs=TRUE)
```

We then call *rxFisherTest* on the resulting table:

```
rxFisherTest(admissCTabs)
```

```
 Fisher's Exact Test for Count Data
  estimate 1 95% CI Lower 95% CI Upper      p-value
    1.840856     1.621356     2.091246 4.835903e-22
    HA: two.sided
    H0:  odds ratio = 1
```

The chi-squared test works equally well on this example:

```
rxChiSquaredTest(admissCTabs)
```

```
 Chi-squared test of independence between Gender and Admit
  X-squared df      p-value
    91.6096  1 1.055797e-21
```

In both cases, we are given indisputable evidence of the independence of our two predictor factors. For this example, we could have just as easily used the standard R functions *chisq.test* and *fisher.test*. The RevoScaleR enhancements, however, permit *rxChisSquaredTest* and *rxFisherTest* to work on *xtabs* objects with multiple tables. For example, if we expand our examination of the admissions data to include the department info, we obtain a multi-way contingency table:

```
admissCTabs2 <- rxCrossTabs(Freq ~ Gender:Admit:Dept, data = UCBADF,
    returnXtabs=TRUE)
```

The chi-squared and Fisher's exact test results are shown below; notice that they provide a test of independence between Gender and Admit for each level of Dept:

```
rxChiSquaredTest(admissCTabs2)
```

```
 Chi-squared test of independence between Gender and Admit
           X-squared df      p-value
 Dept==A 16.37177373  1 5.205468e-05
```

```
 Dept==B  0.08509801  1 7.705041e-01
 Dept==C  0.63322380  1 4.261753e-01
 Dept==D  0.22159370  1 6.378283e-01
 Dept==E  0.80804765  1 3.686981e-01
 Dept==F  0.21824336  1 6.403817e-01
```

```
rxFisherTest(admissCTabs2)
```

```
 Fisher's Exact Test for Count Data
        odds ratio 95% CI Lower 95% CI Upper      p-value
 Dept==A  0.3495628    0.1970420    0.5920417 1.669189e-05
 Dept==B  0.8028124    0.2944986    2.0040231 6.770899e-01
 Dept==C  1.1329004    0.8452173    1.5162918 3.866166e-01
 Dept==D  0.9213798    0.6789572    1.2504742 5.994965e-01
 Dept==E  1.2211852    0.8064776    1.8385155 3.603964e-01
 Dept==F  0.8280944    0.4332888    1.5756278 5.458408e-01
    HA: two.sided
    H0:  odds ratio = 1
```

Like Fisher's exact test, the Kendall tau correlation test works best on smaller contingency tables. Here is an example of what it returns when applied to our admissions data (the results will differ from run to run as the underlying algorithm relies on sampling):

```
rxKendallCor(admissCTabs2)
```

```
               taub p-value
 Dept==A -0.13596550   0.000
 Dept==B -0.02082575   0.666
 Dept==C  0.02865045   0.380
 Dept==D -0.01939676   0.585
 Dept==E  0.04140240   0.383
 Dept==F -0.02319366   0.530
    HA: two.sided
```

7.7 Odds Ratios and Risk Ratios

Another common task associated with 2 x 2 contingency tables is the calculation of odds ratios and risk ratios (also known as relative risk). The two functions *rxOddsRatio* and *rxRiskRatio* in RevoScaleR can be used to compute these quantities. The odds ratio and the risk ratio are closely related: the odds ratio computes the relative odds of an event among two or more groups, while the risk ratio computes the relative probabilities of an event. Consider again the contingency table *admissCTabs*:

```
#  Odds Ratios and Risk Ratios
```

```
admissCTabs
```

```
         Admit
 Gender   Admitted Rejected
   Male       1198     1493
   Female      557     1278
```

In this example, the odds of being admitted as a male are 1198/1493, or about 4 to 5 against. The odds of being admitted as a female are 557/1278, or about 4 to 9 against. The odds ratio is (1198/1493)/(557/1278), or 1.8 greater odds that a male will be admitted as opposed to a woman.

```
rxOddsRatio(admissCTabs)
```

```
 data:
 Z = 0.6104, p-value < 2.2e-16
 alternative hypothesis: two.sided
 95 percent confidence interval:
  1.624377 2.086693
 sample estimates:
 oddsRatio
   1.84108
```

The risk ratio, by contrast, compares the probabilities of being *rejected*, that is, 1493/(1198+1493) for a man versus 1278/(557+1278) for a woman. So here the risk ratio is 0.697 (the probability of a woman being rejected) divided by 0.555 (the probability of a man being rejected), or 1.255:

```
rxRiskRatio(admissCTabs)
```

```
 data:
 Z.Female = 0.2274, p-value < 2.2e-16
 alternative hypothesis: two.sided
 95 percent confidence interval:
  1.199631 1.313560
 sample estimates:
 riskRatio.Female
         1.255303
```

Chapter 8.

Fitting Linear Models

Linear regression models are fitted in RevoScaleR using the *rxLinMod* function. Like other RevoScaleR functions, *rxLinMod* uses an updating algorithm to compute the regression model. The R object returned by *rxLinMod* includes the estimated model coefficients and the call used to generate the model, together with other information that allows RevoScaleR to recompute the model—because *rxLinMod* is designed to work with arbitrarily large data sets, quantities such as residuals and fitted values are not included in the return object, although these can be obtained easily once the model has been fitted.

As a simple example, let's use the sample data set AirlineDemoSmall.xdf and fit the arrival delay by day of week:

```
##########################################################
# Chapter 8: Fitting Linear Models
Ch8Start <- Sys.time()


readPath <- rxGetOption("sampleDataDir")
airlineDemoSmall <- file.path(readPath, "AirlineDemoSmall.xdf")
rxLinMod(ArrDelay ~ DayOfWeek, data = airlineDemoSmall)

 Call:
 rxLinMod(formula = ArrDelay ~ DayOfWeek, data = airlineDemoSmall)
```

```
Linear Regression Results for: ArrDelay ~ DayOfWeek
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-3.2.2\library\
RevoScaleR\SampleData\AirlineDemoSmall.xdf
Dependent variable(s): ArrDelay
Total independent variables: 8 (Including number dropped: 1)
Number of valid observations: 582628
Number of missing observations: 17372

Coefficients:
                    ArrDelay
(Intercept)         10.3318058
DayOfWeek=Monday     1.6937981
DayOfWeek=Tuesday    0.9620019
DayOfWeek=Wednesday -0.1752668
DayOfWeek=Thursday  -1.6737983
DayOfWeek=Friday     4.4725290
DayOfWeek=Saturday   1.5435207
DayOfWeek=Sunday       Dropped
```

Because our predictor is categorical, we can use the *cube* argument to *rxLinMod* to perform the regression using a partitioned inverse, which may be faster and may use less memory than the standard algorithm. The output object also includes a data frame with the averages or counts for each category:

```
arrDelayLm1 <- rxLinMod(ArrDelay ~ DayOfWeek, cube = TRUE,
    data = airlineDemoSmall)
```

Typing the name of the object arrDelayLm1 yields the following output:

```
Call:
rxLinMod(formula = ArrDelay ~ DayOfWeek, data = airlineDemoSmall,
    cube = TRUE)

Cube Linear Regression Results for: ArrDelay ~ DayOfWeek
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-3.2.2\library\
RevoScaleR\SampleData\AirlineDemoSmall.xdf
Dependent variable(s): ArrDelay
Total independent variables: 7
Number of valid observations: 582628
Number of missing observations: 17372

Coefficients:
                   ArrDelay
DayOfWeek=Monday    12.025604
DayOfWeek=Tuesday   11.293808
DayOfWeek=Wednesday 10.156539
DayOfWeek=Thursday   8.658007
DayOfWeek=Friday    14.804335
DayOfWeek=Saturday  11.875326
DayOfWeek=Sunday    10.331806
```

8.1 Obtaining a Summary of the Model

The print method for the rxLinMod model object shows only the call and the coefficients. You can obtain more information about the model by calling the summary method:

```
#  Obtaining a Summary of a Model

summary(arrDelayLm1)
```

This produces the following output, which includes substantially more information about the model coefficients, together with the residual standard error, multiple R-squared, and adjusted R-squared:

```
Call:
rxLinMod(formula = ArrDelay ~ DayOfWeek, data = airlineDemoSmall,
    cube = TRUE)

Cube Linear Regression Results for: ArrDelay ~ DayOfWeek
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-3.2.2\library\
RevoScaleR\SampleData\AirlineDemoSmall.xdf
Dependent variable(s): ArrDelay
Total independent variables: 7
Number of valid observations: 582628
Number of missing observations: 17372

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)     | Counts
DayOfWeek=Monday     12.0256     0.1317   91.32 2.22e-16 *** |  95298
DayOfWeek=Tuesday    11.2938     0.1494   75.58 2.22e-16 *** |  74011
DayOfWeek=Wednesday  10.1565     0.1467   69.23 2.22e-16 *** |  76786
DayOfWeek=Thursday    8.6580     0.1445   59.92 2.22e-16 *** |  79145
DayOfWeek=Friday     14.8043     0.1436  103.10 2.22e-16 *** |  80142
DayOfWeek=Saturday   11.8753     0.1404   84.59 2.22e-16 *** |  83851
DayOfWeek=Sunday     10.3318     0.1330   77.67 2.22e-16 *** |  93395
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 40.65 on 582621 degrees of freedom
Multiple R-squared: 0.001869 (as if intercept included)
Adjusted R-squared: 0.001858
F-statistic: 181.8 on 6 and 582621 DF,  p-value: < 2.2e-16
Condition number: 1
```

8.2 Using Probability Weights

Probability weights are common in survey data; they represent the probability that a case was selected into the sample from the population, and are calculated as the inverse of the sampling fraction. The variable *perwt* in the census data represents a probability weight. You pass probability weights to the RevoScaleR analysis functions using the *pweights* argument, as in the following example:

```
#  Using Probability Weights

rxLinMod(incwage ~ F(age), pweights = "perwt", data = censusWorkers)
```

This yields the following output:

```
Call:
```

```
rxLinMod(formula = incwage ~ F(age), data = censusWorkers, pweights = "perwt")

Linear Regression Results for: incwage ~ F(age)
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Probability weights: perwt
Dependent variable(s): incwage
Total independent variables: 47 (Including number dropped: 1)
Number of valid observations: 351121
Number of missing observations: 0

Coefficients:
               incwage
(Intercept)  32111.3012
F_age=20    -19488.0874
F_age=21    -18043.7738
F_age=22    -15928.5538
F_age=23    -13498.2138
F_age=24    -11248.8583
F_age=25     -7948.6603
F_age=26     -5667.3599
F_age=27     -4682.8375
F_age=28     -3024.1648
F_age=29     -1480.8682
F_age=30      -971.4461
F_age=31       143.5648
F_age=32      2009.0019
F_age=33      2861.3031
F_age=34      2797.9986
F_age=35      4038.2131
F_age=36      5511.8633
F_age=37      5148.1841
F_age=38      5957.2190
F_age=39      7652.9870
F_age=40      6969.9630
F_age=41      8387.6821
F_age=42      9150.0006
F_age=43      8936.7590
F_age=44      9267.0820
F_age=45     10148.1702
F_age=46      9099.0659
F_age=47      9996.0450
F_age=48     10408.1712
F_age=49     10281.1324
F_age=50     12029.6751
F_age=51     10247.2529
F_age=52     12105.0654
F_age=53     10957.8211
F_age=54     11881.4307
F_age=55     11490.8457
F_age=56      9442.3856
F_age=57      9331.2347
F_age=58      9353.1980
F_age=59      7526.4912
F_age=60      6078.4463
F_age=61      4636.6756
F_age=62      3129.5531
F_age=63      2535.4858
F_age=64      1520.3707
F_age=65        Dropped
```

8.3 Using Frequency Weights

Frequency weights are useful when your data has a particular form: a set of data in which one or more cases is exactly replicated. If you then compact the data to remove duplicated observations and create a variable to store the number of replications of each observation, you can use that new variable as a frequency weights variable in the RevoScaleR analysis functions.

For example, the sample data set fourthgraders.xdf contains the following 44 rows:

```
   height eyecolor   male reps
14     44     Blue   Male    1
23     44    Brown   Male    3
9      44    Brown Female    1
38     44    Green Female    1
8      45     Blue   Male    1
31     45     Blue Female    5
2      45    Brown   Male    2
51     45    Brown Female    1
6      45    Green   Male    1
47     45    Hazel Female    1
37     46     Blue   Male    1
21     46     Blue Female    3
12     46    Brown   Male    2
5      46    Brown Female    4
19     46    Green   Male    1
80     46    Green Female    3
64     47     Blue   Male    1
69     47     Blue Female    3
39     47    Brown   Male    4
18     47    Brown Female    3
41     47    Green   Male    2
7      47    Green Female    4
26     47    Hazel   Male    3
17     48     Blue   Male    4
36     48     Blue Female    3
13     48    Brown   Male    6
62     48    Brown Female    4
61     48    Green Female    2
56     48    Hazel   Male    1
10     49     Blue   Male    1
15     49     Blue Female    5
22     49    Brown   Male    2
4      49    Brown Female    5
3      49    Green   Male    3
91     49    Green Female    1
94     50     Blue   Male    1
96     50     Blue Female    1
97     50    Brown   Male    1
1      50    Brown Female    1
28     50    Green   Male    4
52     50    Hazel   Male    1
98     51     Blue   Male    1
57     51    Brown Female    1
90     51    Green Female    1
```

The *reps* column shows the number of replications for each observation; the sum of the reps column indicates the total number of observations, in this case 100. We can fit a model (admittedly not very useful) of height on eye color with *rxLinMod* as follows:

```
#  Using Frequency Weights

fourthgraders <- file.path(rxGetOption("sampleDataDir"),
    "fourthgraders.xdf")
fourthgradersLm <- rxLinMod(height ~ eyecolor, data = fourthgraders,
    fweights="reps")
```

Typing the name of the object shows the following output:

```
Call:
rxLinMod(formula = height ~ eyecolor, data = fourthgraders, fweights = "reps")

Linear Regression Results for: height ~ eyecolor
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\fourthgraders.xdf
Linear Regression Results for: height ~ eyecolor
Frequency weights: reps
Dependent variable(s): height
Total independent variables: 5 (Including number dropped: 1)
Number of valid observations: 44
Number of missing observations: 0

Coefficients:
                  height
(Intercept)    47.33333333
eyecolor=Blue  -0.01075269
eyecolor=Brown -0.08333333
eyecolor=Green  0.40579710
eyecolor=Hazel     Dropped
```

8.4 Using rxLinMod with R Data Frames

While RevoScaleR is primarily designed to work with data on disk, it can also be used with in-memory R data frames. As an example, consider the R sample data frame “cars”, which contains data recorded in the 1920s on the speed of cars and the distances taken to stop.

```
#  Using rxLinMod with R Data Frames

rxLinMod(dist ~ speed, data = cars)
```

We get the following output (which matches the output given by the R function lm):

```
Call:
rxLinMod(formula = dist ~ speed, data = cars)

Linear Regression Results for: dist ~ speed
Data: cars
Dependent variable(s): dist
Total independent variables: 2
Number of valid observations: 50
```

```
Number of missing observations: 0

Coefficients:
                  dist
(Intercept) -17.579095
speed         3.932409
```

8.5 Using the Cube Option for Conditional Predictions

If the cube argument is set to TRUE and the first term of the independent variables is categorical, *rxLinMod* will compute and return a data frame with category counts. If there are no other independent variables, or if the *cubePredictions* argument is set to TRUE, the data frame will also contain predicted values. Let's create a simple data frame to illustrate:

```
#  Using the Cube Option for Conditional Predictions

xfac1 <- factor(c(1,1,1,1,2,2,2,2,3,3,3,3), labels=c("One1", "Two1", "Three1"))
xfac2 <- factor(c(1,1,1,1,1,1,2,2,2,3,3,3), labels=c("One2", "Two2", "Three2"))
set.seed(100)
y <- as.integer(xfac1) + as.integer(xfac2)* 2 + rnorm(12)
myData <- data.frame(y, xfac1, xfac2)
```

If we estimate a simple linear regression of y on xfac1, the coefficients are equal to the within-group means:

```
myLinMod <- rxLinMod(y ~ xfac1, data = myData, cube = TRUE)
myLinMod

 Call:
 rxLinMod(formula = y ~ xfac1, data = myData, cube = TRUE)

 Cube Linear Regression Results for: y ~ xfac1
 Data: myData
 Dependent variable(s): y
 Total independent variables: 3
 Number of valid observations: 12
 Number of missing observations: 0

 Coefficients:
                      y
 xfac1=One1   3.109302
 xfac1=Two1   5.142086
 xfac1=Three1 8.250260
```

In addition to the standard output, the returned object contains a *countDF* data frame with information on within-group means and counts in each category. In this simple case the within-group means are the same as the coefficients:

```
myLinMod$countDF

    xfac1        y Counts
 1   One1 3.109302      4
 2   Two1 5.142086      4
 3 Three1 8.250260      4
```

Using *rxLinMod* with the cube option also allows us to compute conditional within-group means. For example:

```
myLinMod1 <- rxLinMod(y~xfac1 + xfac2, data = myData,
    cube = TRUE, cubePredictions = TRUE)
myLinMod1

 Call:
 rxLinMod(formula = y ~ xfac1 + xfac2, data = myData, cube = TRUE,
        cubePredictions=TRUE)

 Cube Linear Regression Results for: y ~ xfac1 + xfac2
 Data: myData
 Dependent variable(s): y
 Total independent variables: 6 (Including number dropped: 1)
 Number of valid observations: 12
 Number of missing observations: 0

 Coefficients:
                       y
 xfac1=One1     7.725231
 xfac1=Two1     8.833730
 xfac1=Three1   8.942099
 xfac2=One2    -4.615929
 xfac2=Two2    -2.767359
 xfac2=Three2    Dropped
```

If we look at the *countDF*, we will see the within-group means, conditional on the average value of the conditioning variable, *xfac2*:

```
myLinMod1$countDF

    xfac1        y Counts
 1   One1 4.725427      4
 2   Two1 5.833926      4
 3 Three1 5.942295      4
```

For the variable *xfac2*, 50% of the observations have the value “One2”, 25% of the observations have the value “Two2”, and 25% have the value “Three2”. We can compute the weighted average of the coefficients for *xfac2* as:

```
myCoef <- coef(myLinMod1)
avexfac2c <- .5*myCoef[4] + .25*myCoef[5]
```

To compute the conditional within-group mean shown in the countDF for xfac1 equal to “One1”, we add this to the coefficient computed for “One1”:

```
condMean1 <- myCoef[1] + avexfac2c
condMean1

 xfac1=One1
   4.725427
```

Conditional within-group means can also be computed using additional continuous independent variables.

8.6 Fitted Values, Residuals, and Prediction

When you fit a model with lm or any of the other core R model-fitting functions, you get back an object that includes as components both the fitted values for the response variable and the model residuals. For models fit with rxLinMod or other RevoScaleR functions, it is usually impractical to include these components, as they can be many megabytes in size. Instead, they are computed on demand using the rxPredict function. This function takes an rxLinMod object as its first argument, an input data set as its second argument, and an output data set as its third argument. If the input data set is the same as the data set used to fit the rxLinMod object, the resulting predictions are the fitted values for the model. If the input data set is a different data set (but one containing the same variable names used in fitting the rxLinMod object), the resulting predictions are true predictions of the response for the new data from the original model. In either case, residuals for the predicted values can be obtained by setting the flag computeResiduals to TRUE.

For example, we can draw from the 7% sample of the large airline data set (available online) training and prediction data sets as follows (remember to customize the first line below for your own system):

```
#  Fitted Values, Residuals, and Prediction


bigDataDir <- "C:/MRS/Data"
sampleAirData <- file.path(bigDataDir, "AirOnTime7Pct.xdf")
trainingDataFile <- "AirlineData06to07.xdf"
targetInfile <- "AirlineData08.xdf"

rxDataStep(sampleAirData, trainingDataFile, rowSelection = Year == 1999 |
     Year == 2000 | Year == 2001 | Year == 2002 | Year == 2003 |
     Year == 2004 | Year == 2005 | Year == 2006 | Year == 2007)
rxDataStep(sampleAirData, targetInfile, rowSelection = Year == 2008)
```

We can then fit a linear model with the training data and compute predicted values on the prediction data set as follows:

```
arrDelayLm2 <- rxLinMod(ArrDelay ~ DayOfWeek + UniqueCarrier + Dest,
    data = trainingDataFile)
rxPredict(arrDelayLm2, data = targetInfile, outData = targetInfile)
```

To see the first few rows of the result, use *rxGetInfo* as follows:

```
rxGetInfo(targetInfile,  numRows = 5)
```

```
 File name: C:\MRS\Data\OutData\AirlineData08.xdf
 Number of observations: 489792
 Number of variables: 14
 Number of blocks: 2
 Compression type: zlib
 Data (5 rows starting with row 1):
   Year DayOfWeek UniqueCarrier Origin Dest CRSDepTime DepDelay TaxiOut TaxiIn
```

```
 1 2008       Mon            9E    ATL  HOU   7.250000       -2       14       5
 2 2008       Mon            9E    ATL  HOU   7.250000       -2       16       2
 3 2008       Sat            9E    ATL  HOU   7.250000        0       18       5
 4 2008       Wed            9E    ATL  SRQ  12.666667        6       20       4
 5 2008       Sat            9E    HOU  ATL   9.083333       -9       15       9
   ArrDelay ArrDel15 CRSElapsedTime Distance ArrDelay_Pred
1      -15    FALSE            140      696      8.981548
2        0    FALSE            140      696      8.981548
3        0    FALSE            140      696      5.377572
4        6    FALSE             86      445      7.377952
5      -23    FALSE            120      696      6.552242
```

8.7 Prediction Standard Errors, Confidence Intervals, and Prediction Intervals

You can also use rxPredict to obtain prediction standard errors, provided you have included the variance-covariance matrix in the original rxLinMod fit. If you choose to compute the prediction standard errors, you can also obtain either of two kinds of intervals: *confidence intervals* that for a given confidence level tell us how confident we are that the expected value is within the given interval, and *prediction intervals* that specify, for a given confidence level, how likely future observations are to fall within the interval given what has already been observed. Standard error computations are computationally intensive, and they may become prohibitive on large data sets with a large number of predictors. To illustrate the computation, we start with a small data set, using the example on page 132 of *Introduction to the Practice of Statistics,* (5th Edition)(Moore & McCabe, 2006). The predictor, neaInc, is the increase in "non-exercise activity" in response to an increase in caloric intake. The response, fatGain, is the associated increase in fat. We first read in the data and create a data frame to use in our analysis:

```
# Standard Errors, Confidence Intervals, and Prediction Intervals

neaInc <- c(-94, -57, -29, 135, 143, 151, 245, 355, 392, 473, 486, 535, 571,
    580, 620, 690)
fatGain <- c( 4.2, 3.0, 3.7, 2.7, 3.2, 3.6, 2.4, 1.3, 3.8, 1.7, 1.6, 2.2, 1.0,
    0.4, 2.3, 1.1)
ips132df <- data.frame(neaInc = neaInc, fatGain=fatGain)
```

Next we fit the linear model with rxLinMod, setting covCoef=TRUE to ensure we have the variance-covariance matrix in our model object:

```
ips132lm <- rxLinMod(fatGain ~ neaInc, data=ips132df, covCoef=TRUE)
```

Now we use rxPredict to obtain the fitted values, prediction standard errors, and confidence intervals. By setting *writeModelVars* to *TRUE*, the variables used in the model will also be included in the output data set. In this first example, we obtain confidence intervals:

```
ips132lmPred <- rxPredict(ips132lm, data=ips132df, computeStdErrors=TRUE,
    interval="confidence", writeModelVars = TRUE)
```

The standard errors are by default put into a variable named by concatenating the name of the response variable with an underscore and the string “StdErr”:

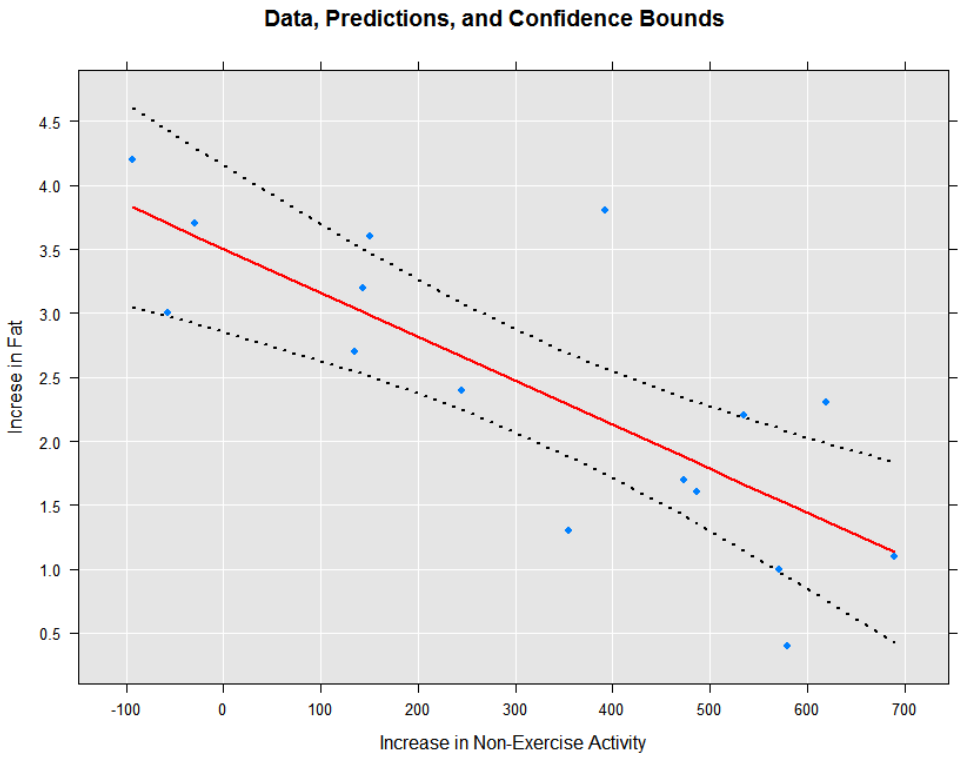
```
ips132lmPred$fatGain_StdErr
```

```
  [1] 0.3613863 0.3381111 0.3209344 0.2323853 0.2288433 0.2254018 0.1941840
  [8] 0.1863180 0.1915656 0.2151569 0.2202366 0.2418892 0.2598922 0.2646223
 [15] 0.2865818 0.3279390
```

We can view the original data, the fitted prediction line, and the confidence intervals as follows:

```
rxLinePlot(fatGain + fatGain_Pred + fatGain_Upper + fatGain_Lower ~ neaInc,
     data = ips132lmPred, type = "b",
     lineStyle = c("blank", "solid", "dotted", "dotted"),
     lineColor = c(NA, "red", "black", "black"),
     symbolStyle = c("solid circle", "blank", "blank", "blank"),
     title = "Data, Predictions, and Confidence Bounds",
     xTitle = "Increase in Non-Exercise Activity",
     yTitle = "Increse in Fat", legend = FALSE)
```

The resulting plot is shown below:

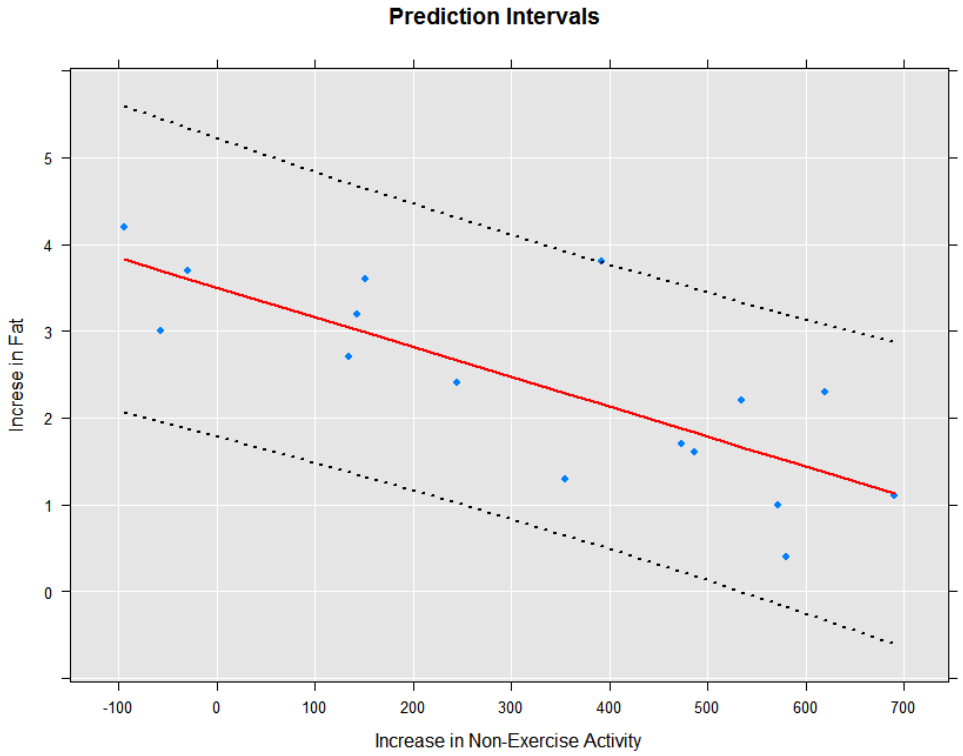


The prediction intervals can be obtained and plotted as follows:

```
ips132lmPred2 <- rxPredict(ips132lm, data=ips132df, computeStdErrors=TRUE,
    interval="prediction", writeModelVars = TRUE)
rxLinePlot(fatGain + fatGain_Pred + fatGain_Upper + fatGain_Lower ~ neaInc,
     data = ips132lmPred2, type = "b",
     lineStyle = c("blank", "solid", "dotted", "dotted"),
     lineColor = c(NA, "red", "black", "black"),
```

```
    symbolStyle = c("solid circle", "blank", "blank", "blank"),
    title = "Prediction Intervals",
    xTitle = "Increase in Non-Exercise Activity",
    yTitle = "Increse in Fat", legend = FALSE)
```

The resulting plot is shown below:



We can fit the prediction standard errors on our big airline regression model if we first refit it with covCoef=TRUE:

```
arrDelayLmVC <- rxLinMod(ArrDelay ~ DayOfWeek + UniqueCarrier + Dest,
    data = trainingDataFile, covCoef=TRUE)
```

We can then obtain the prediction standard errors and a confidence interval as before:

```
rxPredict(arrDelayLmVC, data = targetInfile, outData = targetInfile,
    computeStdErrors=TRUE, interval = "confidence", overwrite=TRUE)
```

We can then look at the first few lines of targetInfile to see the first few predictions and standard errors:

```
rxGetInfo(targetInfile, numRows=10)
```

```
 File name: C:\YourOutputPath\AirlineData08.xdf
 Number of observations: 489792
 Number of variables: 17
 Number of blocks: 2
 Compression type: zlib
 Data (10 rows starting with row 1):
    Year DayOfWeek UniqueCarrier Origin Dest CRSDepTime DepDelay TaxiOut TaxiIn
```

```
1  2008       Mon            9E    ATL  HOU   7.250000       -2      14      5
2  2008       Mon            9E    ATL  HOU   7.250000       -2      16      2
3  2008       Sat            9E    ATL  HOU   7.250000        0      18      5
4  2008       Wed            9E    ATL  SRQ  12.666667        6      20      4
5  2008       Sat            9E    HOU  ATL   9.083333       -9      15      9
6  2008       Mon            9E    ATL  IAH  16.416666       -3      25      4
7  2008      Thur            9E    IAH  ATL  18.500000        9      12      7
8  2008       Sat            9E    IAH  ATL  18.500000       -3      19      8
9  2008       Mon            9E    IAH  ATL  18.500000       -5      16      6
10 2008      Thur            9E    ATL  IAH  13.250000       -2      15      7
   ArrDelay ArrDel15 CRSElapsedTime Distance ArrDelay_Pred ArrDelay_StdErr
1       -15    FALSE            140      696      8.981548       0.3287748
2         0    FALSE            140      696      8.981548       0.3287748
3         0    FALSE            140      696      5.377572       0.3293198
4         6    FALSE             86      445      7.377952       0.6380760
5       -23    FALSE            120      696      6.552242       0.2838803
6       -11    FALSE            145      689      7.530244       0.2952031
7        -8    FALSE            125      689     12.168922       0.2833356
8       -16    FALSE            125      689      6.552242       0.2838803
9       -24    FALSE            125      689     10.156218       0.2833283
10       21     TRUE            130      689      9.542948       0.2952058
   ArrDelay_Lower ArrDelay_Upper
1        8.337161       9.625935
2        8.337161       9.625935
3        4.732117       6.023028
4        6.127346       8.628559
5        5.995847       7.108638
6        6.951657       8.108832
7       11.613594      12.724249
8        5.995847       7.108638
9        9.600905      10.711532
10       8.964355      10.121540
```

8.8 Stepwise Variable Selection

Stepwise linear regression is an algorithm that helps you determine which variables are most important to a regression model. You provide a minimal, or lower, model formula and a maximal, or upper, model formula, and using forward selection, backward elimination, or bidirectional search, the algorithm determines the model formula that provides the best fit based on an AIC selection criterion.

In SAS, stepwise linear regression is implemented through PROC REG. In open source R, it is implemented through the function *step*. The problem with using the function *step* in R is that the size of the data set that can be analyzed is severely limited by the requirement that all computations must be done in memory.

RevoScaleR provides an implementation of stepwise linear regression that is not constrained by the use of "in-memory" algorithms. Stepwise linear regression in RevoScaleR is implemented by the functions *rxLinMod* and *rxStepControl*.

Stepwise linear regression begins with an initial model of some sort. Consider for example the airline training data set AirlineData06to07.xdf we created in section 8.6:

```
#  Stepwise Linear Regression

rxGetVarInfo(trainingDataFile)
```

```
 Var 1: Year, Type: integer, Low/High: (1999, 2007)
 Var 2: DayOfWeek
        7 factor levels: Mon Tues Wed Thur Fri Sat Sun
 Var 3: UniqueCarrier
        30 factor levels: AA US AS CO DL ... OH F9 YV 9E VX
 Var 4: Origin
        373 factor levels: JFK LAX HNL OGG DFW ... IMT ISN AZA SHD LAR
 Var 5: Dest
        377 factor levels: LAX HNL JFK OGG DFW ... ESC IMT ISN AZA SHD
 Var 6: CRSDepTime, Type: numeric, Storage: float32, Low/High: (0.0000, 23.9833)
 Var 7: DepDelay, Type: integer, Low/High: (-1199, 1930)
 Var 8: TaxiOut, Type: integer, Low/High: (0, 1439)
 Var 9: TaxiIn, Type: integer, Low/High: (0, 1439)
 Var 10: ArrDelay, Type: integer, Low/High: (-926, 1925)
 Var 11: ArrDel15, Type: logical, Low/High: (0, 1)
 Var 12: CRSElapsedTime, Type: integer, Low/High: (-34, 1295)
 Var 13: Distance, Type: integer, Low/High: (11, 4962)
```

We are interested in fitting a model that will predict arrival delay (*ArrDelay*) as a function of some of the other variables. To keep things simple, we'll start with our by now familiar model of arrival delay as a function of *DayOfWeek* and *CRSDepTime*:

```
initialModel <- rxLinMod(ArrDelay ~ DayOfWeek + CRSDepTime,
    data = trainingDataFile)
initialModel
```

```
 Call:
 rxLinMod(formula = ArrDelay ~ DayOfWeek + CRSDepTime, data = trainingDataFile)

 Linear Regression Results for: ArrDelay ~ DayOfWeek + CRSDepTime
 File name:
     C:\MyWorkingDir\Documents\MRS\LMPrediction\AirlineData06to07.xdf
 Dependent variable(s): ArrDelay
 Total independent variables: 9 (Including number dropped: 1)
 Number of valid observations: 3945964
 Number of missing observations: 98378

 Coefficients:
                   ArrDelay
 (Intercept)    -4.91416806
 DayOfWeek=Mon   0.49172258
 DayOfWeek=Tues -1.41878850
 DayOfWeek=Wed   0.09677481
 DayOfWeek=Thur  2.52841304
 DayOfWeek=Fri   3.29474667
 DayOfWeek=Sat  -2.86217838
 DayOfWeek=Sun      Dropped
 CRSDepTime      0.86703378
```

The question is, can we improve this model by adding more predictors? If so, which ones? To use stepwise selection in RevoScaleR, you add the *variableSelection* argument to your call to *rxLinMod*. The *variableSelection* argument is a list, most conveniently created by using the *rxStepControl* function. Using *rxStepControl*, you specify the method (the default,

"stepwise", specifies a bidirectional search), the scope (lower and upper formulas for the search), and various control parameters. With our model, we first want to try some more numeric predictors, so we specify our model as follows:

```
airlineStepModel <- rxLinMod(ArrDelay ~ DayOfWeek + CRSDepTime,
     data = trainingDataFile,
     variableSelection = rxStepControl(method="stepwise",
        scope = ~ DayOfWeek + CRSDepTime + CRSElapsedTime +
              Distance + TaxiIn + TaxiOut ))
```

```
Call:
rxLinMod(formula = ArrDelay ~ DayOfWeek + CRSDepTime, data = trainingDataFile,
    variableSelection = rxStepControl(method = "stepwise", scope = ~DayOfWeek +
        CRSDepTime + CRSElapsedTime + Distance + TaxiIn + TaxiOut))

Linear Regression Results for: ArrDelay ~ DayOfWeek + CRSDepTime +
    CRSElapsedTime + Distance + TaxiIn + TaxiOut
File name:
    C:\MyWorkingDir\Documents\MRS\LMPrediction\AirlineData06to07.xdf
Dependent variable(s): ArrDelay
Total independent variables: 13 (Including number dropped: 1)
Number of valid observations: 3945964
Number of missing observations: 98378

Coefficients:
                  ArrDelay
(Intercept)    -9.87474950
DayOfWeek=Mon   0.09830827
DayOfWeek=Tues -1.81998781
DayOfWeek=Wed  -0.62761606
DayOfWeek=Thur  1.53941124
DayOfWeek=Fri   2.45565510
DayOfWeek=Sat  -2.20111789
DayOfWeek=Sun      Dropped
CRSDepTime      0.75995355
CRSElapsedTime -0.20256102
Distance        0.02135381
TaxiIn          0.16194266
TaxiOut         0.99814931
```

8.8.1 Methods of Variable Selection

Three methods of variable selection are supported by rxLinMod:

- *"forward"*: starting from the minimal model, variables are added one at a time until no additional variable satisfies the selection criterion, or until the maximal model is reached.
- *"backward"*: starting from the maximal model, variables are removed one at a time until the removal of another variable won't satisfy the selection criterion, or until the minimal model is reached.
- *"stepwise"* (the default): a combination of forward and backward selection, in which variables are added to the minimal model, but at each step, the model is reanalyzed to see if any variables that have been added are candidates for deletion from the current model.

You specify the desired method by supplying a named component *"method"* in the list supplied for the *variableSelection* argument, or by specifying the *method* argument in a call to *rxStepControl* that is then passed as the *variableSelection* argument.

8.8.2 Variable Selection with Wide Data

We've found that generalized linear models do not converge if the number of predictors is greater than the number of observations. If your data has more variables, it won't be possible to include all of them in the maximal model for stepwise selection. We recommend you use domain experience and insights from initial data explorations to choose a subset of the variables to serve as the maximal model before performing stepwise selection.

There are a few things you can do to reduce the number of predictors. If there are a lot of variables that measure the same quantitative or qualitative entity, try to select one variable that represents the entity best. For example, include a variable that identifies a person's political party affiliation instead of including many variables representing how the person feels about individual issues. If your goal with linear modeling is the interpretation of individual predictors, you want to ensure that correlation between variables in the model is minimal to avoid multicollinearity. This means checking for these correlations before modeling. Sometimes it is useful to combine correlated variables into a composite variable. Height and weight are often correlated, but can be transformed into BMI. Combining variables allows you to reduce the number of variables without losing any information. Ultimately, the variables you select will depend on how you plan to use the results of your linear model.

8.8.3 Specifying Model Scope

You use the *scope* argument in *rxStepControl* (or a named component *"scope"* in the list supplied for the *variableSelection* argument) to specify which variables should be considered for inclusion in the final model selection and which should be ignored. Whether you specify a separate value for scope also determines which models the algorithm will try next.

You can specify the scope as a simple formula (which will be treated as the upper bound, or maximal model), or as a named list with components *"lower"* and *"upper"* (either of which may be missing). For example, to analyze the iris data with a minimal model involving the single predictor *Sepal.Width* and a maximal model involving *Sepal.Width*, *Petal.Length*, and the interaction between *Petal.Width* and *Species*, we can specify our variable selection model as follows:

```
#     Specifying Model Scope

form <- Sepal.Length ~ Sepal.Width + Petal.Length
scope <- list(
    lower = ~ Sepal.Width,
    upper = ~ Sepal.Width + Petal.Length + Petal.Width * Species)
```

```
varsel <- rxStepControl(method = "stepwise", scope = scope)
rxlm.step <- rxLinMod(form, data = iris, variableSelection = varsel,
    verbose = 1, dropMain = FALSE, coefLabelStyle = "R")
```

In general, the models considered are determined from the *scope* argument as follows:

- *"lower"* scope only: All models considered will include this lower model up to the base model specified in the *formula* argument to *rxLinMod*.
- *"upper"* scope only: All models considered will include the terms in the base model (specified by the *formula* argument to *rxLinMod*), plus additional terms as specified in the upper scope.
- Both *"lower"* and *"upper"* scope supplied: All models considered will include at least the terms in the lower scope and additional terms will be added using terms from the upper scope until the stopping criterion is reached or the full upper scope model is selected.
- No scope supplied: The minimal model will include just the intercept term and the maximal model will include at most the terms specified in the base model.

(This convention is identical to that used by R's *step* function.)

8.8.4 Specifying the Selection Criterion

By default, variable selection is determined using the Akaike Information Criterion, or AIC; this is the R standard. If you want a stepwise selection that is more SAS-like, you can specify *stepCriterion="SigLevel"*. If this is set, rxLinMod uses either an F-test (default) or Chi-square test to determine whether to add or drop terms from the model. You can specify which test to perform using the *test* argument. For example, we can refit our airline model using the SigLevel step criterion with an F-test as follows:

```
#
# Specifying selection criterion
#
airlineStepModelSigLevel <- rxLinMod(ArrDelay ~ DayOfWeek + CRSDepTime,
      data = trainingDataFile, variableSelection =
         rxStepControl( method = "stepwise", scope = ~ DayOfWeek +
                CRSDepTime + CRSElapsedTime + Distance + TaxiIn + TaxiOut,
                stepCriterion = "SigLevel" ))
```

In this case (and with many other well-behaved models), the results of using the SigLevel step criterion are identical to those using AIC.

You can control the significance levels for adding and dropping models using the *maxSigLevelToAdd* and *minSigLevelToDrop*. The *maxSigLevelToAdd* specifies a significance level below which a variable can be considered for inclusion in the model; the *minSigLevelToDrop* specifies a significance level above which a variable currently included can

be considered for dropping. By default, for *method="stepwise"*, the both levels are set to .15. We can tighten the selection criterion to the .10 level as follows:

```
airlineStepModelSigLevel.10 <- rxLinMod(ArrDelay ~ DayOfWeek + CRSDepTime,
     data = trainingDataFile, variableSelection =
        rxStepControl( method = "stepwise", scope = ~ DayOfWeek +
              CRSDepTime + CRSElapsedTime +Distance + TaxiIn + TaxiOut,
              stepCriterion = "SigLevel",
              maxSigLevelToAdd=.10, minSigLevelToDrop=.10))
```

8.8.5 Plotting Model Coefficients

By default, the values of the parameters at each step of the stepwise selection are not preserved. Using an additional argument, *keepStepCoefs*, in your *rxStepControl* statement saves the values of the coefficients from each step of the regression. This coefficient data can then be plotted using another function, *rxStepPlot*.

Consider the stepwise linear regression on the iris data from section 8.8.3:

```
#
# Plottings Model Coefficients at Each Step
#
form <- Sepal.Length ~ Sepal.Width + Petal.Length
scope <- list(
    lower = ~ Sepal.Width,
    upper = ~ Sepal.Width + Petal.Length + Petal.Width * Species)

varsel <- rxStepControl(method = "stepwise", scope = scope, keepStepCoefs=TRUE)
rxlm.step <- rxLinMod(form, data = iris, variableSelection = varsel,
    verbose = 1, dropMain = FALSE, coefLabelStyle = "R")
```

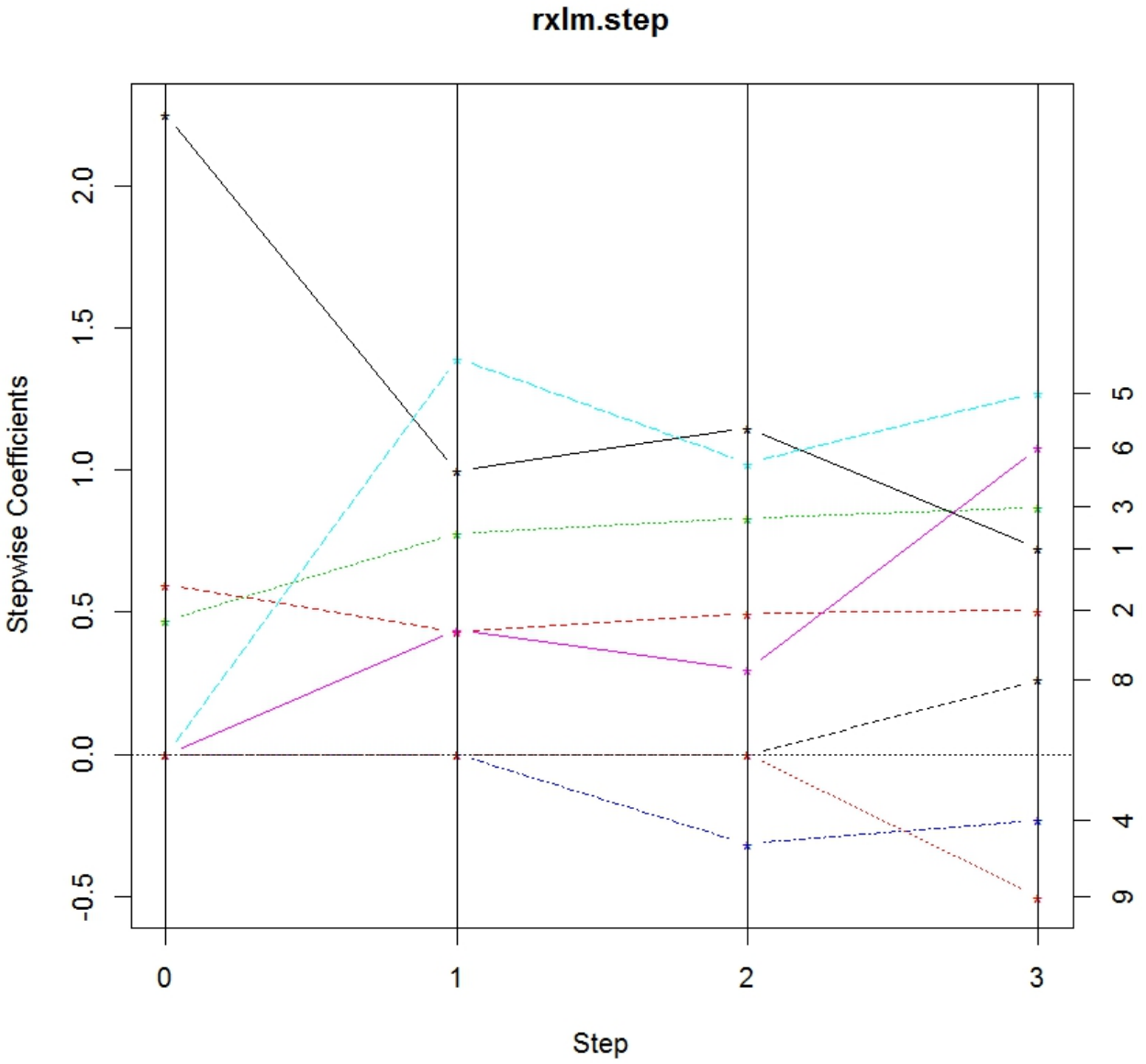
Notice the addition of the argument *keepStepCoefs = TRUE* to the *rxStepContol* call. This produces an extra piece of output in the *rxLinMod* object, a dataframe containing the values of the coefficients at each step of the regression. This dataframe, *stepCoefs*, can be accessed as follows:

```
rxlm.step$stepCoefs
```

```
                            0         1          2          3
 (Intercept)          2.2491402 0.9962913  1.1477685  0.7228228
 Sepal.Width          0.5955247 0.4322172  0.4958889  0.5050955
 Petal.Length         0.4719200 0.7756295  0.8292439  0.8702840
 Petal.Width          0.0000000 0.0000000 -0.3151552 -0.2313888
 Species1             0.0000000 1.3940979  1.0234978  1.2715542
 Species2             0.0000000 0.4382856  0.2999359  1.0781752
 Species3             0.0000000        NA         NA         NA
 Petal.Width:Species1 0.0000000 0.0000000  0.0000000  0.2630978
 Petal.Width:Species2 0.0000000 0.0000000  0.0000000 -0.5012827
 Petal.Width:Species3 0.0000000 0.0000000  0.0000000         NA
```

Trying to glean patterns and information from a table can be difficult. So we've added another function, *rxStepPlot*, which allows the user to plot the parameter values at each step. Using the iris model object, we plot the coefficients:

```
rxStepPlot(rxlm.step)
```

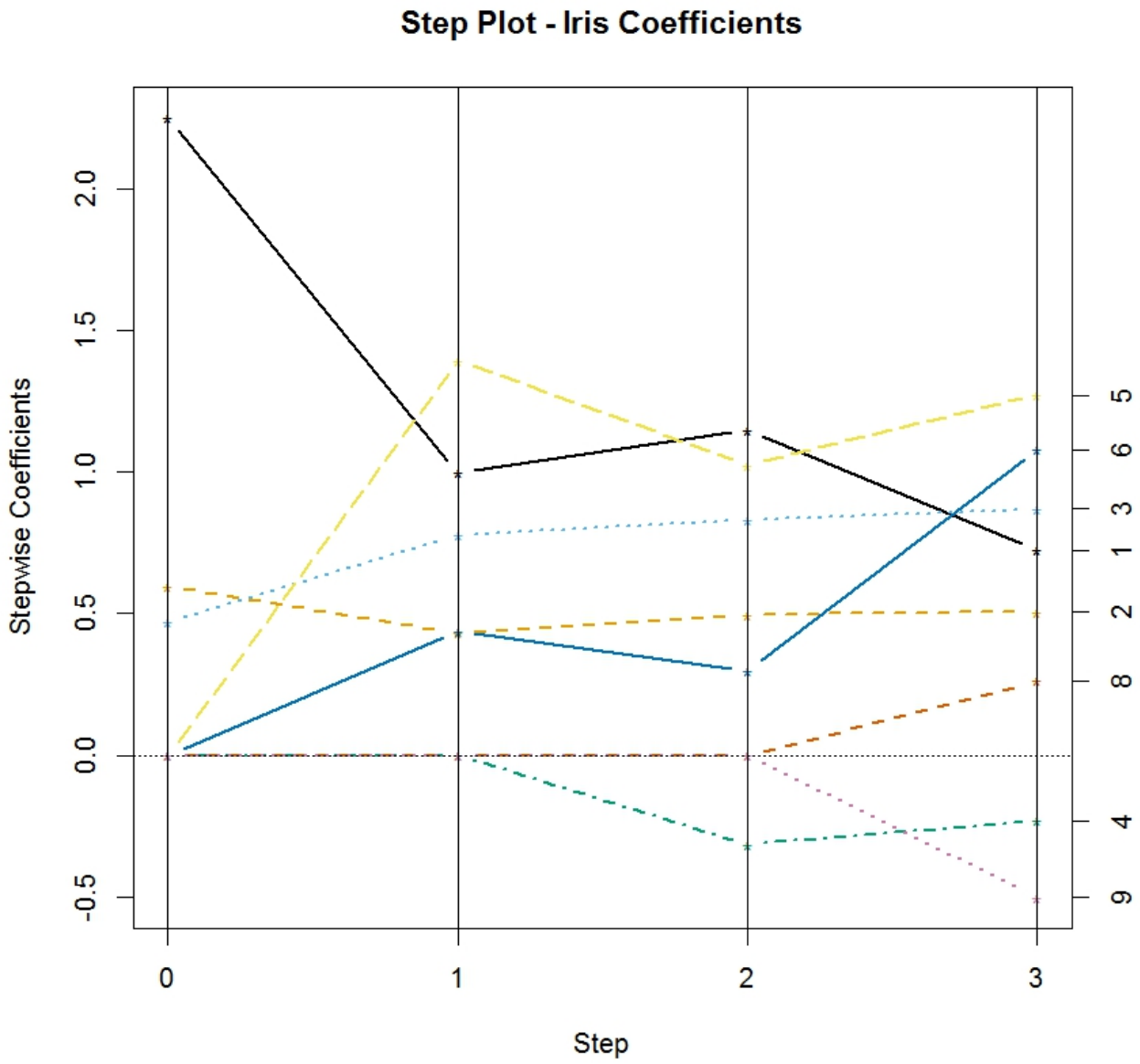


From this plot, we can tell when a variable enters the model by noting the step when it becomes non-zero. Lines are labelled with the numbers on the right axis to indicate the parameter. The numbers correspond to the order they appear in the data frame *stepCoef*. You'll notice that the 7th and 10th parameters don't show up in this plot because the *species3* parameter is the reference category for species.

The function *rxStepPlot* is easily customized by using additional graphical parameters from the *matplot* function from base R. In the following example, we update our orginal call to

rxStepPlot to demonstrate how to specify the colors used for each line, adjust the line width and add a proper title to the plot:

```
colorSelection <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442",
    "#0072B2", "#D55E00", "#CC79A7")
rxStepPlot(rxlm.step, col = colorSelection, lwd = 2,
    main = "Step Plot - Iris Coefficients")
```



By default, the *rxStepPlot* function uses 7 line colors. If the number of parameters exceeds the number of colors, they will be reused in the same order. However, the line types are set to vary from 1 to 5, so lines that have the same color may differ in line type. The line types can also be specified using the *lty* argument in the *rxStepPlot* call.

8.9 Fixed-Effects Models

Fixed-effects models are commonly associated with studies in which multiple observations are recorded for each test subject, for example, yearly observations of median housing price by city, or measurements of tensile strength from samples of steel rods by batch. To fit such a model with rxLinMod, include a factor variable specifying the subject (the cities, or the batch identifier) as the first predictor, and specify *cube=TRUE* to use a partitioned inverse and omit the intercept term.

For example, the MASS library contains the data set *petrol*, which consists of measurements of the yield of a certain refining process with possible predictors including specific gravity, vapor pressure, ASTM 10% point, and volatility measured as the ASTM endpoint for 10 samples of crude oil. Following Venables and Ripley (2002), we first scale the numeric predictors, then fit the fixed-effects model:

```
#  Fixed-Effects Models

library(MASS)
Petrol <- petrol
Petrol[,2:5] <- scale(Petrol[,2:5], scale=F)
rxLinMod(Y ~ No + EP, data=Petrol,cube=TRUE)

 Call:
 rxLinMod(formula = Y ~ No + EP, data = Petrol, cube = TRUE)

 Cube Linear Regression Results for: Y ~ No + EP
 Data: Petrol
 Dependent variable(s): Y
 Total independent variables: 11
 Number of valid observations: 32
 Number of missing observations: 0

 Coefficients:
              Y
 No=A 32.5493917
 No=B 24.2746407
 No=C 27.7820456
 No=D 21.1541642
 No=E 21.5191269
 No=F 20.4355218
 No=G 15.0359067
 No=H 13.0630467
 No=I  9.8053871
 No=J  4.4360767
 EP    0.1587296
```

8.10 Least Squares Dummy Variable (LSDV) Models

RevoScaleR is capable of estimating huge models where fixed effects are estimated by dummy variables, that is, binary variables set to 1 or TRUE if the observation is in a particular category. Creation of these dummy variables is often accomplished by interacting two or more factor

variables using ":" in the formula. If the first term in an rxLinMod (or rxLogit) model is purely categorical and the "cube" argument is set to TRUE, the estimation uses a partitioned inverse to save on computation time and memory.

8.10.1 A Quick Review of Interacting Factors

First, let's do a quick, cautionary review of interacting factor variables by experimenting with a small made-up data set.

```
#  Least Squares Dummy Variable (LSDV) Models
#   A Quick Review of Interacting Factors

set.seed(50)
income <- rep(c(1000,1500,2500,4000), each=5) + 100*rnorm(20)
region <- rep(c("Rural","Urban"), each=10)
sex <- rep(c("Female", "Male"), each=5)
sex <- c(sex,sex)
myData <- data.frame(income, region, sex)
```

The data set has 20 observations with three variables: a numeric variable income and two factor variables representing region and sex. There are three easy ways to compute the within group means of every combination of age and region using RevoScaleR. First, we can use *rxSummary*:

```
rxSummary(income~region:sex, data=myData)
```

which includes in its output:

```
Category                              region sex    Means     StdDev   Min
 income for region=Rural, sex=Female Rural  Female  970.7522 98.01983  827.2396
 income for region=Urban, sex=Female Urban  Female 2501.8303 47.10861 2450.1364
 income for region=Rural, sex=Male   Rural  Male   1480.4378 92.29320 1355.4250
 income for region=Urban, sex=Male   Urban  Male   3944.5127 40.82421 3883.3983
```

Second, we could use *rxCube*:

```
rxCube(income~region:sex, data=myData)
```

which includes in its output:

```
  region    sex    income Counts
1 Rural Female  970.7522      5
2 Urban Female 2501.8303      5
3 Rural   Male 1480.4378      5
4 Urban   Male 3944.5127      5
```

Or, we can use *rxLinMod* with *cube=TRUE*. The intercept is automatically omitted, and four dummy variables are created from the two factors: one for each combination of region and sex. The coefficients are simply the within group means:

```
summary(rxLinMod(income~region:sex, cube=TRUE, data=myData))
```

which includes in its output:

```
Coefficients:
                        Estimate Std. Error t value Pr(>|t|)     | Counts
region=Rural, sex=Female   970.75      33.18   29.26 2.66e-15 *** |      5
region=Urban, sex=Female  2501.83      33.18   75.41 2.22e-16 *** |      5
region=Rural, sex=Male    1480.44      33.18   44.62 2.22e-16 *** |      5
region=Urban, sex=Male    3944.51      33.18  118.90 2.22e-16 *** |      5
```

The same model could be estimated using: `lm(income~region:sex + 0, data=myData)`. Below we will refer to these within group means as *MeanIncRuralFemale*, *MeanIncUrbanFemale*, *MeanIncRuralMale*, and *MeanIncUrbanMale*.

If we add an intercept, we will encounter perfect multicollinearity and one of the coefficients will be dropped. The intercept is then the mean of a reference group and the other coefficients represent the differences or contrasts between the within group means and the reference group. For example,

```
lm(income~region:sex, data=myData)
```

produces:

```
Coefficients:
        (Intercept)  region:Rural:sexFemale  regionUrban:sexFemale
               3945                   -2974                  -1443
  regionRural:sexMale    regionUrban:sexMale
              -2464                     NA
```

We can see that the dummy variable for urban males was dropped; urban males are the reference group and the Intercept is equal to *MeanIncUrbanMale*. The other coefficients represent contrasts from the reference group, so for example, *regionRural:sexFemale* is equal to *MeanIncRuralFemale – MeanIncUrbanMale*.

Another variation is to use "*"in the formula for factor crossing. Using `a*b` is equivalent to using `a + b + a:b`. For example:

```
lm(income~region*sex, data = myData)
```

which results in:

```
Coefficients:
      (Intercept)          regionUrban              sexMale  regionUrban:sexMale
            970.8               1531.1                509.7                933.0
```

Note that the dropping of coefficients in rxLinMod can be controlled to obtain the same results:

```
rxLinMod(income~region*sex, data = myData, dropFirst = TRUE, dropMain = FALSE)
```

Coefficients using this model can be more difficult to interpret, and in fact are highly dependent on the order of the factor levels. In this case, we see the following relationship between the estimated coefficients and the within group means

(Intercept)	*MeanIncRuralFemale*
regionUrban	*MeanIncUrbanFemale – MeanIncRuralFemale*
sexMale	*MeanIncRuralMale – MeanIncRuralFemale*
regionUrban:sexMale	*MeanIncUrbanMale – MeanIncUrbanFemale – MeanIncRuralMale + MeanIncRuralFemale*

If we set up our data slightly differently, we will get quite different results. Let's use the same income data but a different naming convention for the factors:

```
region <- rep(c("Rural","Urban"), each=10)
sex <- rep(c("Woman", "Man"), each=5)
sex <- c(sex,sex)
myData1 <- data.frame(income, region, sex)
```

Using the same model, `lm(income~region*sex, data=myData1)`, results in:

```
Coefficients:
           (Intercept)            regionUrban                sexWoman
                1480.4                 2464.1                  -509.7
regionUrban:sexWoman
                -933.0
```

With this superficial modification to the data, the coefficient for the dummy variable for regionUrban has jumped from $1531 to $2464. This is due to the change in reference group; in this model the Urban coefficient represents the difference between mean urban and rural male income, while in the previous model it was the difference between mean urban and rural female income. That is, the relationship between the within group means and the new coefficients are:

(Intercept)	*MeanIncRuralMale*
regionUrban	*MeanIncUrbanMale – MeanIncRuralMale*
sexWoman	*MeanIncRuralFemale – MeanIncRuralMale*
regionUrban:sexMale	*MeanIncUrbanFemale – MeanIncUrbanMale – MeanIncRuralFemale + MeanIncRuralMale*

Omitting the intercept provides yet another combination of results. For example, using rxLinMod with the original factor labeling:

```
rxLinMod(income~region*sex, data=myData, cube=TRUE)
```

results in:

```
Call:
rxLinMod(formula = income ~ region * sex, data = myData, cube = TRUE)
```

```
Cube Linear Regression Results for: income ~ region * sex
Data: myData
Dependent variable(s): income
Total independent variables: 8 (Including number dropped: 4)
Number of valid observations: 20
Number of missing observations: 0

Coefficients:
                            income
region=Rural              1480.4378
region=Urban              3944.5127
sex=Female               -1442.6824
sex=Male                    Dropped
region=Rural, sex=Female  932.9968
region=Urban, sex=Female   Dropped
region=Rural, sex=Male     Dropped
region=Urban, sex=Male     Dropped
```

region=Rural	*MeanIncRuralMale*
region=Urban	*MeanIncUrbanMale*
Sex=Female	*MeanIncUrbanFemale – MeanIncUrbanMale*
region=Rural, sex=Female	*(MeanIncRuralFemale – MeanIncRuralMale) – (MeanIncUrbanFemale – MeanIncUrbanMale)*

With large data sets it is common to estimate many interaction terms, and if some categories have zero counts, it may not even be obvious what the reference group is. Also note that setting *cube=TRUE* in the above model is of limited use: only the first term from the expanded expression (in this case *region*) is estimated using a partitioned inverse.

8.10.2 Using Dummy Variables in rxLinMod: Letting the Data Speak Example 2

In Chapter 6, we looked at the CensusWorkers.xdf data set and examined the relationship between wage income and age. Now let's add another variable, and examine the relationship between wage income and sex and age.

We can start with a simple dummy variable model, computing the mean wage income by sex:

```
#   Using Dummy Variables in rxLinMod

censusWorkers <- file.path(rxGetOption("sampleDataDir"), "CensusWorkers.xdf")
rxLinMod(incwage~sex, data=censusWorkers, pweights="perwt", cube=TRUE)
```

which computes:

```
Call:
rxLinMod(formula = incwage ~ sex, data = censusWorkers, pweights = "perwt",
    cube = TRUE)

Cube Linear Regression Results for: incwage ~ sex
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Probability weights: perwt
```

```
Dependent variable(s): incwage
Total independent variables: 2
Number of valid observations: 351121
Number of missing observations: 0

Coefficients:
            incwage
sex=Male   43472.71
sex=Female 26721.09
```

Similarly, we could look at a simple linear relationship between wage income and age:

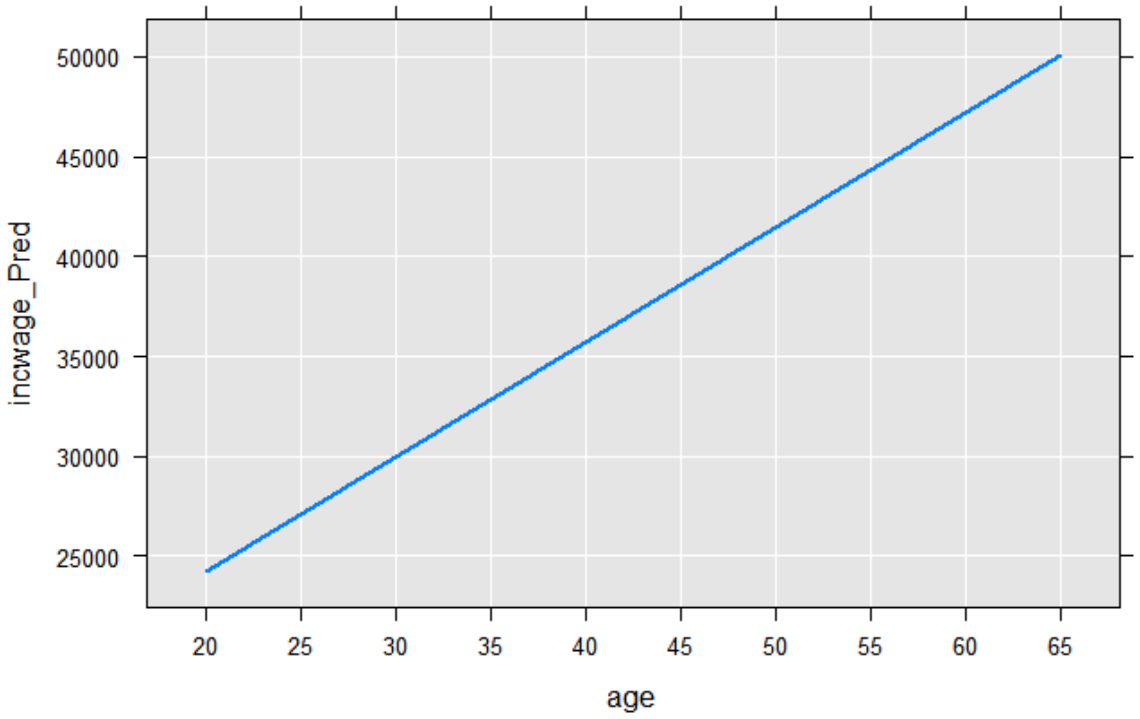
```
linMod1 <- rxLinMod(incwage~age, data=censusWorkers, pweights="perwt")
summary(linMod1)
```

resulting in:

```
Call:
rxLinMod(formula = incwage ~ age, data = censusWorkers, pweights = "perwt")

Linear Regression Results for: incwage ~ age
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Probability weights: perwt
Dependent variable(s): incwage
Total independent variables: 2
Number of valid observations: 351121
Number of missing observations: 0

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 12802.980    247.963   51.63 2.22e-16 ***
age           572.980      5.947   96.35 2.22e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 180800 on 351119 degrees of freedom
Multiple R-squared: 0.02576
Adjusted R-squared: 0.02576
F-statistic:  9284 on 1 and 351119 DF,  p-value: < 2.2e-16
Condition number: 1
```

Computing the two end points on the regression line, we can plot it:

```
age <- c(20,65)
coefLinMod1 <- coef(linMod1)
incwage_Pred <- coefLinMod1[1] + age*coefLinMod1[2]
plotData1 <- data.frame(age, incwage_Pred)
rxLinePlot(incwage_Pred~age, data=plotData1)
```



The next typical step is to combine the two approaches by estimating separate intercepts for males and females:

```
linMod2 <- rxLinMod(incwage~sex+age, data = censusWorkers, pweights = "perwt",
cube=TRUE)
summary(linMod2)
```

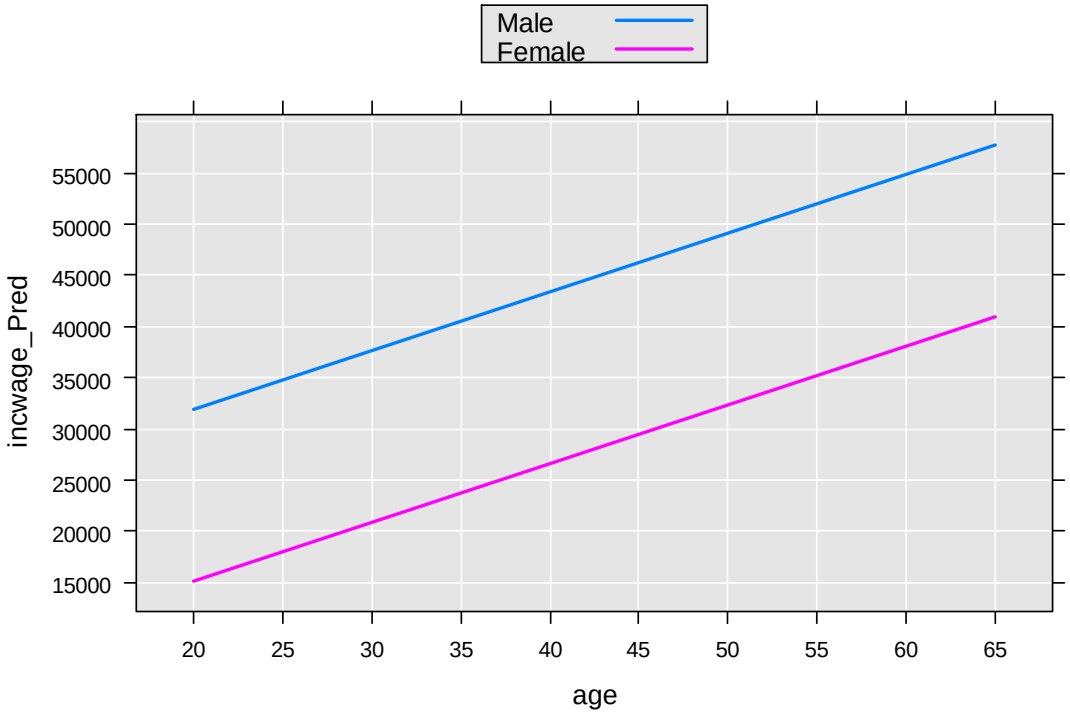
which results in:

```
Call:
rxLinMod(formula = incwage ~ sex + age, data = censusWorkers,
    pweights = "perwt", cube = TRUE)

Cube Linear Regression Results for: incwage ~ sex + age
File name:
C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Probability weights: perwt
Dependent variable(s): incwage
Total independent variables: 3
Number of valid observations: 351121
Number of missing observations: 0

Coefficients:
            Estimate Std. Error t value Pr(>|t|)     |  Counts
sex=Male   20479.178    250.033   81.91 2.22e-16 *** | 3866542
sex=Female  3723.067    252.968   14.72 2.22e-16 *** | 3276744
age          573.232      5.816   98.56 2.22e-16 *** |
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 176800 on 351118 degrees of freedom
Multiple R-squared: 0.06804 (as if intercept included)
Adjusted R-squared: 0.06804
F-statistic: 1.282e+04 on 2 and 351118 DF,  p-value: < 2.2e-16
Condition number: 1
```

We will create a small sample data set with the same variables we use in censusWorkers, but with only four observations representing the high and low value of age for both sexes. Using the *rxPredict* function, the predicted values for each one of these sample observations is computed, which we then plot:

```
age <- c(20,65,20,65)
sex <- factor(rep(c(1, 2), each=2), labels=c("Male", "Female"))
perwt <- rep(1, times=4)
incwage <- rep(0, times=4)
plotData2 <- data.frame(age, sex, perwt, incwage)
plotData2p <- rxPredict(linMod2, data=plotData2, outData=plotData2)
rxLinePlot(incwage_Pred~age, groups=sex, data=plotData2p)
```



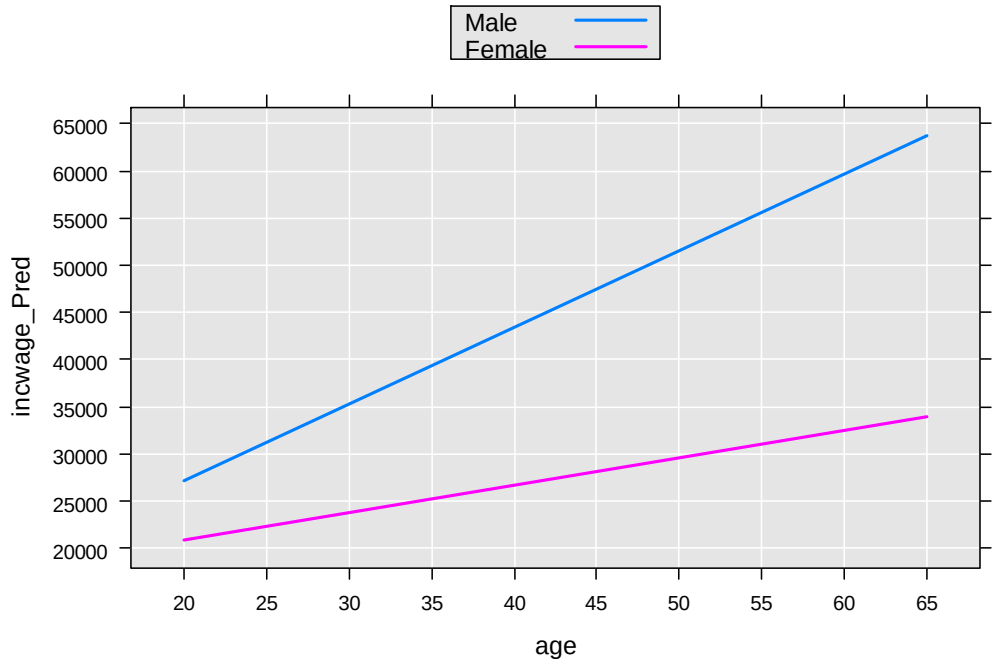
These types of models are often relaxed further by allowing both the slope and itercept to vary by group:

```
linMod3 <- rxLinMod(incwage~sex+sex:age, data = censusWorkers,
     pweights = "perwt", cube=TRUE)
summary(linMod3)

 Call:
 rxLinMod(formula = incwage ~ sex + sex:age, data = censusWorkers,
     pweights = "perwt", cube = TRUE)
```

```
Cube Linear Regression Results for: incwage ~ sex + sex:age
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Probability weights: perwt
Dependent variable(s): incwage
Total independent variables: 4
Number of valid observations: 351121
Number of missing observations: 0

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)     |  Counts
sex=Male           10783.449    328.871   32.79 2.22e-16 *** | 3866542
sex=Female         15131.422    356.806   42.41 2.22e-16 *** | 3276744
age for sex=Male     814.948      7.888  103.31 2.22e-16 *** |
age for sex=Female   288.876      8.556   33.76 2.22e-16 *** |
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 176300 on 351117 degrees of freedom
Multiple R-squared: 0.07343 (as if intercept included)
Adjusted R-squared: 0.07343
F-statistic:  9276 on 3 and 351117 DF,  p-value: < 2.2e-16
Condition number: 1.1764
```

Again getting predictions and plotting:

```
plotData3p <- rxPredict(linMod3, data=plotData2, outData=plotData2)
rxLinePlot(incwage_Pred~age, groups=sex, data=plotData3p)
```



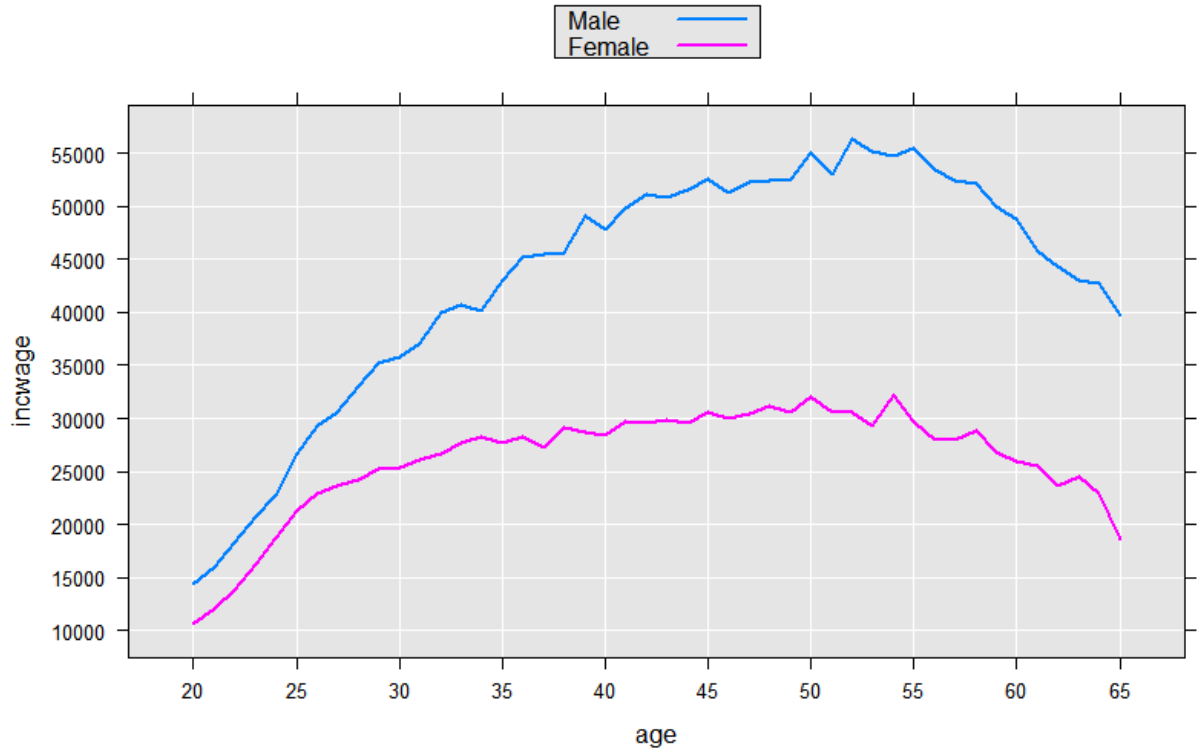
We could continue the process, experimenting with functional forms for age. But, since we have many observations (and therefore many degrees of freedom), we can take advantage of the F() function available in revoScaleR to let the data speak for itself. As we saw in Chapter 6,

the F() function creates a factor variable from a numeric variable “on-the-fly”, creating a level for every integer value. This allows us to compute and observe the shape of the functional form using a purely dummy variable model:

```
linMod4 <- rxLinMod(incwage~sex:F(age), data=censusWorkers, pweights="perwt",
cube=TRUE)
```

This model estimated a total of 92 coefficients, all for dummy variables representing every age in the range of 20 to 65 for each sex. To visually examine the coefficients we could add observations to our plotData data frame and use rxPredict to compute predicted values for each of the 92 groups represented, but since the model contains only dummy variables in an initial cube term, we can instead use the “counts” data frame returned with the rxLinMod object:

```
plotData4 <- linMod4$countDF
# Convert the age factor variable back to an integer
plotData4$age <- as.integer(levels(plotData4$F.age.))[plotData4$F.age.]
rxLinePlot(incwage~age, groups=sex, data=plotData4)
```



8.11 Intercept-Only Models

You may have seen intercept-only models fitted with R’s `lm` function, where the model formula is of the form response ~ 1. In RevoScaleR these models should be fitted using `rxSummary`, because the intercept-only model simply returns the mean of the response. For example:

```
#  Intercept-Only Models

airlineDF <- rxDataStep(inData =
     file.path(rxGetOption("sampleDataDir"), "AirlineDemoSmall.xdf"))
lm(ArrDelay ~ 1, data = airlineDF)

 Call:
 lm(formula = ArrDelay ~ 1, data = airlineDF)

 Coefficients:
 (Intercept)
       11.32


rxSummary(~ ArrDelay, data = airlineDF)

 Call:
 rxSummary(formula = ~ArrDelay, data = airlineDF)

 Summary Statistics Results for: ~ArrDelay
 Data: airlineDF
 Number of valid observations: 6e+05
 Number of missing observations: 0

  Name     Mean     StdDev   Min Max  ValidObs MissingObs
  ArrDelay 11.31794 40.68854 -86 1490 582628   17372
```

Chapter 9.

Fitting Logistic Regression Models

Logistic regression is a standard tool for modeling data with a binary response variable. In R, you fit a logistic regression using the *glm* function, specifying a binomial family and the logit link function. In RevoScaleR, you can use *rxGlm* in the same way (see Chapter 10, Fitting Generalized Linear Models) or you can fit a logistic regression using the optimized *rxLogit* function; because this function is specific to logistic regression, you need not specify a family or link function.

9.1 A Simple Logistic Regression Example

As an example, consider the *kyphosis* data set in the *rpart* package. This data set consists of 81 observations of four variables (Age, Number, Kyphosis, Start) in children following corrective spinal surgery; it is used as the initial example of *glm* in the White Book(Chambers & Hastie, 1992). The variable Kyphosis reports the absence or presence of this deformity.

We can use *rxLogit* to model the probability that kyphosis is present as follows:

```
#######################################################
# Chapter 9: Fitting Logistic Regression Models
Ch9Start <- Sys.time()


library(rpart)
```

```
rxLogit(Kyphosis ~ Age + Start + Number, data = kyphosis)
```

The following output is returned:

```
Logistic Regression Results for: Kyphosis ~ Age + Start + Number
Data: kyphosis
Dependent variable(s): Kyphosis
Total independent variables: 4
Number of valid observations: 81
Number of missing observations: 0

Coefficients:
                Kyphosis
(Intercept) -2.03693354
Age          0.01093048
Start       -0.20651005
Number       0.41060119
```

The same model can be fit with *glm* (or *rxGlm*) as follows:

```
glm(Kyphosis ~ Age + Start + Number, family = binomial, data = kyphosis)


Call:  glm(formula = Kyphosis ~ Age + Start + Number, family = binomial,
data = kyphosis)

Coefficients:
(Intercept)          Age        Start       Number
   -2.03693      0.01093     -0.20651      0.41060

Degrees of Freedom: 80 Total (i.e. Null);  77 Residual
Null Deviance:          83.23
Residual Deviance: 61.38   AIC: 69.38
```

9.2 Stepwise Logistic Regression

Stepwise logistic regression is an algorithm that helps you determine which variables are most important to a logistic model. You provide a minimal, or lower, model formula and a maximal, or upper, model formula, and using forward selection, backward elimination, or bidirectional search, the algorithm determines the model formula that provides the best fit based on an AIC or significance level selection criterion.

RevoScaleR provides an implementation of stepwise logistic regression that is not constrained by the use of "in-memory" algorithms. Stepwise linear regression in RevoScaleR is implemented by the functions *rxLogit* and *rxStepControl*.

Stepwise logistic regression begins with an initial model of some sort. We can look at the kyphosis data again and start with a simpler model: Kyphosis ~ Age:

```
initModel <- rxLogit(Kyphosis ~ Age, data=kyphosis)
initModel

 Logistic Regression Results for: Kyphosis ~ Age
 Data: kyphosis
 Dependent variable(s): Kyphosis
```

```
Total independent variables: 2
Number of valid observations: 81
Number of missing observations: 0

Coefficients:
                Kyphosis
(Intercept) -1.809351230
Age          0.005441758
```

We can specify a stepwise model using rxLogit and rxStepControl as follows:

```
KyphStepModel <-  rxLogit(Kyphosis ~ Age,
     data = kyphosis,
     variableSelection = rxStepControl(method="stepwise",
        scope = ~ Age + Start + Number ))
KyphStepModel
```

```
Logistic Regression Results for: Kyphosis ~ Age + Start + Number
Data: kyphosis
Dependent variable(s): Kyphosis
Total independent variables: 4
Number of valid observations: 81
Number of missing observations: 0

Coefficients:
               Kyphosis
(Intercept) -2.03693354
Age          0.01093048
Start       -0.20651005
Number       0.41060119
```

The methods for variable selection (forward, backward, and stepwise), the definition of model scope, and the available selection criteria are all the same as for stepwise linear regression; see section 8.8 and the rxStepControl help file for more details.

9.2.1 Plotting Model Coefficients

The ability to save model coefficients using the argument `keepStepCoefs = TRUE` within the `rxStepControl` call and to plot them with the function `rxStepPlot` was described in great detail for stepwise `rxLinMod` in section 8.8.5. This functionality is also available for stepwise `rxLogit` objects.

9.3 Prediction

As described above for linear models, the objects returned by the RevoScaleR model-fitting functions do not include fitted values or residuals. We can obtain them, however, by calling `rxPredict` on our fitted model object, supplying the original data used to fit the model as the data to be used for prediction.

For example, consider the mortgage default example in Section 6 of the manual *RevoScaleR: Getting Started Guide.* For that example, we used ten input data files to create the data set used to fit the model. But suppose instead we use nine input data files to create the training

data set and use the remaining data set for prediction. We can do that as follows (again, remember to modify the first line for your own system):

```
#  Logistic Regression Prediction


bigDataDir <- "C:/MRS/Data"
mortCsvDataName <- file.path(bigDataDir, "mortDefault", "mortDefault")
trainingDataFileName <- "mortDefaultTraining"
mortCsv2009 <- paste(mortCsvDataName, "2009.csv", sep = "")
targetDataFileName <- "mortDefault2009.xdf"
ageLevels <- as.character(c(0:40))
yearLevels <- as.character(c(2000:2009))
colInfo <- list(list(name = "houseAge", type = "factor",
    levels = ageLevels), list(name = "year", type = "factor",
    levels = yearLevels))
append= FALSE
for (i in 2000:2008)
{
    importFile <- paste(mortCsvDataName, i, ".csv", sep = "")
    rxImport(inData = importFile, outFile = trainingDataFileName,
     colInfo = colInfo, append = append)
    append = TRUE
}


rxImport(inData = mortCsv2009, outFile = targetDataFileName,
   colInfo = colInfo)
```

We can then fit a logistic regression model to the training data and predict with the prediction data set as follows:

```
logitObj <- rxLogit(default ~ year + creditScore + yearsEmploy + ccDebt,
     data = trainingDataFileName, blocksPerRead = 2, verbose = 1,
     reportProgress=2)
rxPredict(logitObj, data = targetDataFileName,
     outData = targetDataFileName, computeResiduals = TRUE)
```

To view the first 30 rows of the output data file, use `rxGetInfo` as follows:

```
rxGetInfo(targetDataFileName, numRows = 30)
```

9.4 Prediction Standard Errors and Confidence Intervals

You can use rxPredict to obtain prediction standard errors and confidence intervals for models fit with rxLogit in the same way as for those fit with rxLinMod. The original model must be fit with covCoef=TRUE:

```
#  Prediction Standard Errors and Confidence Intervals

logitObj2 <- rxLogit(default ~ year + creditScore + yearsEmploy + ccDebt,
     data = trainingDataFileName, blocksPerRead = 2, verbose = 1,
     reportProgress=2, covCoef=TRUE)
```

You then specify *computeStdErr=TRUE* to obtain prediction standard errors; if this is TRUE, you can also specify *interval="confidence"* to obtain a confidence interval:

```
rxPredict(logitObj2, data = targetDataFileName,
     outData = targetDataFileName, computeStdErr = TRUE,
     interval = "confidence", overwrite=TRUE)
```

The first ten lines of the file with predictions can be viewed as follows:

```
rxGetInfo(targetDataFileName, numRows=10)
```

```
 File name: C:\Users\yourname\Documents\MRS\mortDefault2009.xdf
 Number of observations: 1e+06
 Number of variables: 10
 Number of blocks: 2
 Compression type: zlib
 Data (10 rows starting with row 1):
    creditScore houseAge yearsEmploy ccDebt year default default_Pred
 1          617       20           8   4410 2009       0 6.620773e-06
 2          623       11           7   5609 2009       0 4.610861e-05
 3          758       17           4   7250 2009       0 4.259884e-04
 4          687       22           5   3761 2009       0 3.770789e-06
 5          663       15           6   6746 2009       0 2.312827e-04
 6          676       10           2   7106 2009       0 1.092593e-03
 7          721       23           2   2280 2009       0 8.515912e-07
 8          680       18           7   2831 2009       0 6.011109e-07
 9          734        9           5   3867 2009       0 3.144299e-06
 10         688       16           8   6238 2009       0 5.350031e-05
    default_StdErr default_Lower default_Upper
 1    3.143695e-07  6.032422e-06  7.266507e-06
 2    1.953612e-06  4.243427e-05  5.010109e-05
 3    1.594783e-05  3.958500e-04  4.584203e-04
 4    1.739047e-07  3.444893e-06  4.127516e-06
 5    8.733193e-06  2.147838e-04  2.490486e-04
 6    3.952975e-05  1.017797e-03  1.172880e-03
 7    4.396314e-08  7.696409e-07  9.422675e-07
 8    3.091885e-08  5.434655e-07  6.648706e-07
 9    1.469334e-07  2.869109e-06  3.445883e-06
 10   2.224102e-06  4.931401e-05  5.804197e-05
```

9.5 Using ROC Curves to Evaluate Estimated Binary Response Models

A *receiver operating characteristic* (ROC) curve can be used to visually assess binary response models. It plots the *True Positive Rate* (the number of correctly predicted TRUE responses divided by the actual number of TRUE responses) against the *False Positive Rate* (the number of incorrectly predicted TRUE responses divided by the actual number of FALSE responses), calculated at various thresholds. The *True Positive Rate* is the same as the *sensitivity*, and the *False Positive Rate* is equal to one minus the *specificity*.

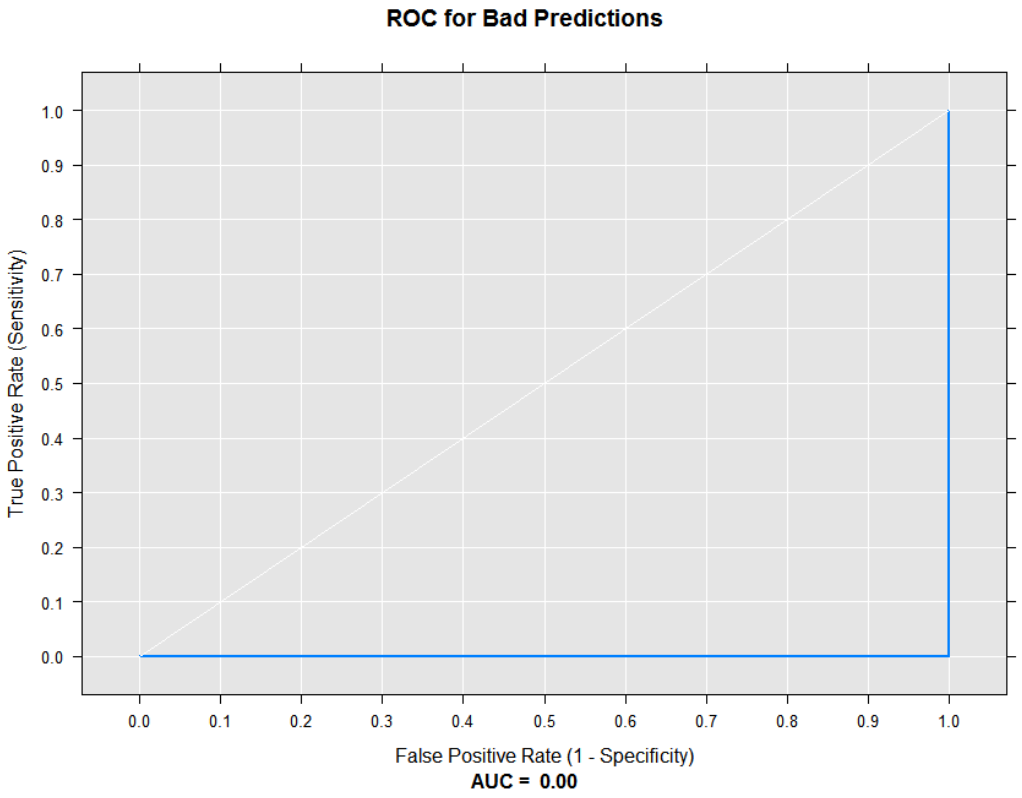
Let's start with a simple example. Suppose we have a data set with 10 observations. The variable *actual* contains the actual responses, or the 'truth'. The variable *badPred* are the

predicted responses from a very poor model. The variable *goodPred* contains the predicted responses from a great model.

```
# Using ROC Curves for Binary Response Models

sampleDF <- data.frame(
    actual = c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1),
    badPred = c(.99, .99, .99, .99, .99, .01, .01, .01, .01, .01),
    goodPred = c( .01, .01, .01, .01, .01,.99, .99, .99, .99, .99))
```

We can now call the *rxRocCurve* function to compute the sensitivity and specificty for the 'bad' predictions, and draw the ROC curve. The numBreaks argument indicates the number of breaks to use in determining the thresholds for computing the true and false positive rates.

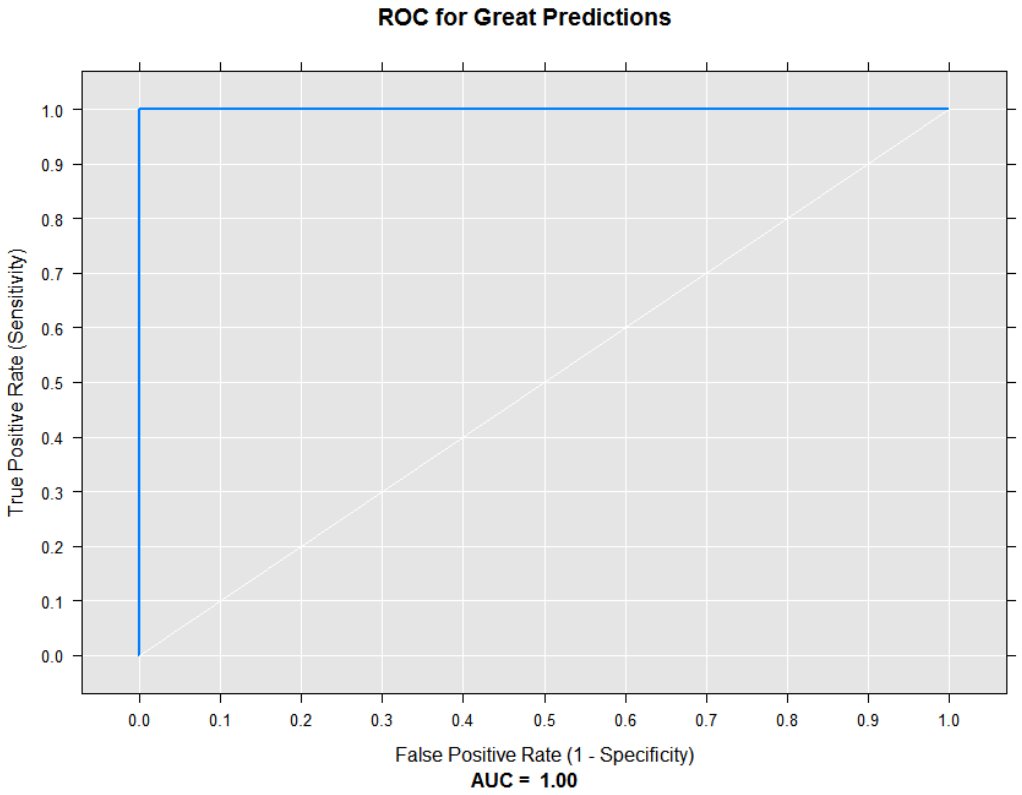
```
rxRocCurve(actualVarName = "actual", predVarNames = "badPred",
      data = sampleDF, numBreaks = 10, title = "ROC for Bad Predictions")
```



Since all of our predictions are wrong at every threshold, the ROC curve is a flat line at 0. The *Area Under the Curve* (AUC) summary statistic is 0.

At the other extreme, let's draw an ROC curve for our great model:

```
rxRocCurve(actualVarName = "actual", predVarNames = "goodPred",
      data = sampleDF, numBreaks = 10, title = "ROC for Great Predictions")
```



With perfect predictions, we see the the True Positive Rate is 1 for all thresholds, and the AUC is 1. We'd expect a random guess ROC curve to lie along with white diagonal line.

Now let's use actual model predictions in an ROC curve. We'll use the small mortgage default sample data to estimate a logistic model and them compute predicted values:

```
# Using mortDefaultSmall for predictions and an ROC curve

mortXdf <- file.path(rxGetOption("sampleDataDir"), "mortDefaultSmall")
logitOut1 <- rxLogit(default ~ creditScore + yearsEmploy + ccDebt,
      data = mortXdf, blocksPerRead = 5)

predFile <- "mortPred.xdf"

predOutXdf <- rxPredict(modelObject = logitOut1, data = mortXdf,
      writeModelVars = TRUE, predVarNames = "Model1", outData = predFile)
```

Now, let's estimate a different model (with 1 less independent variable), and add the predictions from that model to our output data set:

```
# Estimate a second model without ccDebt
logitOut2 <- rxLogit(default ~ creditScore + yearsEmploy,
     data = predOutXdf, blocksPerRead = 5)

# Add preditions to prediction data file
predOutXdf <- rxPredict(modelObject = logitOut2, data = predOutXdf,

 predVarNames = "Model2")
```

Now we can compute the sensitivity and specificity for both models, using rxRoc:

```
rocOut <- rxRoc(actualVarName = "default",
     predVarNames = c("Model1", "Model2"),
     data = predOutXdf)
rocOut
```

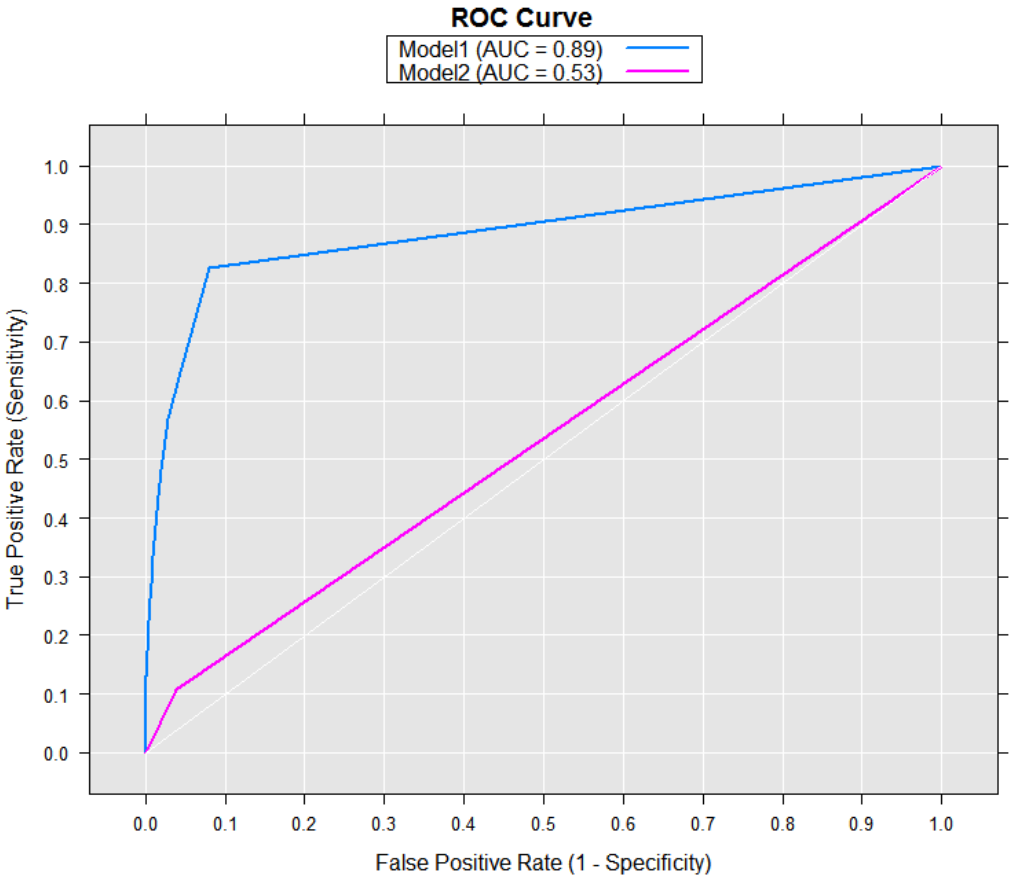
```
    threshold predVarName sensitivity specificity
 1       0.00      Model1 1.000000000   0.0000000
 2       0.01      Model1 0.825902335   0.9197118
 3       0.02      Model1 0.647558386   0.9567965
 4       0.03      Model1 0.569002123   0.9721488
 5       0.04      Model1 0.481953291   0.9797647
 6       0.05      Model1 0.437367304   0.9845472
 7       0.06      Model1 0.386411890   0.9877825
 8       0.07      Model1 0.335456476   0.9900130
 9       0.08      Model1 0.305732484   0.9916406
 10      0.09      Model1 0.288747346   0.9930272
 11      0.10      Model1 0.261146497   0.9940520
 12      0.11      Model1 0.237791932   0.9947252
 13      0.12      Model1 0.225053079   0.9953682
 14      0.13      Model1 0.208067941   0.9959107
 15      0.14      Model1 0.197452229   0.9963528
 16      0.15      Model1 0.182590234   0.9967648
 17      0.16      Model1 0.171974522   0.9971064
 18      0.17      Model1 0.161358811   0.9973877
 19      0.18      Model1 0.152866242   0.9975886
 20      0.19      Model1 0.150743100   0.9978298
 21      0.20      Model1 0.144373673   0.9980307
 22      0.21      Model1 0.138004246   0.9982518
 23      0.22      Model1 0.131634820   0.9984527
 24      0.23      Model1 0.131634820   0.9986034
 25      0.24      Model1 0.129511677   0.9987340
 26      0.25      Model1 0.123142251   0.9987843
 27      0.26      Model1 0.116772824   0.9988546
 28      0.27      Model1 0.116772824   0.9989149
 29      0.28      Model1 0.114649682   0.9989752
 30      0.29      Model1 0.108280255   0.9990355
 31      0.30      Model1 0.101910828   0.9991158
 32      0.31      Model1 0.099787686   0.9991661
 33      0.32      Model1 0.091295117   0.9992264
 34      0.33      Model1 0.087048832   0.9992866
 35      0.34      Model1 0.082802548   0.9993469
 36      0.35      Model1 0.080679406   0.9994072
 37      0.36      Model1 0.074309979   0.9994474
 38      0.37      Model1 0.072186837   0.9994675
 39      0.38      Model1 0.070063694   0.9995077
 40      0.39      Model1 0.067940552   0.9995780
 41      0.40      Model1 0.063694268   0.9995881
 42      0.41      Model1 0.063694268   0.9996182
 43      0.42      Model1 0.063694268   0.9996684
 44      0.43      Model1 0.055201699   0.9996986
```

```
45      0.44      Model1 0.050955414   0.9997287
46      0.45      Model1 0.048832272   0.9997790
47      0.46      Model1 0.046709130   0.9997790
48      0.47      Model1 0.042462845   0.9997991
49      0.48      Model1 0.040339703   0.9998091
50      0.49      Model1 0.040339703   0.9998292
51      0.50      Model1 0.040339703   0.9998493
52      0.51      Model1 0.040339703   0.9998794
53      0.52      Model1 0.033970276   0.9998895
54      0.53      Model1 0.031847134   0.9999096
55      0.54      Model1 0.031847134   0.9999196
56      0.55      Model1 0.031847134   0.9999297
57      0.58      Model1 0.029723992   0.9999397
58      0.59      Model1 0.027600849   0.9999498
59      0.60      Model1 0.023354565   0.9999598
60      0.61      Model1 0.016985138   0.9999598
61      0.63      Model1 0.014861996   0.9999598
62      0.65      Model1 0.014861996   0.9999799
63      0.70      Model1 0.014861996   0.9999900
64      0.72      Model1 0.012738854   0.9999900
65      0.74      Model1 0.010615711   0.9999900
66      0.78      Model1 0.010615711   1.0000000
67      0.80      Model1 0.008492569   1.0000000
68      0.83      Model1 0.006369427   1.0000000
69      0.89      Model1 0.004246285   1.0000000
70      0.91      Model1 0.000000000   1.0000000
71      0.00      Model2 1.000000000   0.0000000
72      0.01      Model2 0.108280255   0.9612776
73      0.02      Model2 0.000000000   0.9994474
74      0.03      Model2 0.000000000   1.0000000
```

With the *removeDups* argument set to its default of *TRUE*, rows containing duplicate entries for sensitivity and specificity were removed from the returned data frame. In this case, it results in many fewer rows for Model2 than Model1. We can use the *rxRoc plot* method to render our ROC curve using the computed results.

```
plot(rocOut)
```

The resulting plot shows that the second model is much closer to the “random” diagonal line than the first model.


ROC Curve
Model1 (AUC = 0.89)
Model2 (AUC = 0.53)
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0

Chapter 10.

Fitting Generalized Linear Models

Generalized linear models (GLM) are a framework for a wide range of analyses. They relax the assumptions for a standard linear model in two ways. First, a functional form can be specified for the conditional mean of the predictor. This is referred to as the "link" function. Second, you can specify a distribution for the response variable. The rxGlm function in RevoScaleR provides the ability to estimate generalized linear models on large data sets.

The following family/link combinations are implemented in C++ for performance enhancements: binomial/logit, gamma/log, poisson/log, and Tweedie. Other family/link combinations use a combination of C++ and R code. Any valid R family object that can be used with glm() can be used with rxGlm(), including those that are user-defined. The following table shows all of the supported family/link combinations (in addition to user-defined):

Family	Default Link Function	Other Available Link Functions

binomial	"logit"	"probit", "cauchit", "log", "cloglog"
gaussian	"identity"	"log", "inverse"
Gamma	"inverse"	"identity", "log"
inverse.gaussian	"1/mu^2"	"inverse", "identity", "log"
poisson	"log"	"identity", "sqrt"
quasi	"identity" with variance = "constant"	"logit", "probit", "cloglog", "inverse", "log", "1/mu^2", "sqrt"
quasibinomial	"logit"	Same as binomial, but dispersion parameter not fixed at one
quasipoisson	"log"	Same as poisson, but dispersion parameter not fixed at one
rxTweedie	requires arguments instead of link function	

10.1 A Simple Example Using the Poisson Family

The Poisson family is used to estimate models of count data. Examples from the literature include the following types of response variables:

- Number of drinks on a Saturday night
- Number of bacterial colonies in a Petri dish
- Number of children born to married women
- Number of credit cards a person has

We'll start with a simple example from Kabacoff's **R in Action** book (2011), using data provided with the ***robust*** R package. The data are from a placebo-controlled clinical trial of 59 epileptics. Patients with partial seizures were enrolled in a randomized clinical trial of the anti-epileptic drug, progabide. Counts of epileptic seizures were recorded during the trial. The data set also includes a baseline 8-week seizure count and the age of the patient.

To access this data, first make sure the ***robust*** package is installed, then use the `data` command to load the the data frame:

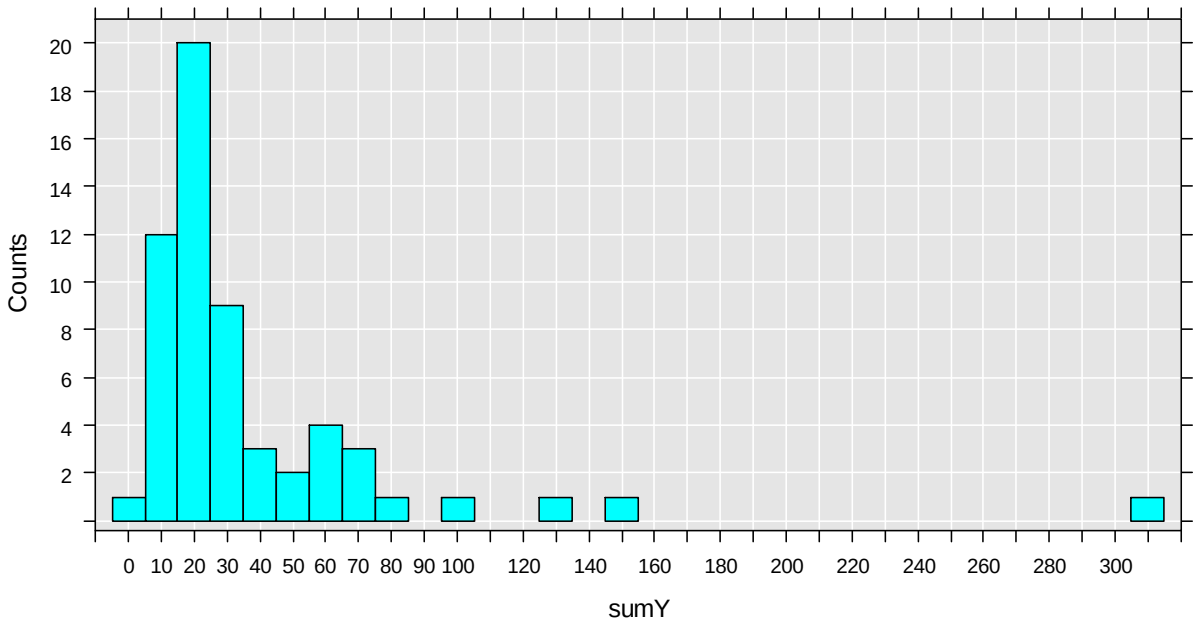
```
#########################################################
# Chapter 10: Fitting Generalized Linear Models
  #  A Simple Example Using the Poisson Family
Ch10Start <- Sys.time()


if ("robust" %in% .packages()){
data(breslow.dat, package = "robust")
```

First, let's get some basic information on the data set, then draw a histogram of the sumY variable, containing the total count of seizures during the trial.

```
rxGetInfo(breslow.dat, getVarInfo = TRUE)
rxHistogram( ~sumY, numBreaks = 25, data = breslow.dat)
```

The data set has 59 observations, and 12 variables. The variables of interest are *Base*, *Age*, *Trt*, and *sumY*.

```
Data frame: breslow.dat
Number of observations: 59
Number of variables: 12
Variable information:
Var 1: ID, Type: integer, Low/High: (101, 238)
Var 2: Y1, Type: integer, Low/High: (0, 102)
Var 3: Y2, Type: integer, Low/High: (0, 65)
Var 4: Y3, Type: integer, Low/High: (0, 76)
Var 5: Y4, Type: integer, Low/High: (0, 63)
Var 6: Base, Type: integer, Low/High: (6, 151)
Var 7: Age, Type: integer, Low/High: (18, 42)
Var 8: Trt
       2 factor levels: placebo progabide
Var 9: Ysum, Type: integer, Low/High: (0, 302)
Var 10: sumY, Type: integer, Low/High: (0, 302)
Var 11: Age10, Type: numeric, Low/High: (1.8000, 4.2000)
Var 12: Base4, Type: numeric, Low/High: (1.5000, 37.7500)
```



To estimate a model with *sumY* as the response variable and the *Base* number of seizures, *Age*, and the treatment as explanatory variables, we can use *rxGlm*. A benefit to using *rxGlm* is that the code will scale for use with a much bigger data set.

```
myGlm <- rxGlm(sumY~ Base + Age + Trt, dropFirst = TRUE,
    data = breslow.dat, family = poisson())
summary(myGlm)
```

This results in:

```
Call:
rxGlm(formula = sumY ~ Base + Age + Trt, data = breslow.dat,
    family = poisson(), dropFirst = TRUE)

Generalized Linear Model Results for: sumY ~ Base + Age + Trt
Data: breslow.dat
Dependent variable(s): sumY
Total independent variables: 5 (Including number dropped: 1)
Number of valid observations: 59
Number of missing observations: 0
Family-link: poisson-log

Residual deviance: 559.4437 (on 55 degrees of freedom)

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)    1.9488259  0.1356191  14.370 2.22e-16 ***
Base           0.0226517  0.0005093  44.476 2.22e-16 ***
Age            0.0227401  0.0040240   5.651 5.85e-07 ***
Trt=placebo      Dropped    Dropped Dropped  Dropped
Trt=progabide -0.1527009  0.0478051  -3.194  0.00232 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Condition number of final variance-covariance matrix: 3.3382
Number of iterations: 4
```

To interpret the coefficients, it is sometimes useful to transform them back to the original scale of the dependent variable. In this case:

```
exp(coef(myGlm))
```

```
   (Intercept)           Base            Age   Trt=placebo Trt=progabide
     7.0204403      1.0229102      1.0230007             NA      0.8583864
```

This suggests that, controlling for the base number of seizures and age, those taking progabide during the trial had 85% of the expected number seizures compared with those who didn't.

A common method of checking for overdispersion is to calculate the ratio of the residual deviance with the degrees of freedom, which should be about 1 to fit the assumptions of the model.

```
myGlm$deviance/myGlm$df[2]
```

```
 [1] 10.1717
```

We can see that the ratio is well above one.

The quasi-poisson family can be used to handle over-dispersion. In this case, instead of assuming that the variance and mean are one, a relationship is estimated from the data:

```
myGlm1 <- rxGlm(sumY ~ Base + Age + Trt, dropFirst = TRUE,
    data = breslow.dat, family = quasipoisson())

summary(myGlm1)
} # End of if for robust package
```

```
 Call:
 rxGlm(formula = sumY ~ Base + Age + Trt, data = breslow.dat,
     family = quasipoisson(), dropFirst = TRUE)

 Generalized Linear Model Results for: sumY ~ Base + Age + Trt
 Data: breslow.dat
 Dependent variable(s): sumY
 Total independent variables: 5 (Including number dropped: 1)
 Number of valid observations: 59
 Number of missing observations: 0
 Family-link: quasipoisson-log

 Residual deviance: 559.4437 (on 55 degrees of freedom)

 Coefficients:
                Estimate Std. Error t value Pr(>|t|)
 (Intercept)    1.948826   0.465091   4.190 0.000102 ***
 Base           0.022652   0.001747  12.969 2.22e-16 ***
 Age            0.022740   0.013800   1.648 0.105085
 Trt=placebo     Dropped    Dropped Dropped  Dropped
 Trt=progabide -0.152701   0.163943  -0.931 0.355702
 ---
 Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 (Dispersion parameter for quasipoisson family taken to be 11.76075)

 Condition number of final variance-covariance matrix: 3.3382
 Number of iterations: 4
```

Notice that the coefficients are the same as when using the poisson family, but that the standard errors are larger; the effect of the treatment is no longer significant.

10.2 An Example Using the Gamma Family

The Gamma family is used with data containing positive values with a positive skew. A classic example is estimating the value of auto insurance claims. Using the sample *claims.xdf* data set:

```
#  An Example Using the Gamma Family

claimsXdf <- file.path(rxGetOption("sampleDataDir"),"claims.xdf")

claimsGlm <- rxGlm(cost ~ age + car.age + type, family = Gamma,
                   dropFirst = TRUE, data = claimsXdf)
summary(claimsGlm)


 Call:
 rxGlm(formula = cost ~ age + car.age + type, data = claimsXdf,
     family = Gamma, dropFirst = TRUE)

 Generalized Linear Model Results for: cost ~ age + car.age + type
 File name:
     C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
 3.2.2\library\RevoScaleR\SampleData\claims.xdf
 Dependent variable(s): cost
 Total independent variables: 17 (Including number dropped: 3)
 Number of valid observations: 123
 Number of missing observations: 5
 Family-link: Gamma-inverse

 Residual deviance: 15.6397 (on 109 degrees of freedom)

 Coefficients:
              Estimate Std. Error t value Pr(>|t|)
 (Intercept)  0.0032807  0.0005126   6.400 4.02e-09 ***
 age=17-20      Dropped    Dropped Dropped  Dropped
 age=21-24    0.0006593  0.0005471   1.205 0.230843
 age=25-29    0.0003911  0.0005183   0.755 0.452114
 age=30-34    0.0012388  0.0005982   2.071 0.040720 *
 age=35-39    0.0017152  0.0006514   2.633 0.009685 **
 age=40-49    0.0012649  0.0006007   2.106 0.037516 *
 age=50-59    0.0002863  0.0005087   0.563 0.574771
 age=60+      0.0013006  0.0006041   2.153 0.033519 *
 car.age=0-3    Dropped    Dropped Dropped  Dropped
 car.age=4-7  0.0003444  0.0003535   0.974 0.332120
 car.age=8-9  0.0011005  0.0004161   2.645 0.009375 **
 car.age=10+  0.0034437  0.0006107   5.639 1.36e-07 ***
 type=A         Dropped    Dropped Dropped  Dropped
 type=B      -0.0004443  0.0004880  -0.911 0.364508
 type=C      -0.0004189  0.0004912  -0.853 0.395668
 type=D      -0.0016209  0.0004344  -3.732 0.000304 ***
 ---
 Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 (Dispersion parameter for Gamma family taken to be 0.1785316)

 Condition number of final variance-covariance matrix: 12.4648
 Number of iterations: 4
```

But, note that these estimates are conditional on the fact that a claim was made.

10.3 An Example Using the Tweedie Family

The Tweedie family of distributions provide flexible models for estimation. The power parameter *var.power* determines the shape of the distribution, with familiar models as special cases: if *var.power* is set to 0, Tweedie is a normal distribution; when set to 1, it is Poisson; when 2, it is Gamma; when 3, it is inverse Gaussian. If *var.power* is between 1 and 2, it is a compound Poisson distribution and is appropriate for positive data that also contains exact zeros, for example, insurance claims data, rainfall data, or fish-catch data. If *var.power* is greater than 2, it is appropriate for positive data.

In this example, we'll use a subsample from the 5% sample of the U.S. 2000 census. We will consider the annual cost of property insurance for heads of household ages 21 through 89, and its relationship to age, sex, and region. A variable "perwt" in the data set represents the probability weight for that observation. First, to create the subsample (specify the correct data path for your downloaded data):

```
bigDataDir = "C:/MRS/Data"
bigCensusData <- file.path(bigDataDir, "Census5PCT2000.xdf")
propinFile <- "CensusPropertyIns.xdf"

propinDS <- rxDataStep(inData = bigCensusData, outFile = propinFile,
    rowSelection =  (related == 'Head/Householder') & (age > 20) & (age < 90),
    varsToKeep = c("propinsr", "age", "sex", "region", "perwt"),
    blocksPerRead = 10, overwrite = TRUE)
rxGetInfo(propinDS)

 File name: C:\YourWorkingDir\CensusPropertyIns.xdf
 Number of observations: 5175270
 Number of variables: 5
 Number of blocks: 10
 Compression type: zlib
```

An Xdf data source representing the new data file is returned. The new data file has over 5 million observations.

Let's do one more step in data cleaning. The variable *region* has some very long factor level character strings, and it also has a number of levels for which there are no observations. We can see this using *rxSummary*:

```
rxSummary(~region, data = propinDS)

 Call:
 rxSummary(formula = ~region, data = propinDS)

 Summary Statistics Results for: ~region
 File name: C:\YourWorkingDir\CensusPropertyIns.xdf
 Number of valid observations: 5175270


 Category Counts for region
 Number of categories: 17
```

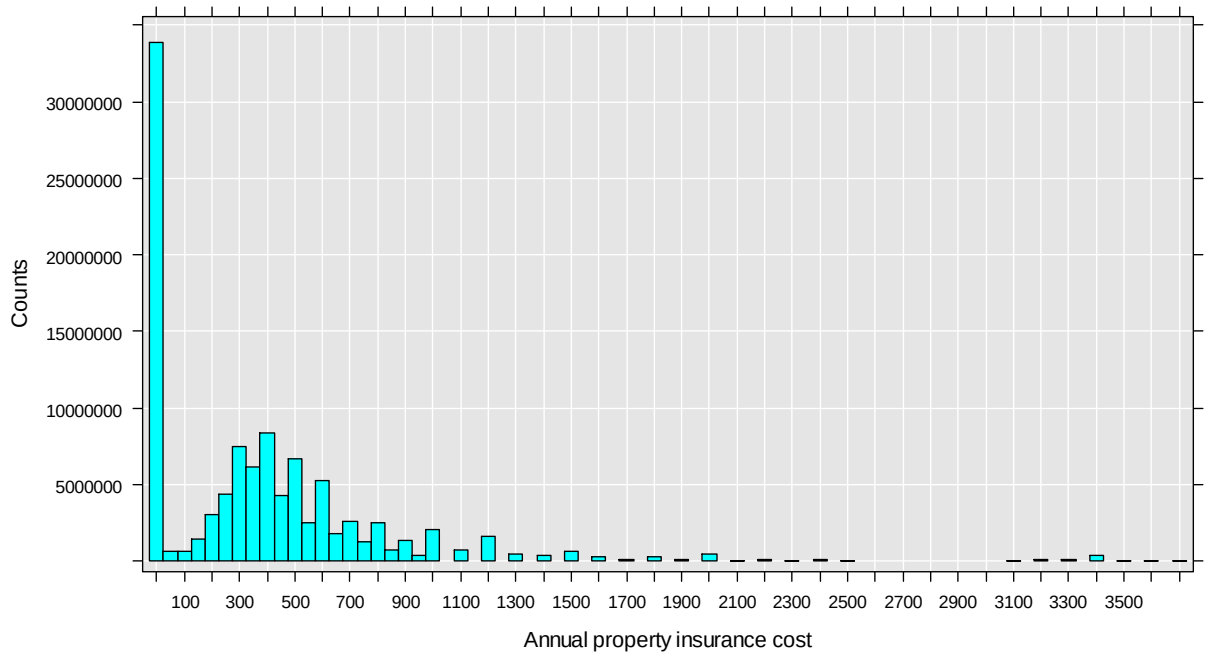
```
Number of valid observations: 5175270
Number of missing observations: 0

 region                                          Counts
 New England Division                            265372
 Middle Atlantic Division                        734585
 Mixed Northeast Divisions (1970 Metro)               0
 East North Central Div.                         847367
 West North Central Div.                         366417
 Mixed Midwest Divisions (1970 Metro)                 0
 South Atlantic Division                         981614
 East South Central Div.                         324003
 West South Central Div.                         553425
 Mixed Southern Divisions (1970 Metro)                0
 Mountain Division                               328940
 Pacific Division                                773547
 Mixed Western Divisions (1970 Metro)                 0
 Military/Military reservations                       0
 PUMA boundaries cross state lines-1% sample          0
 State not identified                                 0
 Inter-regional county group (1970 Metro samples)     0
```

We can use the *rxFactors* function rename and reduce the number of levels:

```
regionLevels <- list( "New England" = "New England Division",
    "Middle Atlantic" = "Middle Atlantic Division",
    "East North Central" = "East North Central Div.",
    "West North Central" = "West North Central Div.",
    "South Atlantic" = "South Atlantic Division",
    "East South Central" = "East South Central Div.",
    "West South Central" = "West South Central Div.",
    "Mountain" ="Mountain Division",
    "Pacific" ="Pacific Division")

rxFactors(inData = propinDS, outFile = propinDS,
    factorInfo = list(region = list(newLevels = regionLevels,
        otherLevel = "Other")),
    overwrite = TRUE)
```

As a first step to analysis, let's look at a histogram of the property insurance cost:

```
rxHistogram(~propinsr, data = propinDS, pweights = "perwt")
```



This appears to be a good match for the Tweedie family with a variance power parameter between 1 and 2, since it has a "clump" of exact zeros in addition to a distribution of positive values.

We can estimate the parameters using *rxGlm*, setting the *var.power* argument to 1.5. As explanatory variables we'll use sex, an "on-the-fly" factor variable with a level for each age, and region:

```
propinGlm <- rxGlm(propinsr~sex + F(age) + region,
    pweights = "perwt", data = propinDS,
    family = rxTweedie(var.power = 1.5), dropFirst = TRUE)
summary(propinGlm)
```

```
Call:
rxGlm(formula = propinsr ~ sex + F(age) + region, data = propinDS,
    family = rxTweedie(var.power = 1.5), pweights = "perwt",
    dropFirst = TRUE)

Generalized Linear Model Results for: propinsr ~ sex + F(age) + region
File name: C:\YourWorkingDir\CensusPropertyIns.xdf
Probability weights: perwt
Dependent variable(s): propinsr
Total independent variables: 82 (Including number dropped: 4)
Number of valid observations: 5175270
Number of missing observations: 0
Family-link: Tweedie-mu^-0.5

Residual deviance: 3292809839.3236 (on 5175192 degrees of freedom)

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

```
(Intercept)                1.231e-01  5.893e-04  208.961 2.22e-16 ***
sex=Male                     Dropped    Dropped  Dropped  Dropped
sex=Female                 9.026e-03  3.164e-05  285.305 2.22e-16 ***
F_age=21                     Dropped    Dropped  Dropped  Dropped
F_age=22                  -9.208e-03  7.523e-04  -12.240 2.22e-16 ***
F_age=23                  -1.980e-02  6.966e-04  -28.430 2.22e-16 ***
F_age=24                  -2.856e-02  6.648e-04  -42.955 2.22e-16 ***
F_age=25                  -3.652e-02  6.432e-04  -56.776 2.22e-16 ***
F_age=26                  -4.371e-02  6.289e-04  -69.500 2.22e-16 ***
F_age=27                  -4.894e-02  6.182e-04  -79.162 2.22e-16 ***
F_age=28                  -5.398e-02  6.099e-04  -88.506 2.22e-16 ***
F_age=29                  -5.787e-02  6.043e-04  -95.749 2.22e-16 ***
F_age=30                  -6.064e-02  6.020e-04 -100.716 2.22e-16 ***
F_age=31                  -6.336e-02  6.004e-04 -105.522 2.22e-16 ***
F_age=32                  -6.526e-02  5.991e-04 -108.933 2.22e-16 ***
F_age=33                  -6.721e-02  5.975e-04 -112.489 2.22e-16 ***
F_age=34                  -6.854e-02  5.962e-04 -114.948 2.22e-16 ***
F_age=35                  -6.942e-02  5.949e-04 -116.688 2.22e-16 ***
F_age=36                  -7.090e-02  5.941e-04 -119.342 2.22e-16 ***
F_age=37                  -7.184e-02  5.936e-04 -121.023 2.22e-16 ***
F_age=38                  -7.265e-02  5.931e-04 -122.498 2.22e-16 ***
F_age=39                  -7.354e-02  5.926e-04 -124.090 2.22e-16 ***
F_age=40                  -7.401e-02  5.923e-04 -124.954 2.22e-16 ***
F_age=41                  -7.462e-02  5.923e-04 -125.994 2.22e-16 ***
F_age=42                  -7.508e-02  5.920e-04 -126.819 2.22e-16 ***
F_age=43                  -7.568e-02  5.920e-04 -127.846 2.22e-16 ***
F_age=44                  -7.597e-02  5.919e-04 -128.344 2.22e-16 ***
F_age=45                  -7.642e-02  5.918e-04 -129.139 2.22e-16 ***
F_age=46                  -7.693e-02  5.919e-04 -129.973 2.22e-16 ***
F_age=47                  -7.727e-02  5.918e-04 -130.564 2.22e-16 ***
F_age=48                  -7.749e-02  5.919e-04 -130.927 2.22e-16 ***
F_age=49                  -7.783e-02  5.919e-04 -131.488 2.22e-16 ***
F_age=50                  -7.809e-02  5.919e-04 -131.941 2.22e-16 ***
F_age=51                  -7.853e-02  5.919e-04 -132.678 2.22e-16 ***
F_age=52                  -7.888e-02  5.916e-04 -133.326 2.22e-16 ***
F_age=53                  -7.919e-02  5.916e-04 -133.859 2.22e-16 ***
F_age=54                  -7.909e-02  5.931e-04 -133.348 2.22e-16 ***
F_age=55                  -7.938e-02  5.929e-04 -133.873 2.22e-16 ***
F_age=56                  -7.930e-02  5.929e-04 -133.751 2.22e-16 ***
F_age=57                  -7.959e-02  5.928e-04 -134.276 2.22e-16 ***
F_age=58                  -7.935e-02  5.937e-04 -133.644 2.22e-16 ***
F_age=59                  -7.923e-02  5.942e-04 -133.336 2.22e-16 ***
F_age=60                  -7.894e-02  5.946e-04 -132.753 2.22e-16 ***
F_age=61                  -7.917e-02  5.947e-04 -133.122 2.22e-16 ***
F_age=62                  -7.912e-02  5.949e-04 -133.003 2.22e-16 ***
F_age=63                  -7.904e-02  5.954e-04 -132.746 2.22e-16 ***
F_age=64                  -7.886e-02  5.956e-04 -132.405 2.22e-16 ***
F_age=65                  -7.878e-02  5.952e-04 -132.359 2.22e-16 ***
F_age=66                  -7.871e-02  5.961e-04 -132.031 2.22e-16 ***
F_age=67                  -7.864e-02  5.963e-04 -131.869 2.22e-16 ***
F_age=68                  -7.861e-02  5.966e-04 -131.766 2.22e-16 ***
F_age=69                  -7.845e-02  5.967e-04 -131.490 2.22e-16 ***
F_age=70                  -7.861e-02  5.965e-04 -131.790 2.22e-16 ***
F_age=71                  -7.856e-02  5.970e-04 -131.600 2.22e-16 ***
F_age=72                  -7.850e-02  5.971e-04 -131.460 2.22e-16 ***
F_age=73                  -7.813e-02  5.977e-04 -130.714 2.22e-16 ***
F_age=74                  -7.818e-02  5.981e-04 -130.722 2.22e-16 ***
F_age=75                  -7.800e-02  5.986e-04 -130.302 2.22e-16 ***
F_age=76                  -7.781e-02  5.993e-04 -129.825 2.22e-16 ***
F_age=77                  -7.763e-02  6.002e-04 -129.342 2.22e-16 ***
F_age=78                  -7.735e-02  6.009e-04 -128.728 2.22e-16 ***
F_age=79                  -7.724e-02  6.024e-04 -128.221 2.22e-16 ***
F_age=80                  -7.646e-02  6.045e-04 -126.495 2.22e-16 ***
```

```
F_age=81                  -7.651e-02  6.060e-04 -126.244 2.22e-16 ***
F_age=82                  -7.643e-02  6.081e-04 -125.693 2.22e-16 ***
F_age=83                  -7.600e-02  6.109e-04 -124.411 2.22e-16 ***
F_age=84                  -7.546e-02  6.145e-04 -122.798 2.22e-16 ***
F_age=85                  -7.529e-02  6.183e-04 -121.775 2.22e-16 ***
F_age=86                  -7.441e-02  6.259e-04 -118.882 2.22e-16 ***
F_age=87                  -7.422e-02  6.324e-04 -117.363 2.22e-16 ***
F_age=88                  -7.339e-02  6.463e-04 -113.553 2.22e-16 ***
F_age=89                  -7.310e-02  6.569e-04 -111.284 2.22e-16 ***
region=New England           Dropped    Dropped  Dropped  Dropped
region=Middle Atlantic     1.710e-03  6.893e-05   24.807 2.22e-16 ***
region=East North Central  3.552e-03  6.867e-05   51.723 2.22e-16 ***
region=West North Central  4.200e-04  7.697e-05    5.457 4.83e-08 ***
region=South Atlantic     -1.227e-03  6.521e-05  -18.821 2.22e-16 ***
region=East South Central -7.894e-04  7.793e-05  -10.130 2.22e-16 ***
region=West South Central -5.857e-03  6.732e-05  -87.011 2.22e-16 ***
region=Mountain            1.821e-03  8.060e-05   22.596 2.22e-16 ***
region=Pacific            -5.990e-04  6.732e-05   -8.897 2.22e-16 ***
region=Other                 Dropped    Dropped  Dropped  Dropped
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Tweedie family taken to be 546.4888)

Condition number of final variance-covariance matrix: 5980.277
Number of iterations: 8
```

A good way to begin examining the results of of the estimated model is to look at predicted values for given explanatory characteristics. For example, let's create a prediction data set for the South Atlantic region for all ages and sexes:

```
# Get the region factor levels
varInfo <- rxGetVarInfo(propinDS)
regionLabels <- varInfo$region$levels

# Create a prediction data set for region 5, all ages, both sexes
region <- factor(rep(5, times=138), levels = 1:10, labels = regionLabels)
age <- c(21:89, 21:89)
sex <- factor(c(rep(1, times=69), rep(2, times=69)),
     levels = 1:2,
     labels = c("Male", "Female"))
predData <- data.frame(age, sex, region)
```

Now we'll use that as a basis for a similar prediction data set for the Middle Atlantic region:

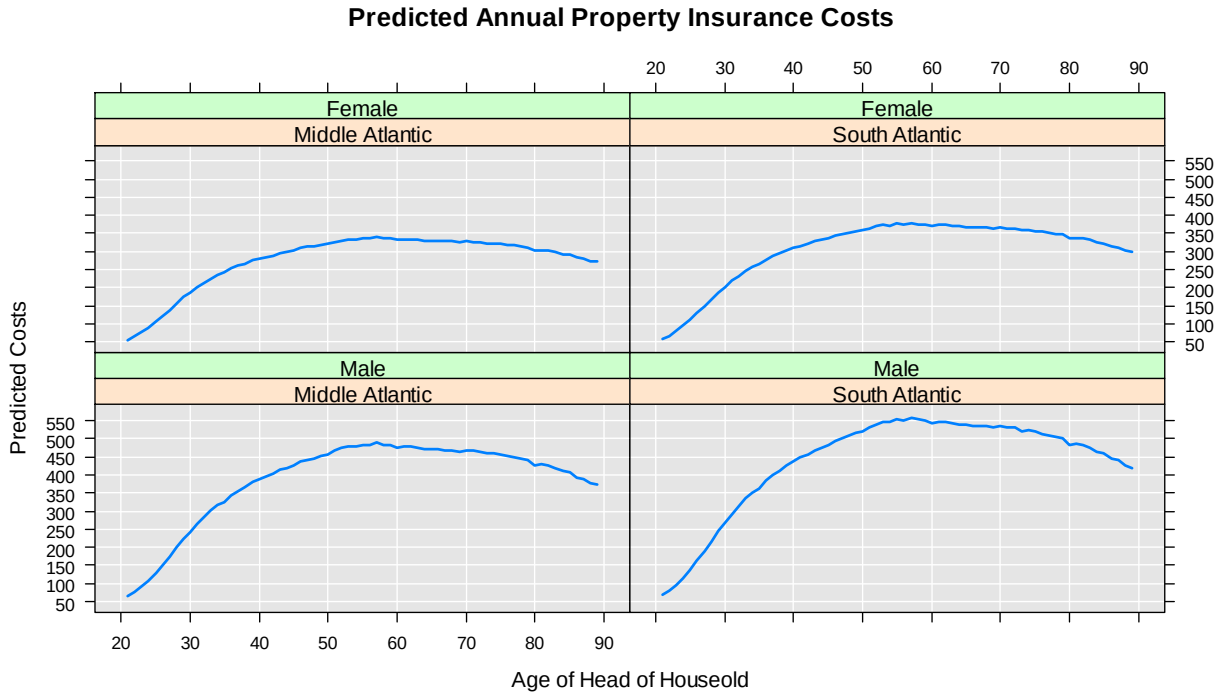
```
# Create a prediction data set for region 2, all ages, both sexes
predData2 <- predData
predData2$region <-factor(rep(2, times=138), levels = 1:10,
     labels = varInfo$region$levels)
```

Next we'll combine the two data sets, and compute the predicted values for annual property insurance cost using our estimated *rxGlm* model:

```
# Combine data sets and compute predictions
predData <- rbind(predData, predData2)
outData <- rxPredict(propinGlm,  data = predData)
```

Last, we can combine the predicted values with our prediction data frame and plot:

```
predData$predicted <- outData$propinsr_Pred
rxLinePlot( predicted ~age|region+sex, data = predData,
  title = "Predicted Annual Property Insurance Costs",
  xTitle = "Age of Head of Household",
  yTitle = "Predicted Costs")
```



10.4 Stepwise Generalized Linear Models

Stepwise generalized linear models help you determine which variables are most important to include in the model. You provide a minimal, or lower, model formula and a maximal, or upper, model formula, and using forward selection, backward elimination, or bidirectional search, the algorithm determines the model formula that provides the best fit based on an AIC selection criterion or a significance level criterion.

As an example, consider again the Gamma family model from section 10.2:

```
claimsXdf <- file.path(rxGetOption("sampleDataDir"),"claims.xdf")
claimsGlm <- rxGlm(cost ~ age + car.age + type, family = Gamma,
                   dropFirst = TRUE, data = claimsXdf)
summary(claimsGlm)
```

We can recast this as a stepwise model by specifying a variableSelection argument using the rxStepControl function to provide our stepwise arguments:

```
claimsGlmStep <- rxGlm(cost ~ age, family = Gamma, dropFirst=TRUE,
                       data=claimsXdf, variableSelection =
                       rxStepControl(scope = ~ age + car.age + type ))
summary(claimsGlmStep)

 Call:
 rxGlm(formula = cost ~ age, data = claimsXdf, family = Gamma,
     variableSelection = rxStepControl(scope = ~age + car.age +
         type), dropFirst = TRUE)

 Generalized Linear Model Results for: cost ~ car.age + type
 File name:
     C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
 3.2.2\library\RevoScaleR\SampleData\claims.xdf
 Dependent variable(s): cost
 Total independent variables: 9 (Including number dropped: 2)
 Number of valid observations: 123
 Number of missing observations: 5
 Family-link: Gamma-inverse

 Residual deviance: 18.0433 (on 116 degrees of freedom)

 Coefficients:
               Estimate Std. Error t value Pr(>|t|)
 (Intercept)  0.0040354  0.0004661   8.657 3.24e-14 ***
 car.age=0-3    Dropped    Dropped Dropped  Dropped
 car.age=4-7  0.0003568  0.0004037   0.884  0.37868
 car.age=8-9  0.0011825  0.0004688   2.522  0.01302 *
 car.age=10+  0.0035478  0.0006853   5.177 9.57e-07 ***
 type=A         Dropped    Dropped Dropped  Dropped
 type=B      -0.0004512  0.0005519  -0.818  0.41528
 type=C      -0.0004135  0.0005558  -0.744  0.45837
 type=D      -0.0016307  0.0004923  -3.313  0.00123 **
 ---
 Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 (Dispersion parameter for Gamma family taken to be 0.2249467)

 Condition number of final variance-covariance matrix: 9.1775
 Number of iterations: 5
```

We see that in the stepwise model fit, age no longer appears in the final model.

10.4.1 Plotting Model Coefficients

The ability to save model coefficients using the argument *keepStepCoefs = TRUE* within the *rxStepControl* call and to plot them with the function *rxStepPlot* was described in great detail for stepwise *rxLinMod* in section 8.8.5. However, this functionality is also available for stepwise *rxGLM* objects.

Chapter 11.

Estimating Decision Tree Models

The `rxDTree` function in RevoScaleR fits tree-based models using a binning-based recursive partitioning algorithm. The resulting model is similar to that produced by the recommended R package `rpart`. Both classification-type trees and regression-type trees are supported; as with `rpart`, the difference is determined by the nature of the response variable: a factor response generates a classification tree; a numeric response generates a regression tree.

11.1 The rxDTree Algorithm

Decision trees are effective algorithms widely used for classification and regression. Building a decision tree generally requires that all continuous variables be sorted in order to decide where to split the data. This sorting step becomes time and memory prohibitive when dealing with large data. Various techniques have been proposed to overcome the sorting obstacle, which can be roughly classified into two groups: performing data pre-sorting or using approximate summary statistic of the data. While pre-sorting techniques follow standard decision tree algorithms more closely, they cannot accommodate very large data sets. These big data decision trees are normally parallelized in various ways to enable large scale learning: data parallelism partitions the data either horizontally or vertically so that different processors see different observations or variables and task parallelism builds different tree nodes on different processors.

The *rxDTree* algorithm is an approximate decision tree algorithm with horizontal data parallelism, especially designed for handling very large data sets. It uses histograms as the approximate compact representation of the data and builds the decision tree in a breadth-first fashion. The algorithm can be executed in parallel settings such as a multicore machine or a distributed environment with a master-worker architecture. Each worker gets only a subset of the observations of the data, but has a view of the complete tree built so far. It builds a histogram from the observations it sees, which essentially compresses the data to a fixed amount of memory. This approximate description of the data is then sent to a master with constant low communication complexity independent of the size of the data set. The master integrates the information received from each of the workers and determines which terminal tree nodes to split and how. Since the histogram is built in parallel, it can be quickly constructed even for extremely large data sets.

With *rxDTree*, you can control the balance between time complexity and prediction accuracy by specifying the maximum number of bins for the histogram. The algorithm builds the histogram with roughly equal number of observations in each bin and takes the boundaries of the bins as the candidate splits for the terminal tree nodes. Since only a limited number of split locations are examined, it is possible that a suboptimal split point is chosen causing the entire tree to be different from the one constructed by a standard algorithm. However, it has been shown analytically that the error rate of the parallel tree approaches the error rate of the serial tree, even though the trees are not identical. You can set the number of bins in the histograms to control the tradeoff between accuracy and speed: a large number of bins allows a more accurate description of the data and thus more accurate results, whereas a small number of bins reduces time complexity and memory usage.

In the case of integer predictors for which the number of bins equals or exceeds the number of observations, the rxDTree algorithm produces the same results as the standard sorting algorithms.

11.2 A Simple Classification Tree

In Chapter 9, we fit a simple logistic regression model to rpart's kyphosis data. That model is easily recast as a classification tree using *rxDTree* as follows:

```
###########################################################
# Chapter 11: Estimating Decision Tree Models
#  A Simple Classification Tree
Ch11Start <- Sys.time()


data("kyphosis", package="rpart")
kyphTree <- rxDTree(Kyphosis ~ Age + Start + Number, data = kyphosis,
      cp=0.01)
```

```
kyphTree

 Call:
 rxDTree(formula = Kyphosis ~ Age + Start + Number, data = kyphosis,
     cp = 0.01)
 Data:  kyphosis
 Number of valid observations:  81
 Number of missing observations:  0

 Tree representation:
 n= 81

 node), split, n, loss, yval, (yprob)
       * denotes terminal node

  1) root 81 17 absent (0.79012346 0.20987654)
    2) Start>=8.5 62  6 absent (0.90322581 0.09677419)
      4) Start>=14.5 29  0 absent (1.00000000 0.00000000) *
      5) Start< 14.5 33  6 absent (0.81818182 0.18181818)
       10) Age< 55 12  0 absent (1.00000000 0.00000000) *
       11) Age>=55 21  6 absent (0.71428571 0.28571429)
         22) Age>=111 14  2 absent (0.85714286 0.14285714) *
         23) Age< 111 7  3 present (0.42857143 0.57142857) *
    3) Start< 8.5 19  8 present (0.42105263 0.57894737) *
```

Recall our conclusions from fitting this model earlier with rxCube: the probability of the post-operative complication Kyphosis seems to be greater if the Start is a cervical vertebra and as more vertebrae are involved in the surgery. Similarly, it appears that the dependence on age is non-linear: it first increases with age, peaks in the range 5-9, and then decreases again.

The rxDTree model seems to confirm these earlier conclusions—for Start < 8.5, 11 of 19 observed subjects developed Kyphosis, while none of the 29 subjects with Start >= 14.5 did. For the remaining 33 subjects, Age was the primary splitting factor, and as we observed earlier, ages 5 to 9 had the highest probability of developing Kyphosis.

The returned object *kyphTree* is an object of class *rxDTree*. The *rxDTree* class is modeled closely on the *rpart* class, so that objects of class *rxDTree* have most essential components of an *rpart* object: frame, cptable, splits, etc. By default, however, *rxDTree* objects do not inherit from class *rpart*. You can, however, use the *rxAddInheritance* function to add *rpart* inheritance to *rxDTree* objects.

11.3 A Simple Regression Tree

As a simple example of a regression tree, consider the *mtcars* data set and let's fit gas mileage (*mpg*) using displacement (*disp*) as a predictor:

```
#  A Simple Regression Tree

mtcarTree <- rxDTree(mpg ~ disp, data=mtcars)
mtcarTree

 Call:
```

```
rxDTree(formula = mpg ~ disp, data = mtcars)
Data:  mtcars
Number of valid observations:  32
Number of missing observations:  0

Tree representation:
n= 32

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

1) root 32 1126.0470 20.09063
  2) disp>=163.5 18  143.5894 15.99444 *
  3) disp< 163.5 14  292.1343 25.35714 *
```

There's a clear split between larger cars (those with engine displacement greater than 163.5 cubic inches) and smaller cars.

11.4 A Larger Regression Tree Model

As a more complex example, we return to the censusWorkers data. We will create a regression tree predicting wage income from age, sex, and weeks worked, using the perwt variable as probability weights:

```
#  A Larger Regression Tree Model

censusWorkers <- file.path(rxGetOption("sampleDataDir"),
    "CensusWorkers.xdf")
rxGetInfo(censusWorkers, getVarInfo=TRUE)
incomeTree <- rxDTree(incwage ~ age + sex + wkswork1, pweights = "perwt",
    maxDepth = 3, minBucket = 30000, data = censusWorkers)
incomeTree
```

```
Call:
rxDTree(formula = incwage ~ age + sex + wkswork1, data = censusWorkers,
    pweights = "perwt", minBucket = 30000, maxDepth = 3)
File:  C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-3.2.2\
library\RevoScaleR\SampleData\CensusWorkers.xdf
Number of valid observations:  351121
Number of missing observations:  0

Tree representation:
n= 351121

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

 1) root 351121 1.177765e+16 35788.47
   2) sex=Female 161777 2.271425e+15 26721.09
     4) wkswork1< 51.5 56874 5.757587e+14 19717.74 *
     5) wkswork1>=51.5 104903 1.608813e+15 30505.87
      10) age< 34.5 31511 2.500078e+14 25836.32 *
      11) age>=34.5 73392 1.338235e+15 32576.74 *
   3) sex=Male 189344 9.008506e+15 43472.71
     6) age< 31.5 48449 6.445334e+14 27577.80 *
     7) age>=31.5 140895 8.010642e+15 49221.82
      14) wkswork1< 51.5 34359 1.550839e+15 37096.62 *
```

```
      15) wkswork1>=51.5 106536 6.326896e+15 53082.08 *
```

The primary split here (not surprising given our analysis of this data set in the *Getting Started Guide*) is sex; women on average earn substantially less than men. The additional splits are also not surprising; older workers earn more than younger workers, and those who work more hours tend to earn more than those who work fewer hours.

11.5 Controlling the Model Fit

The `rxDTree` function has a number of options for controlling the model fit. Most of these control parameters will be familiar to `rpart` users, but the defaults have been modified in some cases to better support large data tree models. A full listing of these options can be found in the `rxDTree` help file, but the following have been found in our testing to be the most useful at controlling the time required to fit a model with `rxDTree`:

- `xVal`: this controls the number of folds used to perform cross-validation. The default of 2 allows for some pruning; once you have closed in a model you may want to increase the value for final fitting and pruning.
- `maxDepth`: this sets the maximum depth of any node of the tree. Computations grow rapidly more expensive as the depth increases, so we recommend a maxDepth of 10 to 15.
- `maxCompete`: this specifies the number of "competitor splits" retained in the output. By default, `rxDTree` sets this to 0, but a setting of 3 or 4 can be useful for diagnostic purposes in determining why a particular split was chosen.
- `maxSurrogate`: this specifies the number of surrogate splits retained in the output. Again, by default `rxDTree` sets this to 0. Surrogate splits are used to assign an observation when the primary split variable is missing for that observation.
- `maxNumBins`: this controls the maximum number of bins used for each variable. Managing the number of bins is important in controlling memory usage. The default is to use the larger of 101 and the square root of the number of observations for small to moderate size data sets (up to about one million observations), but for larger sets to use 1001 bins. For small data sets with continuous predictors, you may find that you need to increase the `maxNumBins` to obtain models that resemble those from rpart.

For large data sets (100000 or more observations), you may need to adjust the following parameters to obtain meaningful models:

- `cp`: this is a complexity parameter and sets the bar for how much a split must reduce the complexity before being accepted. We have set the default to 0 and recommend using `maxDepth` and `minBucket` to control your tree sizes. If you want to specify a `cp` value, start with a conservative value, such as rpart's 0.01; if you don't see an adequate

number of splits, decrease the *cp* by powers of 10 until you do. For our large airline data, we have found interesting models begin with a *cp* of about 1e-4.

- *minSplit*, *minBucket*: these determine how many observations must be in a node before a split is attempted (*minSplit*) and how many must remain in a terminal node (*minBucket*).

11.6 Large Data Tree Models

Scaling decision trees to very large data sets is possible with *rxDTree* but should be done with caution—the wrong choice of model parameters can easily lead to models that take hours or longer to estimate, even in a distributed computing environment. For example, in the *Getting Started Guide*, we estimated linear models using the big airline data and used the variable *Origin* as a predictor in several models. The *Origin* variable is a factor variable with 373 levels with no obvious ordering. Incorporating this variable into an *rxDTree* model that is performing more than two level classification can easily consume hours of computation time. To prevent such unintended consequences, *rxDTree* has a parameter *maxUnorderedLevels* which defaults to 32; in the case of *Origin*, this parameter would flag an error. However, a factor variable of "Region" which groups the airports of *Origin* by location may well be a useful proxy, and can be constructed to have only a limited number of levels. Numeric and ordered factor predictors are much more easily incorporated into the model.

As an example of a large data classification tree, consider the following simple model using the 7% subsample of the full airline data (this uses the variable *ArrDel15* indicating flights with an arrival delay of 15 minutes or more):

```
#  Large Data Tree Models


bigDataDir <- "C:/MRS/Data"
sampleAirData <- file.path(bigDataDir, "AirOnTime7Pct.xdf")
airlineTree <- rxDTree(ArrDel15 ~ CRSDepTime + DayOfWeek, data = sampleAirData,
    blocksPerRead = 30, maxDepth = 5, cp = 1e-5)
```

The default cp of 0 produces a very large number of splits; specifying *cp* = 1e-5 produces a more manageable set of splits in this model:

```
airlineTree

 Call:
 rxDTree(formula = ArrDel15 ~ CRSDepTime + DayOfWeek, data = sampleAirData,
     maxDepth = 5, cp = 1e-05, blocksPerRead = 30)
 File:  C:\MRS\Data\AirOnTime7Pct.xdf
 Number of valid observations:  10186272
 Number of missing observations:  213483

 Tree representation:
 n= 10186272
```

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

 1) root 10186272 1630331.000 0.20008640
   2) CRSDepTime< 13.1745 4941190  642452.000 0.15361830
     4) CRSDepTime< 8.3415 1777685  189395.700 0.12123970
       8) CRSDepTime>=0.658 1717573  178594.900 0.11787560
        16) CRSDepTime< 6.7665 599548   52711.450 0.09740671
          32) CRSDepTime>=1.625 578762   49884.260 0.09526714 *
          33) CRSDepTime< 1.625 20786    2750.772 0.15698070 *
        17) CRSDepTime>=6.7665 1118025  125497.500 0.12885220
          34) DayOfWeek=Sun 134589   11722.540 0.09638975 *
          35) DayOfWeek=Mon,Tues,Wed,Thur,Fri,Sat 983436 113613.80 0.13329490 *
       9) CRSDepTime< 0.658 60112   10225.960 0.21736090
        18) CRSDepTime>=0.2415 9777    1429.046 0.17776410 *
        19) CRSDepTime< 0.2415 50335    8778.609 0.22505220 *
     5) CRSDepTime>=8.3415 3163505  450145.400 0.17181290
      10) CRSDepTime< 11.3415 1964400  268472.400 0.16335320
        20) DayOfWeek=Sun 271900   30839.160 0.13043400
          40) CRSDepTime< 9.7415 126700   13381.800 0.12002370 *
          41) CRSDepTime>=9.7415 145200   17431.650 0.13951790 *
        21) DayOfWeek=Mon,Tues,Wed,Thur,Fri,Sat 1692500  237291.300 0.16864170
          42) DayOfWeek=Tues,Wed,Sat 835355  113384.500 0.16196470 *
          43) DayOfWeek=Mon,Thur,Fri 857145  123833.200 0.17514890 *
      11) CRSDepTime>=11.3415 1199105  181302.000 0.18567180
        22) DayOfWeek=Mon,Tues,Wed,Sat,Sun 852016  124610.900 0.17790390
          44) DayOfWeek=Tues,Sun 342691   48917.520 0.17250230 *
          45) DayOfWeek=Mon,Wed,Sat 509325   75676.600 0.18153830 *
        23) DayOfWeek=Thur,Fri 347089   56513.560 0.20474000 *
   3) CRSDepTime>=13.1745 5245082  967158.500 0.24386220
     6) DayOfWeek=Mon,Tues,Wed,Sat,Sun 3708992  651771.300 0.22746990
      12) DayOfWeek=Sat 635207   96495.570 0.18681000
        24) CRSDepTime>=20.2745 87013   12025.600 0.16564190 *
        25) CRSDepTime< 20.2745 548194   84424.790 0.19016990 *
      13) DayOfWeek=Mon,Tues,Wed,Sun 3073785  554008.600 0.23587240
        26) CRSDepTime< 16.508 1214018  203375.700 0.21281150
          52) CRSDepTime< 15.1325 709846  114523.300 0.20223400 *
          53) CRSDepTime>=15.1325 504172   88661.120 0.22770400 *
        27) CRSDepTime>=16.508 1859767  349565.800 0.25092610
          54) DayOfWeek=Mon,Tues 928523  168050.900 0.23729730 *
          55) DayOfWeek=Wed,Sun 931244  181170.600 0.26451500 *
     7) DayOfWeek=Thur,Fri 1536090  311984.200 0.28344240
      14) CRSDepTime< 15.608 445085   82373.020 0.24519140
        28) CRSDepTime< 14.6825 273682   49360.240 0.23609880 *
        29) CRSDepTime>=14.6825 171403   32954.030 0.25970960 *
      15) CRSDepTime>=15.608 1091005  228694.300 0.29904720
        30) CRSDepTime>=21.9915 64127   11932.930 0.24718140 *
        31) CRSDepTime< 21.9915 1026878  216578.100 0.30228620
          62) CRSDepTime< 17.0745 264085   53451.260 0.28182970 *
          63) CRSDepTime>=17.0745 762793  162978.000 0.30936830 *
```

Looking at the fitted objects cptable component, we can look at whether we have overfitted the model:

```
airlineTree$cptable
```

```
             CP nsplit rel error    xerror         xstd
1  1.270950e-02      0 1.0000000 1.0000002 0.0004697734
2  2.087342e-03      1 0.9872905 0.9873043 0.0004629111
3  1.785488e-03      2 0.9852032 0.9852215 0.0004625035
4  7.772395e-04      3 0.9834177 0.9834381 0.0004608330
```

```
5  6.545095e-04      4 0.9826404 0.9826606 0.0004605065
6  5.623968e-04      5 0.9819859 0.9820200 0.0004602950
7  3.525848e-04      6 0.9814235 0.9814584 0.0004602578
8  2.367018e-04      7 0.9810709 0.9811071 0.0004600062
9  2.274981e-04      8 0.9808342 0.9808700 0.0004597725
10 2.112635e-04      9 0.9806067 0.9806567 0.0004596187
11 2.097651e-04     10 0.9803955 0.9804365 0.0004595150
12 1.173008e-04     11 0.9801857 0.9803311 0.0004594245
13 1.124180e-04     12 0.9800684 0.9800354 0.0004592792
14 1.089414e-04     13 0.9799560 0.9800354 0.0004592792
15 9.890134e-05     14 0.9798471 0.9799851 0.0004592187
16 9.125152e-05     15 0.9797482 0.9798766 0.0004591605
17 4.687397e-05     16 0.9796569 0.9797504 0.0004591074
18 4.510554e-05     17 0.9796100 0.9797292 0.0004590784
19 3.603837e-05     18 0.9795649 0.9796812 0.0004590301
20 2.771093e-05     19 0.9795289 0.9796383 0.0004590247
21 1.577140e-05     20 0.9795012 0.9796013 0.0004590000
22 1.122899e-05     21 0.9794854 0.9795671 0.0004589736
23 1.025944e-05     22 0.9794742 0.9795560 0.0004589678
24 1.000000e-05     23 0.9794639 0.9795455 0.0004589660
```

We see a steady decrease in cross-validation error (xerror) as the number of splits increase, but note that at about nsplit=11 the rate of change slows dramatically. The optimal model is probably very near here. (The total number of passes through the data is equal to a base of *maxDepth* + 3, plus *xVal* times (*maxDepth* + 2), where *xVal* is the number of folds for cross-validation and *maxDepth* is the maximum tree depth. Thus a depth 10 tree with 4-fold cross-validation will require 13 + 48, or 61, passes through the data.)

To prune the tree back, use the *prune.rxDTree* function:

```
airlineTree4 <- prune.rxDTree(airlineTree, cp=1e-4)
airlineTree4

 Call:
 rxDTree(formula = ArrDel15 ~ CRSDepTime + DayOfWeek, data = sampleAirData,
     maxDepth = 5, cp = 1e-05, blocksPerRead = 30)
 File:  C:\MRS\Data\AirOnTime7Pct.xdf
 Number of valid observations:  10186272
 Number of missing observations:  213483

 Tree representation:
 n= 10186272

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

  1) root 10186272 1630331.00 0.20008640
    2) CRSDepTime< 13.1745 4941190  642452.00 0.15361830
      4) CRSDepTime< 8.3415 1777685  189395.70 0.12123970
        8) CRSDepTime>=0.658 1717573  178594.90 0.11787560
         16) CRSDepTime< 6.7665 599548   52711.45 0.09740671 *
         17) CRSDepTime>=6.7665 1118025  125497.50 0.12885220 *
        9) CRSDepTime< 0.658 60112   10225.96 0.21736090 *
      5) CRSDepTime>=8.3415 3163505  450145.40 0.17181290
       10) CRSDepTime< 11.3415 1964400  268472.40 0.16335320
         20) DayOfWeek=Sun 271900   30839.16 0.13043400 *
         21) DayOfWeek=Mon,Tues,Wed,Thur,Fri,Sat 1692500  237291.30 0.16864170 *
       11) CRSDepTime>=11.3415 1199105  181302.00 0.18567180
         22) DayOfWeek=Mon,Tues,Wed,Sat,Sun 852016  124610.90 0.17790390 *
```

```
      23) DayOfWeek=Thur,Fri 347089   56513.56 0.20474000 *
  3) CRSDepTime>=13.1745 5245082  967158.50 0.24386220
    6) DayOfWeek=Mon,Tues,Wed,Sat,Sun 3708992  651771.30 0.22746990
     12) DayOfWeek=Sat 635207   96495.57 0.18681000 *
     13) DayOfWeek=Mon,Tues,Wed,Sun 3073785  554008.60 0.23587240
       26) CRSDepTime< 16.508 1214018  203375.70 0.21281150
         52) CRSDepTime< 15.1325 709846  114523.30 0.20223400 *
         53) CRSDepTime>=15.1325 504172   88661.12 0.22770400 *
       27) CRSDepTime>=16.508 1859767  349565.80 0.25092610
         54) DayOfWeek=Mon,Tues 928523  168050.90 0.23729730 *
         55) DayOfWeek=Wed,Sun 931244  181170.60 0.26451500 *
    7) DayOfWeek=Thur,Fri 1536090  311984.20 0.28344240
     14) CRSDepTime< 15.608 445085   82373.02 0.24519140 *
     15) CRSDepTime>=15.608 1091005  228694.30 0.29904720
       30) CRSDepTime>=21.9915 64127   11932.93 0.24718140 *
       31) CRSDepTime< 21.9915 1026878  216578.10 0.30228620 *
```

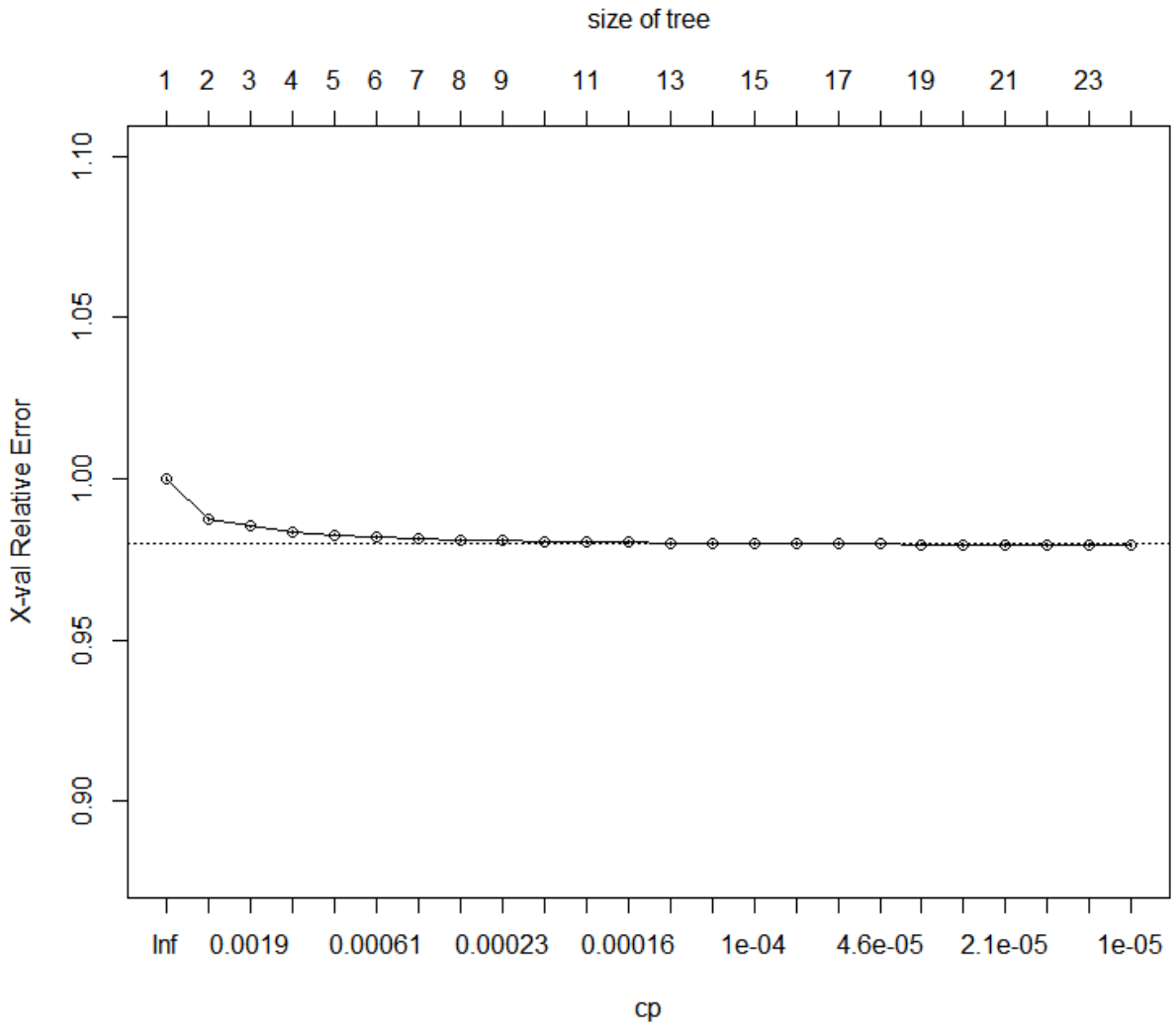
If rpart is installed, *prune.rxDTree* acts as a method for the *prune* function, so you can call it more simply:

```
airlineTree4 <- prune(airlineTree, cp=1e-4)
```

For models fit with 2-fold or greater cross-validation, it is useful to use the cross-validation standard error (part of the cptable component) as a guide to pruning. The rpart function plotcp can be useful for this:

```
plotcp(rxAddInheritance(airlineTree))
```

This yields the following plot:



From this plot, it appears we can prune even further, to perhaps seven or eight splits. Looking again at the cptable, a cp of 2.5e-4 seems a reasonable pruning choice:

```
airlineTreePruned <- prune.rxDTree(airlineTree, cp=2.5e-4)
airlineTreePruned

 Call:
 rxDTree(formula = ArrDel15 ~ CRSDepTime + DayOfWeek, data = sampleAirData,
     maxDepth = 5, cp = 1e-05, blocksPerRead = 30)
 File:  C:\MRS\Data\AirOnTime7Pct.xdf
 Number of valid observations:  10186272
 Number of missing observations:  213483

 Tree representation:
 n= 10186272

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

  1) root 10186272 1630331.00 0.2000864
    2) CRSDepTime< 13.1745 4941190  642452.00 0.1536183
```

```
   4) CRSDepTime< 8.3415 1777685  189395.70 0.1212397
     8) CRSDepTime>=0.658 1717573  178594.90 0.1178756 *
     9) CRSDepTime< 0.658 60112   10225.96 0.2173609 *
   5) CRSDepTime>=8.3415 3163505  450145.40 0.1718129 *
 3) CRSDepTime>=13.1745 5245082  967158.50 0.2438622
   6) DayOfWeek=Mon,Tues,Wed,Sat,Sun 3708992  651771.30 0.2274699
    12) DayOfWeek=Sat 635207   96495.57 0.1868100 *
    13) DayOfWeek=Mon,Tues,Wed,Sun 3073785  554008.60 0.2358724
      26) CRSDepTime< 16.508 1214018  203375.70 0.2128115 *
      27) CRSDepTime>=16.508 1859767  349565.80 0.2509261 *
   7) DayOfWeek=Thur,Fri 1536090  311984.20 0.2834424
    14) CRSDepTime< 15.608 445085   82373.02 0.2451914 *
    15) CRSDepTime>=15.608 1091005  228694.30 0.2990472 *
```

11.7 Handling Missing Values

The *removeMissings* argument to *rxDTree*, as in most RevoScaleR analysis functions, controls how the function deals with missing data in the model fit. If *TRUE*, all rows containing missing values for the response or any predictor variable are removed before model fitting. If *FALSE* (the default), only those rows for which the value of the response or all values of the predictor variables are missing are removed. Using *removeMissings=TRUE* is roughly equivalent to the effect of the *na.omit* function for *rpart*, in that if the file is written out, all rows containing NAs are simply removed. There is no equivalent for *rxDTree* to the *na.exclude* function, which pads the output with NAs for observations that cannot be predicted. Using *removeMissings=FALSE* is the equivalent of using the *na.rpart* or *na.pass* functions; the data is passed through unchanged, but rows which have no data for either all predictors or the response are excluded from the model.

11.8 Prediction

As with other RevoScaleR analysis functions, prediction is performed using the *rxPredict* function, to which you supply a fitted model object and a set of new data (which may be the original data set, but in any event must contain the variables used in the original model).

The adult data set (Kohavi, 1996) is a widely used machine learning data set, similar to the censusWorkers data we have already analyzed. The data set is available from the machine learning data repository at UC Irvine (http://archive.ics.uci.edu/ml/datasets/Adult) ((Frank & Asuncion, 2010) and comes in two pieces: a training data set (adult.data) and a test data set (adult.test). This makes it ready-made for use in prediction. To run the examples below, download this data and add a .txt extension, so that you have adult.data.txt and adult.test.txt. (A third file, adult.names, gives a description of the variables; we use this in the code below as a source for the variable names, which are not part of the data files):

```
#  Prediction

if (bHasAdultData){
```

```
bigDataDir <- "C:/MRS/Data"
adultDataFile <- file.path(bigDataDir, "adult.data.txt")
adultTestFile <- file.path(bigDataDir, "adult.test.txt")

newNames <- c("age", "workclass", "fnlwgt", "education",
      "education_num", "marital_status", "occupation", "relationship",
      "ethnicity", "sex", "capital_gain", "capital_loss", "hours_per_week",
      "native_country", "income")
adultTrain <- rxImport(adultDataFile, stringsAsFactors = TRUE)
names(adultTrain) <- newNames
adultTest <- rxImport(adultTestFile, rowsToSkip = 1,
    stringsAsFactors=TRUE)
names(adultTest) <- newNames
adultTree <- rxDTree(income ~ age + sex + hours_per_week, pweights = "fnlwgt",
    data = adultTrain)
adultPred <- rxPredict(adultTree, data = adultTest, type="vector")
sum(adultPred == as.integer(adultTest$income))/length(adultTest$income)
} # End of bHasAdultData
```

```
 [1] 0.7734169
```

The result shows that the fitted model accurately classifies about 77% of the test data.

When using *rxPredict* with *rxDTree* objects, you should keep in mind how it differs from *predict* with *rpart* objects. First, a *data* argument is always required—this can be either the original data or new data; there is no *newData* argument as in *rpart*. Prediction with the original data provides fitted values, not predictions, but the predicted variable name still defaults to *varname_Pred*.

11.9 Visualizing Trees

The RevoTreeView package can be used to plot decision trees from *rxDTree* or *rpart* in an HTML page. Both classification and regression trees are supported. By plotting the tree objects returned by RevoTreeView's *createTreeView* function in a browser, you can interact with your decision tree. The resulting tree's HTML page can also be shared with other people or displayed on different machines using the package's *zipTreeView* function.

As an example, consider a classification tree built from the *kyphosis* data that is included in the *rpart* package. It produces the following text output:

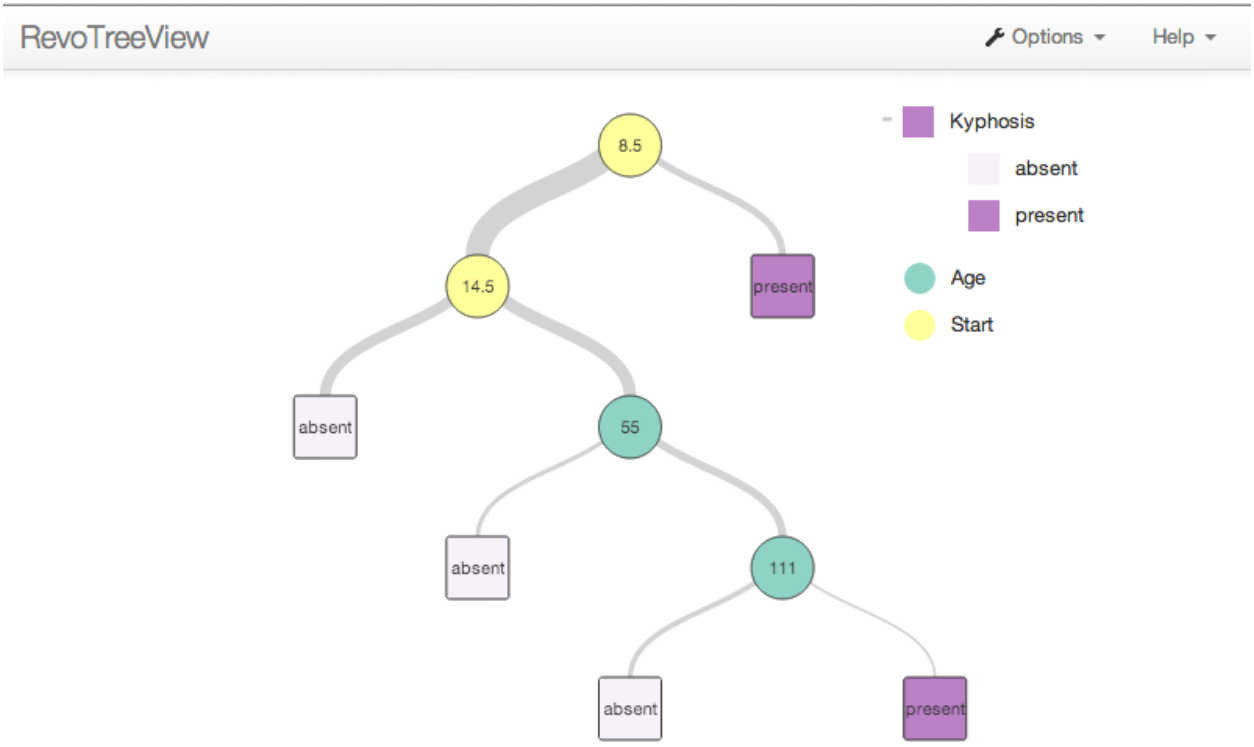
```
data("kyphosis", package="rpart")
kyphTree <- rxDTree(Kyphosis ~ Age + Start + Number,
data = kyphosis, cp=0.01)
kyphTree
```

```
Call:
rxDTree(formula = Kyphosis ~ Age + Start + Number, data = kyphosis,
     cp = 0.01)
Data: kyphosis
Number of valid observations: 81
Number of missing observations: 0

Tree representation:
n= 81
```

```
node), split, n, loss, yval, (yprob)
      * denotes terminal node
 1) root 81 17 absent (0.79012346 0.20987654)
   2) Start>=8.5 62 6 absent (0.90322581 0.09677419)
     4) Start>=14.5 29 0 absent (1.00000000 0.00000000) *
     5) Start< 14.5 33 6 absent (0.81818182 0.18181818)
      10) Age< 55 12 0 absent (1.00000000 0.00000000) *
      11) Age>=55 21 6 absent (0.71428571 0.28571429)
        22) Age>=111 14 2 absent (0.85714286 0.14285714) *
        23) Age< 111 7 3 present (0.42857143 0.57142857) *
   3) Start< 8.5 19 8 present (0.42105263 0.57894737) *
```

Now, you can display a HTML version of the tree output by plotting the object produced by the *createTreeView* function. After running the preceding R code, run the following to load the *RevoTreeView* package and display an interactive decision tree in your browser:

```
library(RevoTreeView)
plot(createTreeView(kyphTree))
```



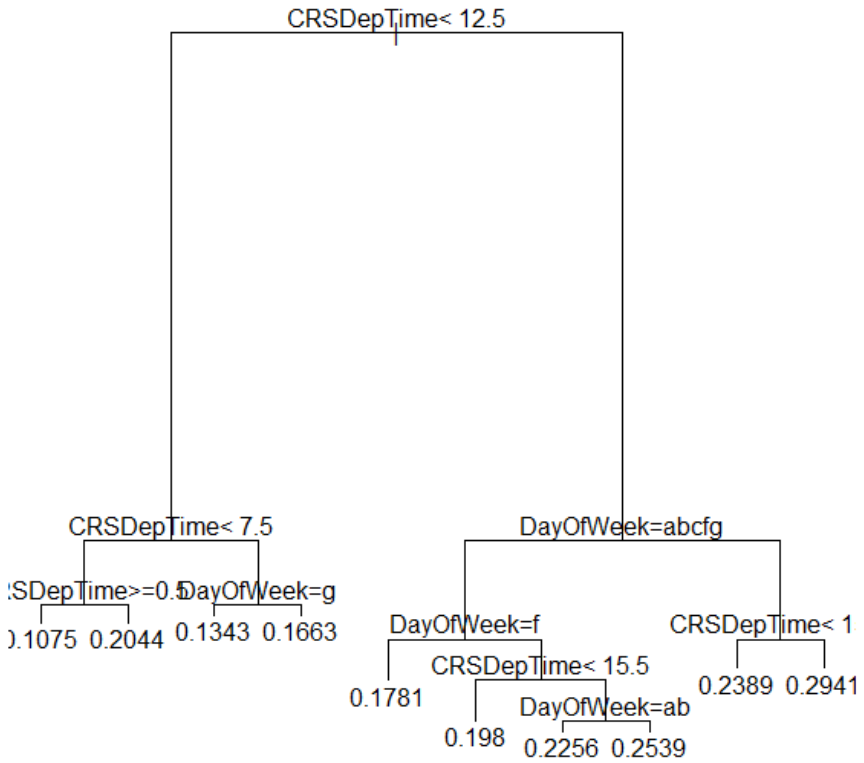
In this interactive tree, click on the circular split nodes to expand or collapse the tree branch. Clicking a node will expand and collapse the node to the last view of that branch. If you use a *CTRL + Click*, the tree will display only the children of the selected node. If you click *ALT + Click*, the tree will display all levels below the selected node. The square-shaped nodes, called leaf or terminal nodes, cannot be expanded.

To get additional information, hover over the node to expose the node details such as its name, the next split variable, its value, the *n*, the predicted value, and other details such as loss or deviance.

You can also use the rpart `plot` and `text` methods with `rxDTree` objects, provided you use the `rxAddInheritance` function to provide rpart inheritance:

```
#  Plotting Trees

plot(rxAddInheritance(airlineTreePruned))
text(rxAddInheritance(airlineTreePruned))
```

This provides the following plot:



Chapter 12.

Estimating Decision Forest Models

The `rxDForest` function in RevoScaleR fits a *decision forest*, which is an ensemble of decision trees. Each tree is fitted to a bootstrap sample of the original data, which leaves about 1/3 of the data unused in the fitting of each tree. Each data point in the original data is fed through each of the trees for which it was unused; the decision forest prediction for that data point is the statistical *mode* of the individual tree predictions, that is, the majority prediction (for classification; for regression problems, the prediction is the mean of the individual predictions).

Unlike individual decision trees, decision forests are not prone to overfitting, and they are consistently shown to be among the best machine learning algorithms. RevoScaleR implements decision forests in the `rxDForest` function, which uses the same basic tree-fitting algorithm as `rxDTree` (see Section 11.1, The `rxDTree` Algorithm). To create the forest, you specify the number of trees using the `nTree` argument and the number of variables to consider for splitting in each tree using the `mTry` argument. In most cases, you will also want to specify the maximum depth to grow the individual trees: greater depth typically results in greater accuracy, but as with `rxDTree`, also results in significantly longer fitting times.

12.1 A Simple Classification Forest

In Chapter 11, we fit a simple classification tree model to rpart's kyphosis data. That model is easily recast as a classification decision forest using *rxDForest* as follows (we set the *seed* argument to ensure reproducibility; in most cases you can omit this):

```
#########################################################
# Chapter 12: Estimating Decision Forest Models
#  A Simple Classification Forest
Ch12Start <- Sys.time()


data("kyphosis", package="rpart")
kyphForest <- rxDForest(Kyphosis ~ Age + Start + Number, seed = 10,
     data = kyphosis, cp=0.01, nTree=500, mTry=3)
kyphForest
```

```
 Call:
 rxDForest(formula = Kyphosis ~ Age + Start + Number, data = kyphosis,
     cp = 0.01, nTree = 500, mTry = 3, seed = 10)


              Type of decision forest: class
                     Number of trees: 500
 No. of variables tried at each split: 3

          OOB estimate of error rate: 19.75%
 Confusion matrix:
          Predicted
 Kyphosis  absent present class.error
   absent      56       8   0.1250000
   present      8       9   0.4705882
```

While decision forests do not produce a unified model, as logistic regression and decision trees do, they do produce reasonable predictions for each data point. In this case, we can obtain predictions using *rxPredict* as follows:

```
dfPreds <- rxPredict(kyphForest, data=kyphosis)
```

Comparing this to the Kyphosis variable in the original kyphosis data, we see that approximately 88 percent of cases are classified correctly:

```
sum(as.character(dfPreds[,1]) ==
    as.character(kyphosis$Kyphosis))/81
```

```
 [1] 0.8765432
```

12.2 A Simple Regression Forest

As a simple example of a regression forest, consider the classic *stackloss* data set, containing observations from a chemical plant producing nitric acid by the oxidation of ammonia, and let's

fit the stack loss (*stack.loss*) using air flow (*Air.Flow*), water temperature (*Water.Temp*), and acid concentration (*Acid.Conc.*) as predictors:

```
#  A Simple Regression Forest

stackForest <- rxDForest(stack.loss ~ Air.Flow + Water.Temp + Acid.Conc.,
     data=stackloss, nTree=200, mTry=2)
stackForest
```

```
 Call:
 rxDForest(formula = stack.loss ~ Air.Flow + Water.Temp + Acid.Conc.,
     data = stackloss, maxDepth = 3, nTree = 200, mTry = 2)


               Type of decision forest: anova
                       Number of trees: 200
 No. of variables tried at each split: 2

           Mean of squared residuals: 44.54992
                     % Var explained: 65
```

12.3 A Larger Regression Forest Model

As a more complex example, we return to the censusWorkers data to which we earlier fit a decision tree. We will create a regression forest predicting wage income from age, sex, and weeks worked, using the *perwt* variable as probability weights (note that we retain the *maxDepth* and *minBucket* parameters from our earlier decision tree example):

```
#  A Larger Regression Forest Model

censusWorkers <- file.path(rxGetOption("sampleDataDir"),
    "CensusWorkers.xdf")
rxGetInfo(censusWorkers, getVarInfo=TRUE)
incForest <- rxDForest(incwage ~ age + sex + wkswork1, pweights = "perwt",
    maxDepth = 3, minBucket = 30000, mTry=2, nTree=200, data = censusWorkers)
incForest
```

```
 Call:
 rxDForest(formula = incwage ~ age + sex + wkswork1, data = censusData,
     pweights = "perwt", maxDepth = 5, nTree = 200, mTry = 2)


               Type of decision forest: anova
                       Number of trees: 200
 No. of variables tried at each split: 2

           Mean of squared residuals: 1458969472
                     % Var explained: 11
```

.

12.4 Large Data Decision Forest Models

As with decision trees, scaling decision forests to very large data sets should be done with caution—the wrong choice of model parameters can easily lead to models that take hours or longer to estimate, even in a distributed computing environment, or that simply cannot be fit at all. For non-binary classification problems, as with decision trees, categorical predictors should have a small to moderate number of levels.

As an example of a large data classification forest, consider the following simple model using the 7% subsample of the full airline data (this uses the variable *ArrDel15* indicating flights with an arrival delay of 15 minutes or more):

```
#  Large Data Tree Models


bigDataDir <- "C:/MRS/Data"
sampleAirData <- file.path(bigDataDir, "AirOnTime7Pct.xdf")
airlineForest <- rxDForest(ArrDel15 ~ CRSDepTime + DayOfWeek,
    data = sampleAirData, blocksPerRead = 30, maxDepth = 5,
    nTree=20, mTry=2, method="class", seed = 8)
```

This yields the following:

```
airlineForest

 Call:
 rxDForest(formula = ArrDel15 ~ CRSDepTime + DayOfWeek, data = sampleAirData,
     method = "class", maxDepth = 5, nTree = 20, mTry = 2, seed = 8,
     blocksPerRead = 30)


               Type of decision forest: class
                      Number of trees: 20
 No. of variables tried at each split: 2

          OOB estimate of error rate: 20.01%
 Confusion matrix:
         Predicted
 ArrDel15   FALSE TRUE class.error
    FALSE 8147274    0           0
    TRUE  2037941    0           1
```

Looking at the fitted object's forest component, we see that a number of the fitted trees do not split at all:

```
airlineForest$forest

    [[1]]
    Number of valid observations:  6440007
    Number of missing observations:  3959748

    Tree representation:
    n= 10186709
```

```
node), split, n, loss, yval, (yprob)
      * denotes terminal node

1) root 10186709 2038302 FALSE (0.7999057 0.2000943) *

[[2]]
Number of valid observations:  6440530
Number of missing observations:  3959225

Tree representation:
n= 10186445

node), split, n, loss, yval, (yprob)
      * denotes terminal node

1) root 10186445 2038249 FALSE (0.7999057 0.2000943) *

[[3]]
...

[[6]]
Number of valid observations:  6439485
Number of missing observations:  3960270

Tree representation:
n= 10186656

node), split, n, loss, yval, (yprob)
      * denotes terminal node

1) root 10186656 2038291 FALSE (0.7999057 0.2000943) *

[[7]]
Number of valid observations:  6439307
Number of missing observations:  3960448

Tree representation:
n= 10186499

node), split, n, loss, yval, (yprob)
      * denotes terminal node

1) root 10186499 2038260 FALSE (0.7999057 0.2000943) *
. . .
```

This may well be because our response is extremely unbalanced--that is, the percentage of flights that are late by 15 minutes or more is quite small. We can tune the fit by providing a *loss matrix*, which allows us to penalize certain predictions in favor of others. You specify the loss matrix using the parms argument, which takes a list with named components. The loss component is specified as either a matrix, or equivalently, a vector that can be coerced to a matrix. In the binary classification case, it can be useful to start with a loss matrix with a penalty roughly equivalent to the ratio of the two classes. So, in our case we know that the on-time flights outnumber the late flights approximately 4 to 1 :

```
airlineForest2 <- rxDForest(ArrDel15 ~ CRSDepTime + DayOfWeek,
    data = sampleAirData, blocksPerRead = 30, maxDepth = 5, seed = 8,
    nTree=20, mTry=2, method="class", parms=list(loss=c(0,4,1,0)))
```

```
Call:
rxDForest(formula = ArrDel15 ~ CRSDepTime + DayOfWeek, data = sampleAirData,
    method = "class", parms = list(loss = c(0, 4, 1, 0)), maxDepth = 5,
    nTree = 20, mTry = 2, seed = 8, blocksPerRead = 30)


               Type of decision forest: class
                     Number of trees: 20
No. of variables tried at each split: 2

         OOB estimate of error rate: 42.27%
Confusion matrix:
        Predicted
ArrDel15   FALSE    TRUE class.error
   FALSE 4719374 3427900    0.420742
   TRUE   877680 1160261    0.430670
```

This model no longer predicts all flights as on time, but now over-predicts late flights. Adjusting the loss matrix again, this time reducing the penalty, yields the following:

```
Call:
rxDForest(formula = ArrDel15 ~ CRSDepTime + DayOfWeek, data = sampleAirData,
    method = "class", parms = list(loss = c(0, 3, 1, 0)), maxDepth = 5,
    nTree = 20, mTry = 2, seed = 8, blocksPerRead = 30)


               Type of decision forest: class
                     Number of trees: 20
No. of variables tried at each split: 2

         OOB estimate of error rate: 30.15%
Confusion matrix:
        Predicted
ArrDel15   FALSE    TRUE class.error
   FALSE 6465439 1681835   0.2064292
   TRUE  1389092  648849   0.6816154
```

12.5 Controlling the Model Fit

The *rxDForest* function has a number of options for controlling the model fit. Most of these control parameters are identical to the same controls in *rxDTree*. A full listing of these options can be found in the *rxDForest* help file, but the following have been found in our testing to be the most useful at controlling the time required to fit a model with *rxDForest*:

- *maxDepth*: this sets the maximum depth of any node of the tree. Computations grow rapidly more expensive as the depth increases, so we recommend a maxDepth of 10 to 15.
- *maxNumBins*: this controls the maximum number of bins used for each variable. Managing the number of bins is important in controlling memory usage. The default is to use the larger of 101 and the square root of the number of observations for small to moderate size data sets (up to about one million observations), but for larger sets to use 1001 bins. For small data sets with continuous predictors, you may find that you need to increase the *maxNumBins* to obtain models that resemble those from rpart.

- *minSplit*, *minBucket*: these determine how many observations must be in a node before a split is attempted (*minSplit*) and how many must remain in a terminal node (*minBucket*).

Chapter 13.

Estimating Models Using Stochastic Gradient Boosting

The `rxBTrees` function in RevoScaleR, like `rxDForest`, fits a decision forest to your data, but the forest is generated using a stochastic gradient boosting algorithm. This is similar to the decision forest algorithm in that each tree is fitted to a subsample of the training set (sampling without replacement) and predictions are made by aggregating over the predictions of all trees. Unlike the `rxDForest` algorithm, the boosted trees are added one at a time, and at each iteration, a regression tree is fitted to the current pseudo-residuals, i.e., the gradient of the loss functional being minimized.

Like the `rxDForest` function, `rxBTrees` uses the same basic tree-fitting algorithm as `rxDTree` (see Section 11.1, The `rxDTree` Algorithm). To create the forest, you specify the number of trees using the `nTree` argument and the number of variables to consider for splitting at each tree node using the `mTry` argument. In most cases, you will also want to specify the maximum depth to grow the individual trees: shallow trees seem to be sufficient in many applications, but as with `rxDTree` and `rxDForest`, greater depth typically results in longer fitting times.

Different model types are supported by specifying different loss functions, as follows:

- `"gaussian"`, for regression models
- `"bernoulli"`, for binary classification models
- `"multinomial"`, for multi-class classification models

13.1 A Simple Binary Classification Forest

In Chapter 11, we fit a simple classification tree model to rpart's kyphosis data. That model is easily recast as a classification decision forest using `rxBTrees` as follows (we set the `seed` argument to ensure reproducibility; in most cases you can omit this):

```
###########################################################
# Chapter 13: Estimating Models Using Stochastic Gradient Boosting
#  A Simple Classification Forest
Ch13Start <- Sys.time()


data("kyphosis", package="rpart")
kyphBTrees <- rxBTrees(Kyphosis ~ Age + Start + Number, seed = 10,
     data = kyphosis, cp=0.01, nTree=500, mTry=3, lossFunction="bernoulli")
kyphBTrees

 Call:
 rxBTrees(formula = Kyphosis ~ Age + Start + Number, data = kyphosis,
     cp = 0.01, nTree = 500, mTry = 3, seed = 10, lossFunction = "bernoulli")


       Loss function of boosted trees: bernoulli
                 Number of iterations: 500
            OOB estimate of deviance: 0.1441952
```

In this case, we don't need to explicitly specify the loss function; `"bernoulli"` is the default.

13.2 A Simple Regression Forest

As a simple example of a regression forest, consider the classic `stackloss` data set, containing observations from a chemical plant producing nitric acid by the oxidation of ammonia, and let's fit the stack loss (`stack.loss`) using air flow (`Air.Flow`), water temperature (`Water.Temp`), and acid concentration (`Acid.Conc.`) as predictors:

```
#  A Simple Regression Forest

stackBTrees <- rxDForest(stack.loss ~ Air.Flow + Water.Temp + Acid.Conc.,
     data=stackloss, nTree=200, mTry=2, lossFunction="gaussian")
stackBTrees


 Call:
 rxDForest(formula = stack.loss ~ Air.Flow + Water.Temp + Acid.Conc.,
     data = stackloss, nTree = 200, mTry = 2, lossFunction = "gaussian")


       Loss function of boosted trees: gaussian
                 Number of iterations: 200
            OOB estimate of deviance: 1.46797
```

13.3 A Simple Multinomial Forest Model

As a simple multinomial example, we will fit an *rxBTrees* model to the iris data:

```
#  A Multinomial Forest Model

irisBTrees <- rxBTrees(Species ~ Sepal.Length + Sepal.Width +
    Petal.Length + Petal.Width, data=iris,
    nTree=50, seed=0, maxDepth=3, lossFunction="multinomial")
irisBTrees
```

```
Call:
rxBTrees(formula = Species ~ Sepal.Length + Sepal.Width + Petal.Length +
    Petal.Width, data = iris, maxDepth = 3, nTree = 50, seed = 0,
    lossFunction = "multinomial")


      Loss function of boosted trees: multinomial
       Number of boosting iterations: 50
No. of variables tried at each split: 1

            OOB estimate of deviance: 0.02720805
```

13.4 Controlling the Model Fit

The principal parameter controlling the boosting algorithm itself is the *learning rate*. The learning rate (or shrinkage) is used to scale the contribution of each tree when it is added to the ensemble. The default learning rate is 0.1.

The *rxBTrees* function has a number of other options for controlling the model fit. Most of these control parameters are identical to the same controls in *rxDTree*. A full listing of these options can be found in the *rxBTrees* help file, but the following have been found in our testing to be the most useful at controlling the time required to fit a model with *rxBTrees*:

- *maxDepth*: this sets the maximum depth of any node of the tree. Computations grow more expensive as the depth increases, so we recommend starting with maxDepth=1, i.e., boosted stumps.
- *maxNumBins*: this controls the maximum number of bins used for each variable. Managing the number of bins is important in controlling memory usage. The default is to use the larger of 101 and the square root of the number of observations for small to moderate size data sets (up to about one million observations), but for larger sets to use 1001 bins. For small data sets with continuous predictors, you may find that you need to increase the *maxNumBins* to obtain models that resemble those from rpart.

- *minSplit*, *minBucket*: these determine how many observations must be in a node before a split is attempted (*minSplit*) and how many must remain in a terminal node (*minBucket*).

Chapter 14.

Naïve Bayes Classifier

In this Chapter, we describe one simple and effective family of classification methods known as Naïve Bayes. In RevoScaleR, Naïve Bayes classifiers can be implemented using the `rxNaiveBayes` function. Classification, simply put, is the act of dividing observations into classes or categories. Some examples of this are the classification of product reviews into positive or negative categories or the detection of email spam. These classification examples can be achieved manually using a set of rules. However, this is not efficient or scalable. In Naïve Bayes and other machine learning based classification algorithms, the decision criteria for assigning class are learned from a training data set, which has classes assigned manually to each observation.

14.1 The rxNaiveBayes Algorithm

The Naïves Bayes classification method is simple, effective, and robust. This method can be applied to data large or small, it requires minimal training data, and is unlikely to produce a classifier that performs poorly compared to more complex algorthims. This family of classifiers utilizes Bayes Theorem to determine the probability that an observation belongs to a certain class. A training dataset is used to calculate prior probabilities of an observation occurring in a class within the predefined set of classes. In RevoScaleR this is done using the `rxNaiveBayes`

function. These probabilities are then used to calculate posterior probabilities that an observation belongs to each class. The class membership is decided by choosing the class with the largest posterior probability for each observation. This is accomplished with the `rxPredict` function using the Naïve Bayes object from a call to `rxNaiveBayes`. Part of the beauty of Naïve Bayes is its simplicity due to the conditional independent assumption: that the values of each predictor are independent of each other given the class. This assumption reduces the number of parameters needed and in turn makes the algorithm extremely efficient. Naïve Bayes methods differ in their choice of distribution for any continuous independent variables. Our implementation via the `rxNaiveBayes` function assumes the distribution to be Gaussian.

14.2 A Simple Naïve Bayes Classifier

In Chapter 9, we fit a simple logistic regression model to rpart's kyphosis data and in Chapters 11 and 12 we used the kyphosis data again to create classification and regression trees. We can use the same data with our Naïve Bayes classifier to see which patients are more likely to acquire Kyphosis based on age, number, and start. We can train and test our classifier on the kyphosis data for the sake of illustration. We use the `rxNaiveBayes` function to construct a classifier for the kyphosis data:

```
###########################################################
# Chapter 14: Naïve Bayes Classifier
#  A Simple Naïve Bayes Classifier
Ch14Start <- Sys.time()


data("kyphosis", package="rpart")
kyphNaiveBayes <- rxNaiveBayes(Kyphosis ~ Age + Start + Number, data = kyphosis)
kyphNaiveBayes
```

```
Call:
rxNaiveBayes(formula = Kyphosis ~ Age + Start + Number, data = kyphosis)

A priori probabilities:
Kyphosis
   absent   present
0.7901235 0.2098765

Predictor types:
  Variable    Type
1      Age numeric
2    Start numeric
3   Number numeric

Conditional probabilities:
$Age
           Means   StdDev
absent  79.89062 61.86111
present 97.82353 39.27505

$Start
            Means   StdDev
absent  12.609375 4.427967
```

```
present  7.294118 4.283175

$Number
           Means   StdDev
absent  3.750000 1.414214
present 5.176471 1.878673
```

The returned object *kyphNaiveBayes* is an object of class *rxNaiveBayes*. Objects of this class provide the following useful components: *apriori* and *tables*. The *apriori* component contains the conditional probabilities for the response variable, in this case the Kyphosis variable. The *tables* component contains a list of tables, one for each predictor variable. For a categorical variable, the table contains the conditional probabilities of the variable given the target level of the response variable. For a numeric variable, the table contains the mean and standard deviation of the variable given the target level of the response variable. These components are printed in the output above.

We can use our Naïve Bayes object with *rxPredict* to re-classify the Kyphosis variable for each child in our original dataset:

```
kyphPred <- rxPredict(kyphNaiveBayes,kyphosis)
```

When we table the results from the Naïve Bayes classifier with the original Kyphosis variable, it appears that 13 of 81 children are misclassified:

```
table(kyphPred[["Kyphosis_Pred"]], kyphosis[["Kyphosis"]])
```

```
           absent present
   absent      59       8
   present      5       9
```

14.3 A Larger Naïve Bayes Classifier

As a more complex example, consider the mortgage default example used in Chapter 9.3 of this guide. For that example, there are ten input files total and we use nine input data files to create the training data set. We then use the model built from those files to make predictions on the final dataset. In this section we will use the same strategy to build a Naïve Bayes classifier on the first nine data sets and assign the outcome variable for the tenth data set.

The mortgage default data sets are available for download online. With the data downloaded we can create the training data set and test data set as follows (remember to modify the first line to match the location of the mortgage default text data files on your own system):

```
#  A Larger Naïve Bayes Classifier


bigDataDir <- "C:/MRS/Data"
```

```
mortCsvDataName <- file.path(bigDataDir, "mortDefault", "mortDefault")
trainingDataFileName <- "mortDefaultTraining"
mortCsv2009 <- paste(mortCsvDataName, "2009.csv", sep = "")
targetDataFileName <- "mortDefault2009.xdf"
defaultLevels <- as.character(c(0,1))
ageLevels <- as.character(c(0:40))
yearLevels <- as.character(c(2000:2009))
colInfo <- list(list(name  = "default", type = "factor",
    levels = defaultLevels), list(name = "houseAge", type = "factor",
    levels = ageLevels), list(name = "year", type = "factor",
    levels = yearLevels))
append= FALSE
for (i in 2000:2008)
{
    importFile <- paste(mortCsvDataName, i, ".csv", sep = "")
    rxImport(inData = importFile, outFile = trainingDataFileName,
    colInfo = colInfo, append = append, overwrite=TRUE)
    append = TRUE
}

rxImport(inData = mortCsv2009, outFile = targetDataFileName,
    colInfo = colInfo)
```

In the above code the response variable `default` is converted to a factor using the `colInfo` argument to `rxImport`. For the `rxNaiveBayes` function, the response variable must be a factor or you will get an error.

Now that we have training and test data sets we can fit a Naïve Bayes classifier with our training data using `rxNaiveBayes` and assign values of the `default` variable for observations within the test data using `rxPredict`:

```
mortNB <- rxNaiveBayes(default ~ year + creditScore + yearsEmploy + ccDebt,
      data = trainingDataFileName, smoothingFactor = 1)
mortNBPred <- rxPredict(mortNB, data = targetDataFileName)
```

Notice that we added an additional argument, `smoothingFactor`, to our rxNaiveBayes call. This is a useful argument when your data are missing levels of a certain variable that you expect to be in your test data. Based on our training data, the conditional probability for year 2009 will be 0, since it only includes data between the years of 2000 and 2008. If we try to use our classifier on the test data without specifying a smoothing factor in our call to `rxNaiveBayes` the function `rxPredict` produces no results since our test data only has data from 2009. In general, smoothing is used to avoid overfitting your model. It follows that to achieve the optimal classifier you may want to smooth the conditional probabilities even if every level of each variable is observed.

We can compare the predicted values of the `default` variable from the Naïve Bayes classifier with the actual data in the test dataset:

```
results <- table(mortNBPred[["default_Pred"]], rxDataStep(targetDataFileName,
    maxRowsByCols=6000000)[["default"]])
results
```

```
          0      1
   0 877272   3792
   1  97987  20949
```

```
pctMisclassified <- sum(results[2:3])/sum(results)*100
pctMisclassified
```

```
  [1] 10.1779
```

These results demonstrate a 10.2% misclassification rate using our Naïve Bayes classifier.

14.4 Naïve Bayes with Missing Data

You can control the handling of missing data using the *byTerm* argument in the *rxNaiveBayes* function. By default, *byTerm* is set to *TRUE*, which means that missings are removed by variable before computing the conditional probabilities. If you prefer to remove observations with missings in any variable before computations are done, set the *byTerm* argument to *FALSE*.

Chapter 15.

Estimating Correlation and Variance/Covariance Matrices

The `rxCovCor` function in RevoScaleR calculates the covariance, correlation, or sum of squares/cross-product matrix for a set of variables in an .xdf file or data frame. The size of these matrices is determined by the number of variables rather than the number of observations, so typically the results can easily fit into memory in R. A broad category of analyses can be computed from some form of a cross-product matrix, for example, factor analysis and principal components.

A cross-product matrix is a matrix of the form X'X, where X represents an arbitrary set of raw or standardized variables. More generally, this is a matrix of the form X'WX, where W is a diagonal weighting matrix.

15.1 Computing Cross-Product Matrices

While rxCovCor is the primary tool for computing covariance, correlation, and other cross-product matrices, you will seldom call it directly. Instead, it is usually simpler to use one of the following convenience functions:

- rxCov: Use rxCov to return the covariance matrix
- rxCor: Use rxCor to return the correlation matrix

- rxSSCP: Use rxSSCP to return the augmented cross-product matrix, that is, we first add a column of 1's (if no weights are specified) or a column equaling the square root of the weights to the data matrix, and then compute the cross-product.

15.2 Computing a Correlation Matrix for Use in Factor Analysis

The 5% sample of the U.S. 2000 census has over 14 million observations. In this example we will compute the correlation matrix for 16 variables derived from variables in the data set for individuals over the age of 20. This correlation matrix is then used as input into the standard R factor analysis function, *factanal*.

First, we specify the name and location of the data set:

```
#########################################################
# Chapter 15: Estimating Correlation and Variance/Covariance Matrices
#  Computing a Correlation Matrix for Use in Factor Analysis
Ch15Start <- Sys.time()



bigDataDir <- "C:/MRS/Data"
bigCensusData <- file.path(bigDataDir, "Census5PCT2000.xdf"
```

Next, we can take a quick look at some basic demographic and socio-economic variables by calling *rxSummary*. (For more information on variables in the census data, see http://usa.ipums.org/usa-action/variables/group.) Throughout the analysis we will use the probability weighting variable, *perwt*, and restrict the analysis to people over the age of 20.

```
rxSummary(~phone + speakeng + wkswork1 + incwelfr + incss + educrec + metro +
     ownershd + marst + lingisol + nfams + yrsusa1 + movedin + racwht + age,
     data = bigCensusData, blocksPerRead = 5, pweights = "perwt",
     rowSelection = age > 20)
```

This call provides summary information about the variables in this weighted sub-sample, including cell counts for factor variables:

```
Call:
rxSummary(formula = ~phone + speakeng + wkswork1 + incwelfr +
    incss + educrec + metro + ownershd + marst + lingisol + nfams +
    yrsusa1 + movedin + racwht + age, data = censusData, pweights = "perwt",
    rowSelection = age > 20, blocksPerRead = 5)

Summary Statistics Results for: ~phone + speakeng + wkswork1 + incwelfr
    + incss + educrec + metro + ownershd + marst + lingisol + nfams +
    yrsusa1 + movedin + racwht + age
File name: C:\MRS\Data\Census5PCT2000.xdf
Probability weights: perwt
Number of valid observations: 9822124

 Name      Mean         StdDev       Min Max   SumOfWeights MissingWeights
 wkswork1   32.068473   23.2438663  0     52 196971131    0
```

```
 incwelfr   61.155293  711.0955602  0  25500 196971131    0
 incss    1614.604835 3915.7717233  0  26800 196971131    0
 nfams       1.163434    0.5375238  1     48 196971131    0
 yrsusa1     2.868573    9.0098343  0     90 196971131    0
 age        46.813005   17.1797905 21     93 196971131    0

Category Counts for phone
Number of categories: 3

 phone                  Counts
 N/A                     5611380
 No, no phone available   3957030
 Yes, phone available   187402721

Category Counts for speakeng
Number of categories: 10

 speakeng                 Counts
 N/A (Blank)                   0
 Does not speak English  2956934
 Yes, speaks English...        0
 Yes, speaks only English 162425091
 Yes, speaks very well   17664738
 Yes, speaks well         7713303
 Yes, but not well        6211065
 Unknown                       0
 Illegible                     0
 Blank                         0

Category Counts for educrec
Number of categories: 10

 educrec                Counts
 N/A  or No schooling        0
 None or preschool     2757363
 Grade 1, 2, 3, or 4   1439820
 Grade 5, 6, 7, or 8  10180870
 Grade 9               4862980
 Grade 10              5957922
 Grade 11              5763456
 Grade 12             63691961
 1 to 3 years of college 55834997
 4+ years of college  46481762

Category Counts for metro
Number of categories: 5

 metro                                Counts
 Not applicable                       13829398
 Not in metro area                    32533836
 In metro area, central city          32080416
 In metro, area, outside central city 60836302
 Central city status unknown          57691179

Category Counts for ownershd
Number of categories: 8

 ownershd                   Counts
 N/A                         5611380
 Owned or being bought             0
 Check mark (owns?)                0
 Owned free and clear       40546259
 Owned with mortgage or loan 94626060
```

```
 Rents                              0
 No cash rent                 3169987
 With cash rent              53017445

Category Counts for marst
Number of categories: 6

 marst                       Counts
 Married, spouse present    112784037
 Married, spouse absent       5896245
 Separated                    4686951
 Divorced                    21474299
 Widowed                     14605829
 Never married/single (N/A)  37523770

Category Counts for lingisol
Number of categories: 3

 lingisol                     Counts
 N/A (group quarters/vacant)   5611380
 Not linguistically isolated 182633786
 Linguistically isolated       8725965

Category Counts for movedin
Number of categories: 7

 movedin                Counts
 NA                     92708540
 This year or last year 20107246
 2-5 years ago          30328210
 6-10 years ago         16959897
 11-20 years ago        16406155
 21-30 years ago        10339278
 31+ years ago          10121805

Category Counts for racwht
Number of categories: 2

 racwht Counts
 No      40684944
 Yes    156286187
```

Next we will call the *rxCor* function, a convenience function for *rxCovCor* that returns just the Pearson's correlation matrix for the variables specified. We will make heavy use of the *transforms* argument to create a series of logical (or dummy) variables from factor variables to be used in the creation of the correlation matrix.

```
censusCor <- rxCor(formula=~poverty + noPhone + noEnglish  + onSocialSecurity +
     onWelfare + working + incearn + noHighSchool + inCity + renter +
     noSpouse + langIsolated + multFamilies + newArrival + recentMove +
     white + sei + older,
     data = bigCensusData, pweightsb= "perwt", blocksPerRead = 5,
     rowSelection = age > 20,
     transforms= list(
        noPhone = phone == "No, no phone available",
        noEnglish = speakeng == "Does not speak English",
        working = wkswork1 > 20,
        onWelfare = incwelfr > 0,
        onSocialSecurity = incss > 0,
        noHighSchool =
```

```
        !(educrec %in%
        c("Grade 12", "1 to 3 years of college", "4+ years of college")),
    inCity = metro == "In metro area, central city",
    renter = ownershd %in% c("No cash rent", "With cash rent"),
    noSpouse = marst != "Married, spouse present",
    langIsolated = lingisol == "Linguistically isolated",
    multFamilies = nfams > 2,
    newArrival = yrsusa2 == "0-5 years",
    recentMove = movedin == "This year or last year",
    white = racwht == "Yes",
    older = age > 64
    ))
```

The resulting correlation matrix is used as input into the factor analysis function provided by the stats package in R. In interpreting the results, note that the variable *poverty* represents family income as a percentage of a poverty threshold, so increases as family income increases. First, specify two factors:

```
censusFa <- factanal(covmat = censusCor, factors=2)
print(censusFa, digits=2, cutoff = .2, sort= TRUE)
```

This results in:

```
Call:
factanal(factors = 2, covmat = censusCor)

Uniquenesses:
         poverty          noPhone        noEnglish onSocialSecurity
            0.53             0.96             0.93             0.23
       onWelfare          working          incearn     noHighSchool
            0.96             0.51             0.68             0.82
          inCity           renter         noSpouse     langIsolated
            0.97             0.79             0.90             0.90
    multFamilies       newArrival       recentMove            white
            0.96             0.93             0.97             0.88
             sei            older
            0.57             0.24

Loadings:
                 Factor1 Factor2
onSocialSecurity  0.83   -0.29
working          -0.68
sei              -0.59   -0.29
older             0.82   -0.29
poverty          -0.28   -0.63
noPhone
noEnglish                 0.26
onWelfare
incearn          -0.46   -0.34
noHighSchool      0.31    0.29
inCity
renter                    0.45
noSpouse                  0.28
langIsolated              0.31
multFamilies
newArrival                0.26
recentMove
white                    -0.34

                Factor1 Factor2
```

```
SS loadings       2.60    1.67
Proportion Var    0.14    0.09
Cumulative Var    0.14    0.24

The degrees of freedom for the model is 118 and the fit was 0.6019
```

We can use the same correlation matrix to estimate three factors:

```
censusFa <- factanal(covmat = censusCor, factors=3)
print(censusFa, digits=2, cutoff = .2, sort= TRUE)
```

```
Call:
factanal(factors = 3, covmat = censusCor)

Uniquenesses:
         poverty          noPhone        noEnglish onSocialSecurity
            0.49             0.96             0.72             0.24
       onWelfare          working          incearn     noHighSchool
            0.96             0.50             0.62             0.80
          inCity           renter         noSpouse     langIsolated
            0.96             0.80             0.90             0.59
    multFamilies       newArrival       recentMove            white
            0.96             0.79             0.97             0.88
             sei            older
            0.56             0.22

Loadings:
                Factor1 Factor2 Factor3
onSocialSecurity  0.87
working          -0.62    0.34
sei              -0.51    0.42
older             0.88
poverty                   0.68
incearn          -0.36    0.51
noEnglish                          0.53
langIsolated                       0.64
noPhone
onWelfare                -0.21
noHighSchool      0.25   -0.26    0.26
inCity
renter                   -0.36    0.24
noSpouse                 -0.30
multFamilies
newArrival                         0.46
recentMove
white                     0.24   -0.24

               Factor1 Factor2 Factor3
SS loadings       2.41    1.50    1.18
Proportion Var    0.13    0.08    0.07
Cumulative Var    0.13    0.22    0.28

The degrees of freedom for the model is 102 and the fit was 0.343
```

15.3 Computing A Covariance Matrix for Principal Components Analysis

Principal components analysis, or PCA, is a technique closely related to factor analysis. PCA seeks to find a set of orthogonal axes such that the first axis, or *first principal component*, accounts for as much variability as possible and subsequent axes or components are chosen to

maximize variance while maintaining orthogonality with previous axes. Principal components are typically computed either by a singular value decomposition of the data matrix or an eigenvalue decomposition of a covariance or correlation matrix; the latter permits us to use *rxCovCor* and its relatives with the standard R function *princomp*.

As an example, we will use the rxCov function to calculate a covariance matrix for the log of the iris data, and pass this to the princomp function; this will reproduce the example from pages 303-304 of *Modern Applied Statistics with S* (Venables & Ripley, 2002):

```
#  Computing A Covariance Matrix for Principal Components Analysis

irisLog <- as.data.frame(lapply(iris[,1:4], log))
irisSpecies <- iris[,5]
irisCov <- rxCov(~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width,
    data=irisLog)
irisPca <- princomp(covmat=irisCov, cor=TRUE)
summary(irisPca)
```

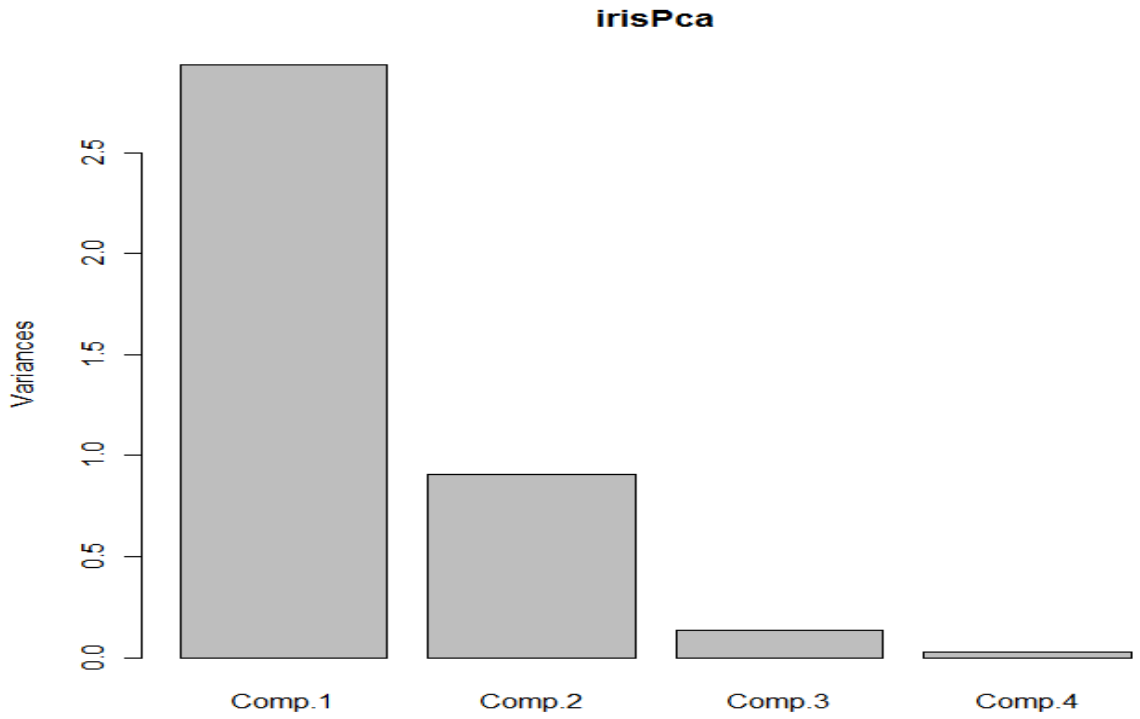
This yields the following:

```
Importance of components:
                          Comp.1    Comp.2     Comp.3    Comp.4
Standard deviation     1.7124583 0.9523797 0.36470294 0.1656840
Proportion of Variance 0.7331284 0.2267568 0.03325206 0.0068628
Cumulative Proportion  0.7331284 0.9598851 0.99313720 1.0000000
```

The default plot method for objects of class princomp is a *screeplot*, which is a barplot of the variances of the principal components. We can obtain the plot as usual by calling plot with our principal components object:

```
plot(irisPca)
```

This yields the following plot:



Another useful bit of output is given by the loadings function, which returns a set of columns showing the linear combinations for each principal component:

```
loadings(irisPca)
```

```
Loadings:
             Comp.1 Comp.2 Comp.3 Comp.4
Sepal.Length  0.504 -0.455  0.709  0.191
Sepal.Width  -0.302 -0.889 -0.331
Petal.Length  0.577        -0.219 -0.786
Petal.Width   0.567        -0.583  0.580

               Comp.1 Comp.2 Comp.3 Comp.4
SS loadings      1.00   1.00   1.00   1.00
Proportion Var   0.25   0.25   0.25   0.25
Cumulative Var   0.25   0.50   0.75   1.00
```

You may have noticed that we supplied the flag cor=TRUE in the call to princomp; this tells princomp to use the correlation matrix rather than the covariance matrix to compute the principal components. We can obtain the same results by omitting the flag but submitting the correlation matrix as returned by rxCor instead:

```
irisCor <- rxCor(~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width,
    data=irisLog)
irisPca2 <- princomp(covmat=irisCor)
summary(irisPca2)
loadings(irisPca2)
```

```
plot(irisPca2)
```

15.4 A Large Data Principal Components Analysis

Stock market data for open, high, low, close, and adjusted close from 1962 to 2010 is available at http://www.infochimps.com/datasets/nyse-daily-1970-2010-open-close-high-low-and-volume/downloads/15407. The full data set includes 9.2 million observations of daily open-high-low-close data for some 2800 stocks. As you might expect, these data are highly correlated, and principal components analysis can be used for data reduction. We read the original data into an .xdf file, NYSE_daily_prices.xdf, using the same process we used in the *Getting Started Guide* to read our mortgage data (set `revoDataDir` to the full path to the NYSE directory containing the .csv files when you unpack the download):

```
#  A Large Data Principal Components Analysis

if (bHasNYSE){

bigDataDir <- "C:/MRS/Data"
nyseCsvFiles <- file.path(bigDataDir, "NYSE_daily_prices","NYSE",
     "NYSE_daily_prices_")

nyseXdf <- "NYSE_daily_prices.xdf"
append <- "none"
for (i in LETTERS)
{
    importFile <- paste(nyseCsvFiles, i, ".csv", sep="")
    rxImport(importFile, nyseXdf, append=append)
    append <- "rows"
}
```

Once we have our .xdf file, we proceed as before:

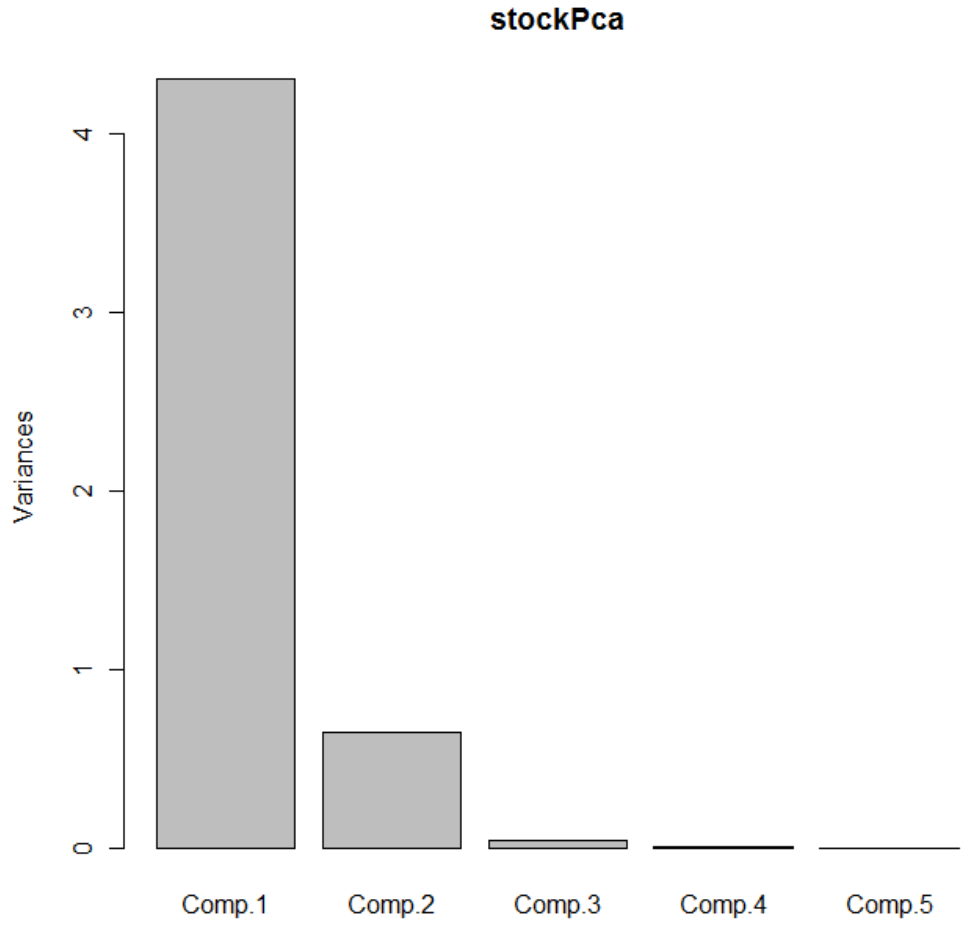
```
stockCor <- rxCor(~ stock_price_open + stock_price_high +
     stock_price_low + stock_price_close +
     stock_price_adj_close, data="NYSE_daily_prices.xdf")
stockPca <- princomp(covmat=stockCor)
summary(stockPca)
loadings(stockPca)
plot(stockPca)
```

This yields the following output:

```
> summary(stockPca)
Importance of components:
                          Comp.1    Comp.2      Comp.3       Comp.4
Standard deviation     2.0756631 0.8063270 0.197632281 0.0454173922
Proportion of Variance 0.8616755 0.1300327 0.007811704 0.0004125479
Cumulative Proportion  0.8616755 0.9917081 0.999519853 0.9999324005
                           Comp.5
Standard deviation     1.838470e-02
Proportion of Variance 6.759946e-05
Cumulative Proportion  1.000000e+00
> loadings(stockPca)

Loadings:
```

```
                     Comp.1 Comp.2 Comp.3 Comp.4 Comp.5
stock_price_open     -0.470 -0.166  0.867
stock_price_high     -0.477 -0.151 -0.276  0.410 -0.711
stock_price_low      -0.477 -0.153 -0.282  0.417  0.704
stock_price_close    -0.477 -0.149 -0.305 -0.811
stock_price_adj_close -0.309  0.951

               Comp.1 Comp.2 Comp.3 Comp.4 Comp.5
SS loadings       1.0    1.0    1.0    1.0    1.0
Proportion Var    0.2    0.2    0.2    0.2    0.2
Cumulative Var    0.2    0.4    0.6    0.8    1.0
```

The screeplot is shown below:



Between them, the first two principal components explain 99% of the variance; we can therefore replace the five original variables by these two principal components with no appreciable loss of information.

```
} # End of bHasNYSE
```

15.5 Ridge Regression

Another application of correlation matrices is to calculate ridge regression, a type of regression that can help deal with multicollinearity and is part of a broader class of models called Penalized Regression Models.

Where the ordinary least squares regression minimizes the sum of squared residuals

$$\sum_i (y_i - x_i^T \boldsymbol{\beta})^2$$

ridge regression minimizes the slightly modified sum

$$\sum_i (y_i - x_i^T \boldsymbol{\beta})^2 + \lambda \sum_{j=1}^{p} \beta_j^2$$

The solution to the ridge regression is

$$\widehat{\boldsymbol{\beta}} = (\boldsymbol{X}^T\boldsymbol{X} + \lambda \boldsymbol{I})^{-1}\boldsymbol{X}^T\boldsymbol{y}$$

where $\boldsymbol{X}$ is the model matrix. This is similar to the ordinary least squares regression solution with a "ridge" added along the diagonal.

Since the model matrix is embedded in the correlation matrix, the following function allows us to compute the ridge regression solution:

```
#  Ridge regression
rxRidgeReg <- function(formula, data, lambda, ...) {
  myTerms <- all.vars(formula)
  newForm <- as.formula(paste("~", paste(myTerms, collapse = "+")))
  myCor <- rxCovCor(newForm, data = data, type = "Cor", ...)
  n <- myCor$valid.obs
  k <- nrow(myCor$CovCor) - 1
  bridgeprime <- do.call(rbind, lapply(lambda,
        function(l) qr.solve(myCor$CovCor[-1,-1] + l*diag(k),
                             myCor$CovCor[-1,1])))
  bridge <-  myCor$StdDevs[1] * sweep(bridgeprime, 2,
        myCor$StdDevs[-1], "/")
  bridge <- cbind(t(myCor$Means[1] -
        tcrossprod(myCor$Means[-1], bridge)), bridge)
  rownames(bridge) <- format(lambda)
  return(bridge)
}
```

The following example shows how ridge regression dramatically improves the solution in a regression involving heavy multicollinearity:

```
set.seed(14)
x <- rnorm(100)
y <- rnorm(100, mean=x, sd=.01)
z <- rnorm(100, mean=2 + x +y)
```

```
data <- data.frame(x=x, y=y, z=z)
lm(z ~ x + y)
```

```
Call:
lm(formula = z ~ x + y)

Coefficients:
(Intercept)            x            y
      1.827        4.359       -2.584
```

```
rxRidgeReg(z ~ x + y, data=data, lambda=0.02)
```

```
                       x         y
0.02 1.827674 0.8917924 0.8723334
```

You can supply a vector of lambdas as a quick way to compare various choices:

```
rxRidgeReg(z ~ x + y, data=data, lambda=c(0, 0.02, 0.2, 2, 20))
```

```
                         x           y
 0.00 1.827112 4.35917238 -2.58387778
 0.02 1.827674 0.89179239  0.87233344
 0.20 1.833899 0.81020130  0.80959911
 2.00 1.865339 0.44512940  0.44575060
20.00 1.896779 0.08092296  0.08105322
```

Notice that for $\lambda = 0$, the ridge regression is identical to ordinary least squares, while as $\lambda \to \infty$, the coefficients of x and y approach 0.

Chapter 16.

Clustering

Clustering is the general name for any of a large number of classification techniques that involve assigning observations to membership in one of two or more clusters on the basis of some distance metric.

16.1 K-means Clustering

K-means clustering is a classification technique that groups observations of numeric data using one of several *iterative relocation* algorithms—that is, starting from some initial classification, which may be random, points are moved from cluster to another so as to minimize sums of squares. In RevoScaleR, the algorithm used is that of Lloyd (1982).

To perform k-means clustering with RevoScaleR, use the `rxKmeans` function.

16.1.1 Clustering the Airline Data

As a first example of k-means clustering, we will cluster the arrival delay and scheduled departure time in the airline data 7% subsample. To start, we extract variables of interest into a new working data set to which we'll be writing additional information:

```
#######################################################
# Chapter 16: Clustering
#  K-means Clustering
```

```
Ch16Start <- Sys.time()
#   Clustering the Airline Data

bigDataDir <- "C:/MRS/Data"
sampleAirData <- file.path(bigDataDir, "AirOnTime7Pct.xdf")
rxDataStep(inData = sampleAirData, outFile = "AirlineDataClusterVars.xdf",
  varsToKeep=c("DayOfWeek", "ArrDelay", "CRSDepTime", "DepDelay"))
```

We specify the variables to cluster as a formula, and specify the number of clusters we'd like; initial centers for these clusters are then chosen at random.

```
kclusts1 <- rxKmeans(formula= ~ArrDelay + CRSDepTime,
     data = "AirlineDataClusterVars.xdf",
     seed = 10,
     outFile = "airlineDataClusterVars.xdf", numClusters=5)
kclusts1
```

This produces the following output (because the initial centers are chosen at random, your output will probably look different):

```
Call:
rxKmeans(formula = ~ArrDelay + CRSDepTime, data = "AirlineDataClusterVars.xdf",
    outFile = "AirlineDataClusterVars.xdf", numClusters = 5)

Data: "AirlineDataClusterVars.xdf"
Number of valid observations: 10186272
Number of missing observations: 213483
Clustering algorithm:

K-means clustering with 5 clusters of sizes 922985, 38192, 4772791, 261779,
4190525

Cluster means:
    ArrDelay CRSDepTime
1  45.258179   14.86596
2 275.363820   14.81432
3 -10.284426   13.08375
4 118.365205   15.52079
5   7.803893   13.53811

Within cluster sum of squares by cluster:
        1         2         3         4         5
223220709 501736748 354763376 233533349 312403604

Available components:
 [1] "centers"       "size"          "withinss"      "valid.obs"
 [5] "missing.obs"   "numIterations" "tot.withinss"  "totss"
 [9] "betweenss"     "cluster"       "params"        "formula"
[13] "call"
```

The value returned by *rxKmeans* is a list similar to the list returned by the standard R kmeans function. The printed output shows a subset of this information, including the number of valid and missing observations, the cluster sizes, the cluster centers, and the within-cluster sums of squares.

The cluster membership component is returned if the input is a data frame, but if the input is an .xdf file, cluster membership is returned only if *outFile* is specified, in which case it is

returned not as part of the return object, but as a column in the specified file. In our example, we specified an *outFile*, and we see the cluster membership variable when we look at the file with *rxGetInfo*:

```
rxGetInfo("AirlineDataClusterVars.xdf", getVarInfo=TRUE)
```

```
File name: AirlineDataClusterVars.xdf
Number of observations: 10399755
Number of variables: 5
Number of blocks: 19
Compression type: zlib
Variable information:
Var 1: DayOfWeek
       7 factor levels: Mon Tues Wed Thur Fri Sat Sun
Var 2: ArrDelay, Type: integer, Low/High: (-1233, 2453)
Var 3: CRSDepTime, Type: numeric, Storage: float32, Low/High: (0.0000, 24.0000)
Var 4: DepDelay, Type: integer, Low/High: (-1199, 2467)
Var 5: .rxCluster, Type: integer, Low/High: (1, 5)
```

16.1.2 Using the Cluster Membership Information

A common follow-up to clustering is to use the cluster membership information to see whether a given model varies appreciably from cluster to cluster. Since we can use the *rowSelection* argument to extract a single cluster on the fly, there is no need to sort the data first. As an example, we fit our original linear model of ArrDelay by DayOfWeek for two of the clusters:

```
#   Using the Cluster Membership Information

clust1Lm <- rxLinMod(ArrDelay ~ DayOfWeek, "AirlineDataClusterVars.xdf",
     rowSelection = .rxCluste r == 1 )
clust5Lm <- rxLinMod(ArrDelay ~ DayOfWeek, "AirlineDataClusterVars.xdf",
     rowSelection = .rxCluster == 5)
summary(clust1Lm)
summary(clust5Lm)
```

Looking at the summary for *clust1Lm* shows the following:

```
Call:
rxLinMod(formula = ArrDelay ~ DayOfWeek, data = "AirlineDataClusterVars.xdf",
    rowSelection = .rxCluster == 1)

Linear Regression Results for: ArrDelay ~ DayOfWeek
File name: AirlineDataClusterVars.xdf
Dependent variable(s): ArrDelay
Total independent variables: 8 (Including number dropped: 1)
Number of valid observations: 922985
Number of missing observations: 0

Coefficients: (1 not defined because of singularities)
               Estimate Std. Error  t value Pr(>|t|)
(Intercept)    45.21591    0.04237 1067.199 2.22e-16 ***
DayOfWeek=Mon   0.23053    0.05893    3.912 9.16e-05 ***
DayOfWeek=Tues -0.06496    0.05968   -1.089   0.2764
DayOfWeek=Wed   0.10139    0.05869    1.727   0.0841 .
DayOfWeek=Thur  0.06098    0.05708    1.068   0.2854
DayOfWeek=Fri   0.23222    0.05660    4.103 4.08e-05 ***
DayOfWeek=Sat  -0.43444    0.06364   -6.827 8.68e-12 ***
```

```
DayOfWeek=Sun   Dropped    Dropped  Dropped  Dropped
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 14.89 on 922978 degrees of freedom
Multiple R-squared: 0.0001705
Adjusted R-squared: 0.000164
F-statistic: 26.24 on 6 and 922978 DF,  p-value: < 2.2e-16
Condition number: 12.8655
```

Similarly, the summary for clust5Lm shows the following:

```
Call:
rxLinMod(formula = ArrDelay ~ DayOfWeek, data = "AirlineDataClusterVars.xdf",
    rowSelection = .rxCluster == 5)

Linear Regression Results for: ArrDelay ~ DayOfWeek
File name: AirlineDataClusterVars.xdf
Dependent variable(s): ArrDelay
Total independent variables: 8 (Including number dropped: 1)
Number of valid observations: 4190525
Number of missing observations: 0

Coefficients: (1 not defined because of singularities)
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     7.808093   0.009593 813.960 2.22e-16 ***
DayOfWeek=Mon  -0.131001   0.013320  -9.835 2.22e-16 ***
DayOfWeek=Tues -0.228087   0.013374 -17.055 2.22e-16 ***
DayOfWeek=Wed  -0.035954   0.013292  -2.705  0.00683 **
DayOfWeek=Thur  0.231958   0.013170  17.613 2.22e-16 ***
DayOfWeek=Fri   0.313961   0.013171  23.838 2.22e-16 ***
DayOfWeek=Sat  -0.257716   0.014036 -18.361 2.22e-16 ***
DayOfWeek=Sun    Dropped    Dropped Dropped  Dropped
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 7.238 on 4190518 degrees of freedom
Multiple R-squared: 0.0007911
Adjusted R-squared: 0.0007897
F-statistic:   553 on 6 and 4190518 DF,  p-value: < 2.2e-16
Condition number: 12.0006
```

Chapter 17.

Converting RevoScaleR Model Objects for Use in PMML

The objects returned by RevoScaleR predictive analytics functions have similarities to objects returned by the predictive analytics functions provided by base and recommended packages in R. A key difference between these two types of model objects is that RevoScaleR model objects typically do not contain any components that have the same length as the number of rows in the original data set. For example, if you use base R's lm function to estimate a linear model, the result object contains not only all of the data used to estimate the model, but components such as residuals and fitted.values that contain values corresponding to every observation in the data set. For estimating models using big data, this is not appropriate.

However, there is overlap in the model object components that can be very useful when working with other packages. For example, the `pmml` package will generate PMML (Predictive Model Markup Language) code for a number of R model types. PMML is an XML-base language which allows users to share models between PMML compliant applications. For more information about PMML, visit http://www.dmg.org .

RevoScaleR provides a set of coercion methods to convert a RevoScaleR model object to a standard R model object: `as.lm`, `as.glm`, `as.rpart`, and `as.kmeans`. As suggested above, these coerced model objects do not have all of the information available in a standard R model object, but do contain information about the fitted model that is similar to standard R.

For example, let's create an rxLinMod object by estimating a linear regression on a very large dataset: the airline data with almost 150 million observations.

```
#########################################################
# Chapter 17: Converting RevoScaleR Model Objects for
#  Use in PMML
#########################################################
Ch17Start <- Sys.time()

bigDataDir <- "C:/MRS/Data"
bigAirData <- file.path(bigDataDir, "AirOnTime87to12/AirOnTime87to12.xdf")

# About 150 million observations
rxLinModObj <- rxLinMod(ArrDelay~Year + DayOfWeek, data = bigAirData,
    blocksPerRead = 10)
```

Next, the R *pmml* package should be downloaded and installed from CRAN. After you have done so, generate the RevoScaleR *rxLinMod* object, and use the *as.lm* method when generating the PMML output:

```
library(pmml)
pmml(as.lm(rxLinModObj))
```

The generated output looks as follows:

```
> pmml(as.lm(rxLinModObj))
<PMML version="4.1" xmlns="http://www.dmg.org/PMML-4_1"
xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:schemaLocation="http://www.dmg.org/PMML-4_1 http://www.dmg.org/v4-1/pmml-4-
1.xsd">
 <Header copyright="Copyright (c) 2013 sue" description="Linear Regression
Model">
  <Extension name="user" value="yourname" extender="Rattle/PMML"/>
  <Application name="Rattle/PMML" version="1.3"/>
  <Timestamp>2013-09-05 11:39:28</Timestamp>
 </Header>
 <DataDictionary numberOfFields="3">
  <DataField name="ArrDelay" optype="continuous" dataType="double"/>
  <DataField name="Year" optype="continuous" dataType="double"/>
  <DataField name="DayOfWeek" optype="categorical" dataType="string">
   <Value value="Mon"/>
   <Value value="Tues"/>
   <Value value="Wed"/>
   <Value value="Thur"/>
   <Value value="Fri"/>
   <Value value="Sat"/>
   <Value value="Sun"/>
  </DataField>
 </DataDictionary>
 <RegressionModel modelName="Linear_Regression_Model" functionName="regression"
algorithmName="least squares" targetFieldName="ArrDelay">
  <MiningSchema>
   <MiningField name="ArrDelay" usageType="predicted"/>
   <MiningField name="Year" usageType="active"/>
   <MiningField name="DayOfWeek" usageType="active"/>
  </MiningSchema>
  <Output>
   <OutputField name="Predicted_ArrDelay" feature="predictedValue"/>
```

```
  </Output>
  <RegressionTable intercept="112.856953212332">
   <NumericPredictor name="Year" exponent="1" coefficient="-
0.0533799688606163"/>
   <CategoricalPredictor name="DayOfWeek" value="Mon"
coefficient="0.303666227836942"/>
   <CategoricalPredictor name="DayOfWeek" value="Tues" coefficient="-
0.593700918634743"/>
   <CategoricalPredictor name="DayOfWeek" value="Wed"
coefficient="0.473693749859764"/>
   <CategoricalPredictor name="DayOfWeek" value="Thur"
coefficient="2.3393087933048"/>
   <CategoricalPredictor name="DayOfWeek" value="Fri"
coefficient="2.91671831592945"/>
   <CategoricalPredictor name="DayOfWeek" value="Sat" coefficient="-
2.31671307739631"/>
   <CategoricalPredictor name="DayOfWeek" value="Sun" coefficient="0"/>
  </RegressionTable>
 </RegressionModel>
</PMML>
```

Similarly, rxLogit and rxGlm functions have as.glm methods:

```
form <- case ~ age + parity + spontaneous + induced
rxLogitObj <- rxLogit(form, data =infert)
pmml(as.glm(rxLogitObj))

rxGlmObj <- rxGlm(form, data=infert, family = binomial())
pmml(as.glm(rxGlmObj))
```

RevoScaleR's *rxKmeans* objects can be coerced to *kmeans* objects:

```
set.seed(17)
irow <- unique(sample.int(nrow(women), 4L,
    replace = TRUE))[seq(2)]
centers <- women[irow,, drop = FALSE]
rxKmeansObj <- rxKmeans(~height + weight, data = women,
    centers = centers)
pmml(as.kmeans(rxKmeansObj))
```

And RevoScaleR's *rxDTree* objects can be coerced to *rpart* objects. (Note that *rpart* is a recommended package that you may need to load.)

```
library(rpart)
method <- "class"
form <- Kyphosis ~ Number + Start
parms <- list(prior = c(0.8, 0.2), loss = c(0, 2, 3, 0),
    split = "gini")
control <- rpart.control(minsplit = 5, minbucket = 2, cp = 0.01,
    maxdepth = 10, maxcompete = 4, maxsurrogate = 5,
    usesurrogate = 2, surrogatestyle = 0, xval = 0)
cost <- 1 + seq(length(attr(terms(form), "term.labels")))

rxDTreeObj <- rxDTree(formula = Kyphosis ~ Number + Start,
    data = kyphosis, method = method, parms = parms,
    control = control, cost = cost)
pmml(as.rpart(rxDTreeObj))
```

Chapter 18.

Transform Functions

In previous chapters, we have used the *transforms* argument and inline transformations within formulas whenever we needed to specify a data transformation, and performed row selection with the *rowSelection* argument. In this chapter, we introduce another method for performing transformations within RevoScaleR that is extremely powerful and can be used both for transforming variables and for creating row selection variables. This method is the use of transform functions.

A transform function is a function that takes as input a list of variables and returns a list of (possibly different) variables. If defined and specified (using the *transformFunc* argument to most RevoScaleR functions), a transform function is evaluated before any transformations specified in the transforms, *rowSelection*, or formula arguments. The list of variables to be passed to the transform function is specified as the *transformVars* argument.

18.1 Creating Variables

Suppose we want to extract five variables from the *CensusWorkers* data set, but also add a factor variable based on the integer variable age. We considered this example in Chapter 4, when we used the *transforms* argument to create the new variable. We can also use a transform function to create new variables. For example, to create our factor variable, we can create the following function:

```
#######################################################
# Chapter 18: Transform Functions
#  Creating Variables
Ch18Start <- Sys.time()


ageTransform <- function(dataList)
{
    dataList$ageFactor <- cut(dataList$age, breaks=seq(from = 20, to = 70,
                                by = 5), right = FALSE)
    return(dataList)
}
```

We can test the function by reading an arbitrary chunk out of the data set. For efficiency reasons, the data passed to the transformation function is stored as a list rather than a data frame, so when reading from the .xdf file we set the *returnDataFrame* argument to FALSE to emulate this behavior. Since we only use the variable *age* in our transformation function, we restrict the variables extracted to that.

```
censusWorkers <- file.path(rxGetOption("sampleDataDir"), "CensusWorkers.xdf")
testData <- rxReadXdf(file = censusWorkers, startRow = 100, numRows = 10,
returnDataFrame = FALSE, varsToKeep = c("age"))

as.data.frame(ageTransform(testData))
```

The resulting list of data (displayed as a data frame) shows us that our transformations are working as expected:

```
 > as.data.frame(ageTransform(testData))
    age ageFactor
1    20    [20,25)
2    48    [45,50)
3    44    [40,45)
4    29    [25,30)
5    28    [25,30)
6    43    [40,45)
7    20    [20,25)
8    23    [20,25)
9    32    [30,35)
10   42    [40,45)
```

In doing a data step operation, RevoScaleR reads in a chunk of data read from the original data set, including only the variables indicated in *varsToKeep*, or omitting variables specified in *varsToDrop*. It then passes the variables needed for data transformations back to R for manipulation. We specify the variables needed to process the transformation in the *transformVars* argument. Including extra variables does not alter the analysis, but it does reduce the efficiency of the data step. In this case, since *ageFactor* depends only on the *age* variable for its creation, the *transformVars* argument needs to specify just that:

```
rxDataStep(inData = censusWorkers, outFile = "newCensusWorkers",
    varsToDrop = c("state"), transformFunc = ageTransform,
    transformVars=c("age"), overwrite=TRUE)
```

The *rxGetInfo* function reveals the added and dropped variables:

```
rxGetInfo("newCensusWorkers", getVarInfo = TRUE)

 File name: C:\YourOutputPath\newCensusWorkers.xdf
 Number of rows: 351121
 Number of variables: 6
 Number of blocks: 6
 Compression type: zlib
 Variable information:
 Var 1: age, Age
        Type: integer, Low/High: (20, 65)
 Var 2: incwage, Wage and salary income
        Type: integer, Low/High: (0, 354000)
 Var 3: perwt, Type: integer, Low/High: (2, 168)
 Var 4: sex, Sex
        2 factor levels: Male Female
 Var 5: wkswork1, Weeks worked last year
        Type: integer, Low/High: (21, 52)
 Var 6: ageFactor
        10 factor levels: [20,25) [25,30) [30,35) [35,40) [40,45) [45,50)
               [50,55) [55,60) [60,65) [65,70)
```

18.2 Using Additional Objects or Data in a Transform Function

It is sometimes useful to access additional information from within a transform function. For example, you might want to match additional data in the process of creating new variables. Transform functions are evaluated in a "sterilized" environment which includes the parent environment of the function closure. To provide access to additional data within the function, you can use the *transformObjects* argument.

For example, suppose you would like to estimate a linear model using wage income as the dependent variable, and want to include state-level of per capita expenditure on education as one of the independent variables. We can define a named vector to contain this state-level data as follows:

```
#  Using Additional Objects or Data in a Transform Function

educExpense <- c(Connecticut=1795.57, Washington=1170.46, Indiana = 1289.66)
```

We can then define a transform function that uses this information as follows:

```
transformFunc <- function(dataList)
{
      # Match each individual's state and add the variable for educ. exp.
     dataList$stateEducExpPC = educExp[match(dataList$state, names(educExp))]
     return(dataList)
}
```

We can then use the transform function and our named vector in a call to *rxLinMod* as follows:

```
censusWorkers <- file.path(rxGetOption("sampleDataDir"), "CensusWorkers.xdf")
linModObj <- rxLinMod(incwage~sex + age + stateEducExpPC,
     data = censusWorkers, pweights = "perwt",
```

```
    transformFun = transformFunc, transformVars = "state",
    transformObjects = list(educExp = educExpense))
summary(linModObj)
```

When the transform function is evaluated, it will have access to the *educExp* object. The final results show:

```
Call:
rxLinMod(formula = incwage ~ sex + age + stateEducExpPC, data = censusWorkers,
    pweights = "perwt", transformObjects = list(educExp = educExp),
    transformFunc = transformFunc, transformVars = "state")

Linear Regression Results for: incwage ~ sex + age + stateEducExpPC
File name:
    C:\Program Files\Microsoft\MRO-for-RRE\8.0\R-
3.2.2\library\RevoScaleR\SampleData\CensusWorkers.xdf
Probability weights: perwt
Dependent variable(s): incwage
Total independent variables: 5 (Including number dropped: 1)
Number of valid observations: 351121
Number of missing observations: 0

Coefficients: (1 not defined because of singularities)
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)    -1.809e+04  4.414e+02  -40.99 2.22e-16 ***
sex=Male        1.689e+04  1.321e+02  127.83 2.22e-16 ***
sex=Female        Dropped    Dropped Dropped  Dropped
age             5.593e+02  5.791e+00   96.58 2.22e-16 ***
stateEducExpPC  1.643e+01  2.731e-01   60.16 2.22e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 175900 on 351117 degrees of freedom
Multiple R-squared: 0.07755
Adjusted R-squared: 0.07754
F-statistic:  9839 on 3 and 351117 DF,  p-value: < 2.2e-16
Condition number: 1.1176
```

18.3 Creating a Row Selection Variable

One common use of the *transformFunc* argument is to create a logical variable to use as a row selection variable. For example, suppose you want to create a random sample from a massive data set. You can use the *transformFunc* argument to specify a transformation that creates a random binomial variable, which can then be coerced to logical and used for row selection. The object name *.rxRowSelection* is reserved for the row selection variable; if RevoScaleR finds this object, it is used for row selection.

Warning: If you both specify a *rowSelection* argument and define a *.rxRowSelection* variable in your transform function, the one specified in your transform function will be overwritten by the contents of the *rowSelection* argument, so that expression takes precedence.

The following code creates a random selection variable to create a data frame with a random 10% subset of the census workers file:

```
#  Creating a Row Selection Variable

createRandomSample <- function(data)
{
    data$.rxRowSelection <- as.logical(rbinom(length(data[[1]]), 1, .10))
     return(data)
}
censusWorkers <- file.path(rxGetOption("sampleDataDir"), "CensusWorkers.xdf")
df <- rxXdfToDataFrame(file = censusWorkers, transformFunc = createRandomSample,
     transformVars = "age")
```

The resulting data frame, `df`, has approximately 35,000 rows. You can look at the first few rows using `head` as follows:

```
rxGetInfo(df)
head(df)
```

```
   age incwage perwt    sex wkswork1   state
1   50    9000    30   Male       48 Indiana
2   41   35000    20 Female       48 Indiana
3   55   40400    21   Male       52 Indiana
4   56   45000    30 Female       52 Indiana
5   46   17200    60 Female       52 Indiana
6   49   35000    21 Female       52 Indiana
```

Equivalently, we could create the temporary row selection variable using the `rowSelection` argument with the internal `.rxNumRows` variable, which provides the number of rows in the current chunk of data being processed:

```
df <- rxDataStep(inData = censusWorkers,
     rowSelection = as.logical(rbinom(.rxNumRows, 1, .10)) == TRUE)
```

18.4 Using Internal Variables in a Transformation Function: An Example Computing Moving Averages

Four additional variables providing information on the RevoScaleR processing are available for use in your transform functions:

- .rxStartRow: The row number from the original data that was read as the first row of the current chunk.
- .rxChunkNum: The current chunk being processed.
- .rxReadFileName: The name of the .xdf file currently being read.
- .rxIsTestChunk: Whether the chunk being processed is being processed as a test sample of data.

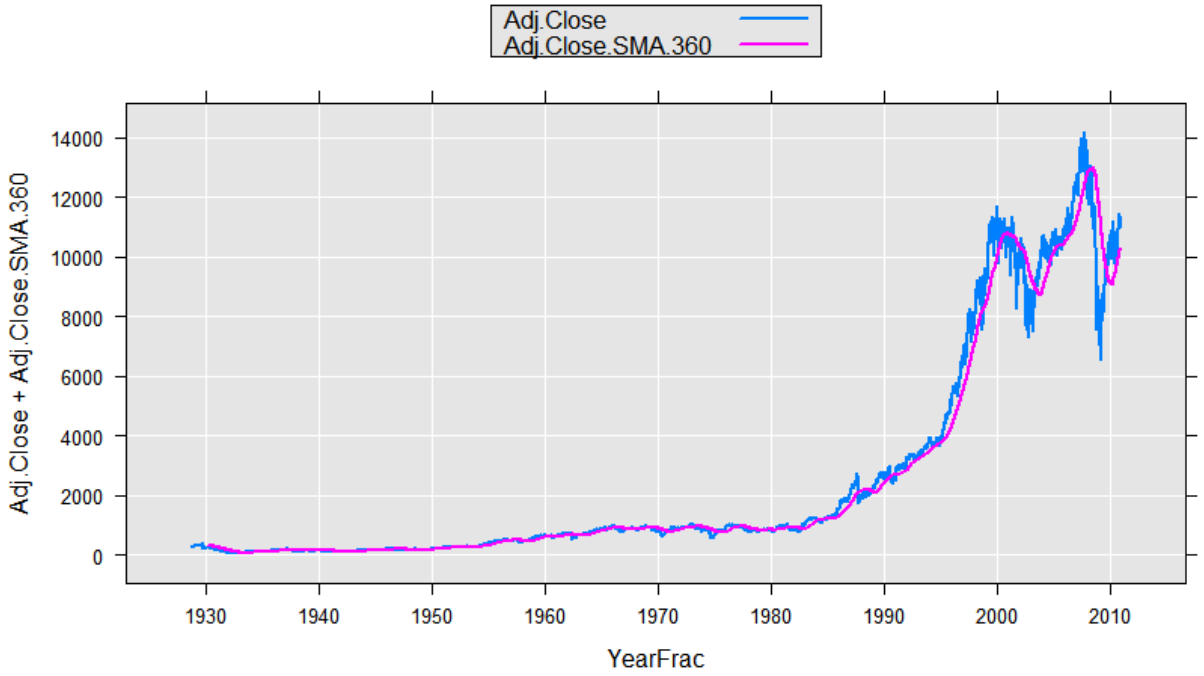
These are particularly useful if you need to access additional rows of data when processing a chunk. This is the case, for example, when you want to include lagged data in a calculation. The following example is a transformation function "generator" to compute a simple moving average. By creating this "function within a function" we are able to easily pass arguments into a transformation function. This one takes as arguments the number of days (or time units) for the moving average, the name of the variable that will be used to compute the moving average, and the name of the new variable to create. The transformation function computes the number of lagged observations to read in, then reads in that data to create a long data vector with the lags. The simple moving average calculations are performed and put into a new variable. The additional lagged rows are removed from the original data vector before returning from the function.

```
#  An Example Computing Moving Averages

makeMoveAveTransFunc <- function(numDays = 10, varName="", newVarName="")
{
    function (dataList)
    {
        numRowsToRead <- 0
        varForMoveAve <- 0
        # If no variable is named, use the first one sent
        # to the transformFunc
        if (is.null(varName) || nchar(varName) == 0)
        {
            varForMoveAve <- names(dataList)[1]
        } else {
            varForMoveAve <- varName
        }

        # Get the number of rows in the current chunk
        numRowsInChunk <- length(dataList[[varForMoveAve]])

        # .rxStartRow is the starting row number of the
        # chunk of data currently being processed
       # Read in previous data if we are not starting at row 1
      if (.rxStartRow > 1)
      {
          # Compute the number of lagged rows we'd like
            numRowsToRead <- numDays - 1
          # Check to see if enough data is available
          if (numRowsToRead >= .rxStartRow)
          {
             numRowsToRead <- .rxStartRow - 1
          }
            # Compute the starting row of previous data to read
          startRow <- .rxStartRow - numRowsToRead
        # Read previous rows from the .xdf file
          previousRowsDataList <- RevoScaleR::rxReadXdf(
                file=.rxReadFileName,
           varsToKeep=names(dataList),
                startRow=startRow, numRows=numRowsToRead,
           returnDataFrame=FALSE)
            # Concatenate the previous rows with the existing rows
           dataList[[varForMoveAve]] <-
                c(previousRowsDataList[[varForMoveAve]],
```

```
                    dataList[[varForMoveAve]])
            }
            # Create variable for simple moving average
              # It will be added as the last variable in the data list
              newVarIdx <- length(dataList) + 1

              # Initialize with NA's
             dataList[[newVarIdx]] <- rep(as.numeric(NA), times=numRowsInChunk)

             for (i in (numRowsToRead+1):(numRowsInChunk + numRowsToRead))
             {
                 j <- i - numRowsToRead
                 lowIdx <- i - numDays + 1
                 if (lowIdx > 0 && ((lowIdx == 1) ||
                      (j > 1 && (is.na(dataList[[newVarIdx]][j-1])))))
             {
                      # If it's the first computation or the previous value
                      # is missing, take the mean of all the relevant lagged data
                   dataList[[newVarIdx]][j] <-
                           mean(dataList[[varForMoveAve]][lowIdx:i])
              } else if (lowIdx > 1)
              {
                      # Add and subtract from the last computation
                    dataList[[newVarIdx]][j] <- dataList[[newVarIdx]][j-1] -
                              dataList[[varForMoveAve]][lowIdx-1]/numDays +
                        dataList[[varForMoveAve]][i]/numDays
              }
              }
             # Remove the extra rows we read in from the original variable
             dataList[[varForMoveAve]] <-

                dataList[[varForMoveAve]][(numRowsToRead + 1):(numRowsToRead +
                    numRowsInChunk)]

             # Name the new variable
             if (is.null(newVarName) || (nchar(newVarName) == 0))
             {
                 # Use a default name if no name specified
                 names(dataList)[newVarIdx] <-
                       paste(varForMoveAve, "SMA", numDays, sep=".")
             } else {
                 names(dataList)[newVarIdx] <- newVarName
             }
            return(dataList)
        }
    }
```

We could use this function with *rxDataStep* to add a variable to our data set, or on-the-fly, for example for plotting. Here we will use the sample data set containing daily information on the Dow Jones Industrial Average. We compute a 360-day moving average for the adjusted close (adjusted for dividends and stock splits) and plot it:

```
DJIAdaily <- file.path(rxGetOption("sampleDataDir"), "DJIAdaily.xdf")
rxLinePlot(Adj.Close+Adj.Close.SMA.360~YearFrac, data=DJIAdaily,
    transformFunc=makeMoveAveTransFunc(numDays=360),
    transformVars=c("Adj.Close"))
```


Adj.Close
Adj.Close.SMA.360
Adj.Close + Adj.Close.SMA.360
14000
12000
10000
8000
6000
4000
2000
0
1930
1940
1950
1960
1970
1980
1990
2000
2010
YearFrac

18.5 How Transforms Are Evaluated

User-defined transforms and transform functions are evaluated in essentially the same way. An evaluation environment is constructed from the base environment together with the utils, stats, and methods packages (you can modify this basic list by setting the rxOption `transformPackages`), packages specified with the `transformPackages` argument, and any specified `transformObjects`, and the closure of the transform function. (User-defined transforms are combined into a single, "hidden" transform function for evaluation.) The transform function is then evaluated in this evaluation environment. Functions that are in packages that are not part of the evaluation environment can be used, but must be prefixed by their package name and two or three colons, depending on whether the function is exported.

18.6 Transformations to Avoid

Transform functions are very powerful, and we recommend their use. However, there are four types of transformation that should be avoided:

1) transformations that change the length of a variable (this includes, naturally, most model-fitting functions)
2) transformations that depend upon all observations simultaneously (because RevoScaleR works on chunks of data, such transformations will not have access to all the data at once). Examples of such transformations are matrix operations such as poly or solve.
3) transformations that have the possibility of creating different mappings of factor codes to factor labels.
4) transformations that involve sampling with replacement. Again, this is because RevoScaleR works on chunks of data, and sampling with replacement chunk by chunk is not equivalent to sampling with replacement from the full data set.

If you change the length of one variable, you will get errors from subsequent analysis functions that not all variables are the same length. If you try to change the length of all variables (essentially, performing some sort of row selection), you need to pass all of your data through the transform function, and this can be very inefficient. We therefore recommend the row selection procedures described in previous chapters.

If you create a factor within a transformation function, you may get unexpected results because all of the data is not in memory at one time. It is recommended that if creating a factor within a transformation function, you always explicitly set the values and labels. For example,

```
dataList$xfac <- as.factor(dataList$x, levels = c(1, 2,3),
     labels = c("One", "Two", "Three"))
```

Chapter 19.

Visualizing Huge Data Sets: An Example from the U.S. Census

By combining the power and flexibility of the open-source R language with the fast computations and rapid access to huge datasets provided by RevoScaleR, it is easy and efficient to not only do fine-grained calculations "on the fly" for plotting, but to visually drill down into these patterns.

This example focuses on a basic demographic pattern: in general, more boys than girls are born and the death rate is higher for males at every age. So, typically we observe a decline in the ratio of males to females as age increases.

19.1 Examining the Data

We can examine this pattern in the United States using the 5% Public Use Microdata Sample (PUMS) of the 2000 United States Census, stored in an .xdf file of about 12 gigabytes.[1] Using the rxGetInfo function, we can get a quick summary of the data set:

```
#########################################################
# Chapter 19: Visualizing Huge Data Sets: An Example from the U.S. Census
#  Examining the Data
Ch19Start <- Sys.time()
```

[1] The analysis in this paper uses the Integrated Public Use Microdata Sample provided by the Minnesota Population Center (Ruggles, et al., 2006) stored in RevoScaleR's .xdf file format.

```
bigDataDir <- "C:/MRS/Data"
bigCensusData <- file.path(bigDataDir,"CensusUS5Pct2000.xdf")
rxGetInfo(bigCensusData)
```

```
 File name: C:\MRS\Data\CensusUS5Pct2000.xdf
 Number of observations: 14058983
 Number of variables: 264
 Number of blocks: 98
 Compression type: zlib
```

It contains over 14 million rows, has 264 variables, and has been stored in 98 data blocks in the .xdf file.

First let's use the rxCube function to count the number of males and females for each age, using the weighting variable provided by the census bureau. We'll read in the data in chunks of 15 blocks, or about 2 million rows at a time.

```
ageSex <- rxCube(~F(age):sex, pweights = "perwt", data = bigCensusData,
blocksPerRead = 15)
```

In the computation, we're treating age as a categorical variable so we'll get counts for each age. Since we'll be converting this factor data back to integers on a regular basis, we'll write a function to do the conversion:

```
factoi <- function(x)
{
     as.integer(levels(x))[x]
}
```

We can now write a simple function in R to take the counts information returned from rxCube and do the arithmetic to compute the sex ratio for each age.

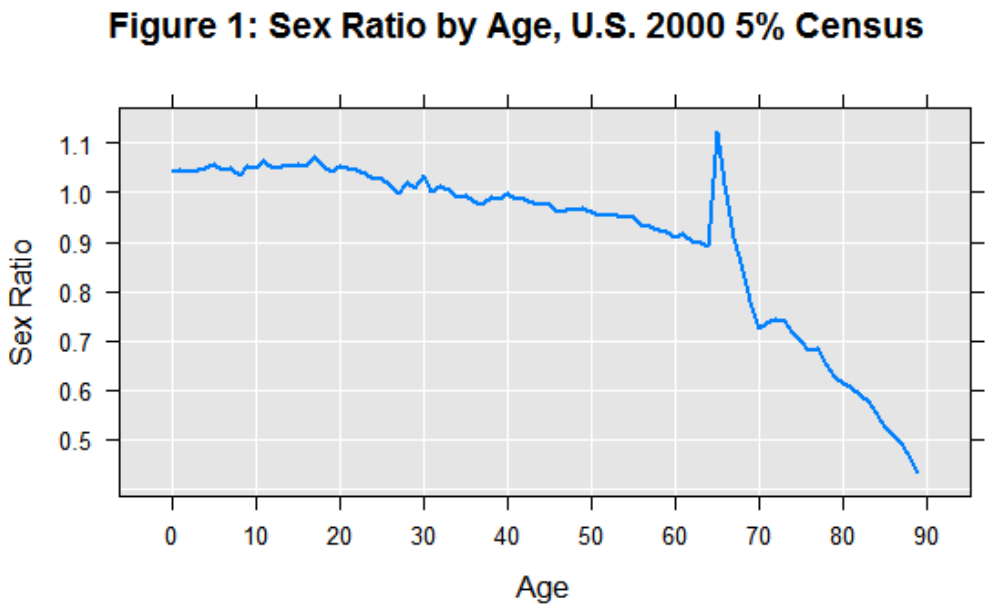
```
getSexRatio <- function(ageSex)
{
    ageSexDF <- as.data.frame(ageSex)
    sexRatioDF <- subset(ageSexDF, sex == 'Male')
    names(sexRatioDF)[names(sexRatioDF) == 'Counts'] <- 'Males'
    sexRatioDF$sex <- NULL
    females <- subset(ageSexDF, sex == 'Female')
    sexRatioDF$Females <- females$Counts
    sexRatioDF$age <- factoi(sexRatioDF$F_age)
    sexRatioDF <- subset(sexRatioDF, Females > 0 & Males > 0 & age <=90)
    sexRatioDF$SexRatio <- sexRatioDF$Males/sexRatioDF$Females
    return(sexRatioDF)
}
```

It returns a data frame with the counts for Males and Females, the SexRatio, and age for all groups in which there are positive counts for both Males and Females. Ages over 90 are also excluded.

Let's use that function and then plot the results:

```
sexRatioDF <- getSexRatio(ageSex)
rxLinePlot(SexRatio~age, data = sexRatioDF,
```

```
xlab = "Age", ylab = "Sex Ratio",
main = "Figure 1: Sex Ratio by Age, U.S. 2000 5% Census")
```



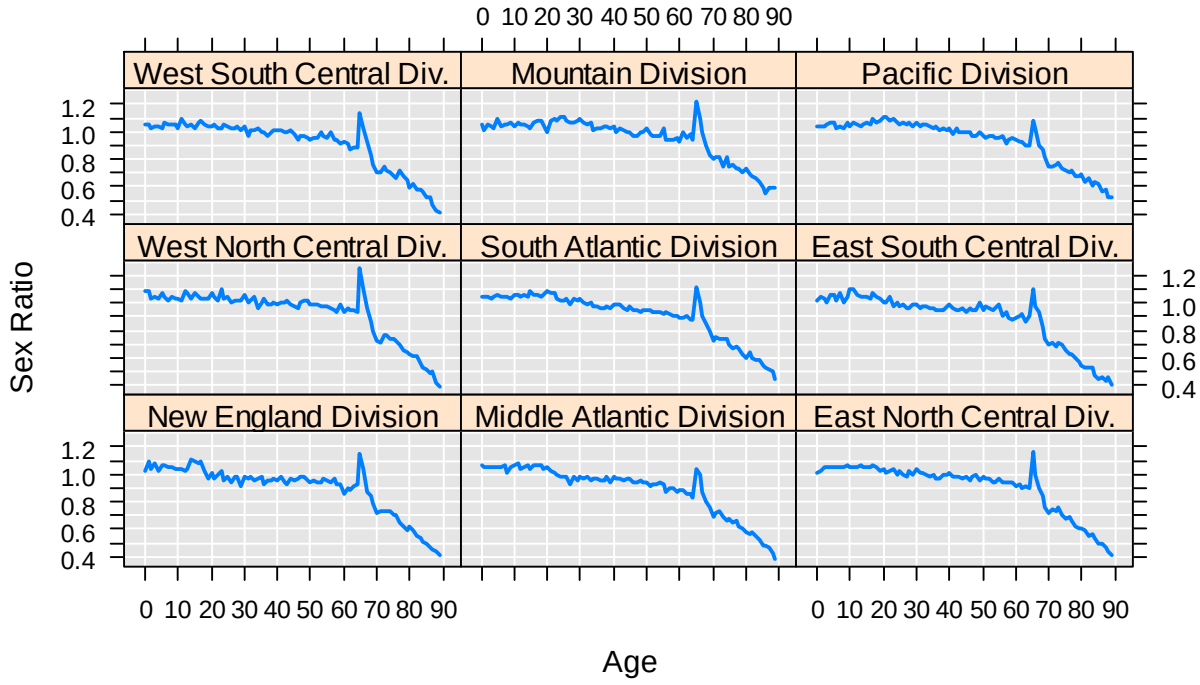
The graph shows the expected downward trend at the younger ages. But look at what happens at the age of 65! At the age of 65, there are suddenly about 12 men for every 10 women.

We can quickly drill down, and do the same computation for each region:

```
ageSex <- rxCube(~F(age):sex:region, pweights = "perwt", data = bigCensusData,
blocksPerRead = 15)
sexRatioDF <- getSexRatio(ageSex)
rxLinePlot(SexRatio~age|region, data = sexRatioDF,
     xlab = "Age", ylab = "Sex Ratio",
     main = "Figure 2: Sex Ratio by Age and Region, U.S. 2000 5% Census")
```

We see the unlikely “spike” at age 65 in all regions:

Figure 2: Sex Ratio by Age and Region, U.S. 2000 5% Census

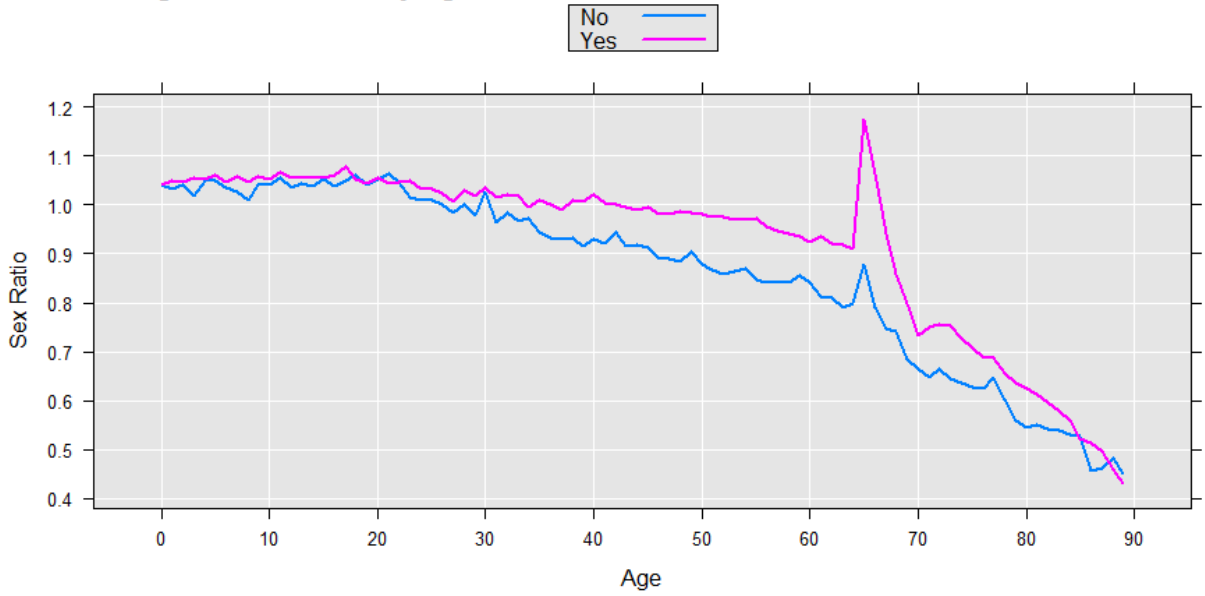


Let's try looking at ethnicity, comparing whites with non-whites.

```
ageSex <- rxCube(~F(age):sex:racwht, pweights = "perwt", data = bigCensusData,
     blocksPerRead = 15)
sexRatioDF <- getSexRatio(ageSex)
rxLinePlot(SexRatio~age, groups = racwht, data = sexRatioDF,
     xlab = "Age", ylab = "Sex Ratio",
main = "Figure 3: Sex Ratio by Age, Conditioned on 'Is White?', U.S. 2000 5%
Census")
```

There are interesting differences between the two groups, but again there is the familiar spike at age 65 in both cases.

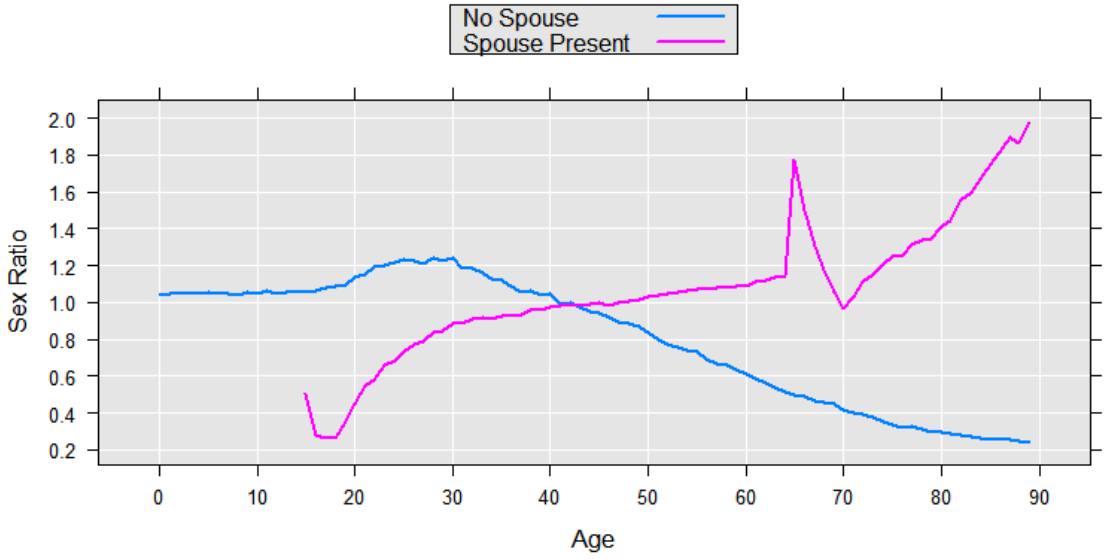
Figure 3: Sex Ratio by Age, Conditioned on 'Is White?', U.S. 2000 5% Census



How about comparing married people with those not living with a spouse? We can create a temporary variable using the transform argument to do this computation:

```
ageSex <- rxCube(~F(age):sex:married, pweights = "perwt", data = bigCensusData,
    transforms = list(married = factor(marst == 'Married, spouse present',
     levels = c(FALSE, TRUE), labels = c("No Spouse", "Spouse Present"))),
    blocksPerRead = 15)
sexRatioDF <- getSexRatio(ageSex)
rxLinePlot(SexRatio~age, groups = married, data = sexRatioDF,
     xlab="Age", ylab = "Sex Ratio",
main="Figure 4: Sex Ratio by Age, Living/Not Living with Spouse, U.S. 2000 5%
Census")
```

Figure 4: Sex Ratio by Age, Living/Not Living with Spouse, U.S. 2000 5% Census



First, notice that the spike at age 65 is absent for unmarried people. But also look at the very different trends. For married 20 year-olds, there are about 5 men for every 10 women, but for married 60 year-olds, there would be about 11 men for every 10 women. This may at first seem counter-intuitive, but it's consistent with the notion that men tend to marry younger women. Let's explore that next.

19.2 Extending the Analysis

We'd like to compare the ages of men with ages of their wives. This is more complicated than the earlier computations because the spouse's age is stored in a different record in the data file. To handle this, we'll create a new data set using RevoScaleR's data step functionality with a transformation function. This transformation function makes use of RevoScaleR's ability to go back and read additional rows from an .xdf file as it is reading through it in chunks. It also uses internal variables that are provided inside a transformation function: `.rxStartRow`, which is the row number from the original data set for the first row of the chunk of data being processed; `.rxReadFileName` gives the name of the file being read. It first checks the spouse location for the relative position of the spouse in the data set. It then determines which of the observations have spouses in the previous, current, or next chunk of data. Then, in each of the three cases, it looks up the spouse information and adds it to the original observation.

```
#  Extending the Analysis

spouseAgeTransform <- function(data)
{
      # Use internal variables
      censusUS2000 <- .rxReadFileName
      startRow <- .rxStartRow

      # Calculate basic information about input data chunk
      numRows <- length(data$sploc)
      endRow <- startRow + numRows - 1

      # Create a new variable. A spouse is present if the spouse locator
      # (relative position of spouse in data) is positive
      data$hasSpouse <- data$sploc > 0

      # Create variables for spouse information
      spouseVars <- c("age", "incwage", "sex")
      data$spouseAge <- rep.int(NA_integer_, numRows)
      data$spouseIncwage <- rep.int(NA_integer_, numRows)
      data$sameSex <- rep.int(NA, numRows)

      # Create temporary row numbers for this block
      rowNum <- seq_len(numRows)
      # Find the temporary row number for the spouse
      spouseRow <- rep.int(NA_integer_, numRows)
      if (any(data$hasSpouse))
      {
         spouseRow[data$hasSpouse] <-
             rowNum[data$hasSpouse] +
             data$sploc[data$hasSpouse] - data$pernum[data$hasSpouse]
```

```
}

#################################################################
# Handle possibility that spouse is in previous or next chunk
# Create a variable indicating if the spouse is in the previous,
# current, or next chunk
blockBreaks <- c(-.Machine$integer.max, 0, numRows, .Machine$integer.max)
blockLabels <- c("previous", "current", "next")
spouseFlag <- cut(spouseRow, breaks = blockBreaks, labels = blockLabels)
blockCounts <- tabulate(spouseFlag, nbins = 3)
names(blockCounts) <- blockLabels

# At least one spouse in previous chunk
if (blockCounts[["previous"]] > 0)
{
   # Go back to the original data set and read the
   # required rows in the previous chunk
   needPreviousRows <- 1 - min(spouseRow, na.rm = TRUE)
   previousData <- rxReadXdf(censusUS2000,
          startRow = startRow - needPreviousRows,
          numRows = needPreviousRows, varsToKeep = spouseVars,
          returnDataFrame = FALSE, reportProgress = 0)

   # Get the spouse locations
   whichPrevious <- which(spouseFlag == "previous")
   spouseRowPrev <- spouseRow[whichPrevious] + needPreviousRows

   # Set the spouse information for everyone with a spouse
   # in the previous chunk
   data$spouseAge[whichPrevious] <- previousData$age[spouseRowPrev]
   data$spouseIncwage[whichPrevious] <- previousData$incwage[spouseRowPrev]
   data$sameSex[whichPrevious] <-
       data$sex[whichPrevious] == previousData$sex[spouseRowPrev]
}

# At least one spouse in current chunk
if (blockCounts[["current"]] > 0)
{
   # Get the spouse locations
    whichCurrent <- which(spouseFlag == "current")
   spouseRowCurr <- spouseRow[whichCurrent]

   # Set the spouse information for everyone with a spouse
   # in the current chunk
   data$spouseAge[whichCurrent] <- data$age[spouseRowCurr]
   data$spouseIncwage[whichCurrent] <- data$incwage[spouseRowCurr]
   data$sameSex[whichCurrent] <-
       data$sex[whichCurrent] == data$sex[spouseRowCurr]
}

# At least one spouse in next chunk
if (blockCounts[["next"]] > 0)
{
   # Go back to the original data set and read the
   # required rows in the next chunk
   needNextRows <- max(spouseRow, na.rm=TRUE) - numRows
   nextData <- rxReadXdf(censusUS2000, startRow = endRow+1,
          numRows = needNextRows, varsToKeep = spouseVars,
          returnDataFrame = FALSE, reportProgress = 0)

   # Get the spouse locations
   whichNext <- which(spouseFlag == "next")
   spouseRowNext <- spouseRow[whichNext] - numRows
```

```
        # Set the spouse information for everyone with a spouse
        # in the next block
        data$spouseAge[whichNext] <- nextData$age[spouseRowNext]
        data$spouseIncwage[whichNext] <- nextData$incwage[spouseRowNext]
        data$sameSex[whichNext] <-
            data$sex[whichNext] == nextData$sex[spouseRowNext]
    }

    # Now caculate age difference
    data$ageDiff <- data$age - data$spouseAge
    data
}
```

We can test the transform function by reading in a small number of rows of data. First we will read in a chunk that has a spouse in the previous block and a spouse in the next block, and call the transform function. We will repeat this, expanding the chunk of data to include both spouses, and double check to make sure the results are the same for the equivalent rows:

```
varsToKeep=c("age", "region", "incwage", "racwht", "nchild", "perwt", "sploc",
     "pernum", "sex")
testDF <- rxReadXdf(bigCensusData, numRows = 6, startRow=9,
     varsToKeep = varsToKeep, returnDataFrame=FALSE)
.rxStartRow <- 9
.rxReadFileName <- bigCensusData
newTestDF <- as.data.frame(spouseAgeTransform(testDF))
.rxStartRow <- 8
testDF2 <- rxReadXdf(bigCensusData, numRows = 8, startRow=8,
     varsToKeep = varsToKeep, returnDataFrame=FALSE)
newTestDF2 <- as.data.frame(spouseAgeTransform(testDF2))
newTestDF[,c("age", "incwage", "sploc", "hasSpouse" ,"spouseAge", "ageDiff")]
newTestDF2[,c("age", "incwage", "sploc", "hasSpouse" ,"spouseAge", "ageDiff")]
```

```
> newTestDF[,c("age", "incwage", "sploc", "hasSpouse" ,"spouseAge", "ageDiff")]
  age incwage sploc hasSpouse spouseAge ageDiff
1  46    1000     1      TRUE        43       3
2  16       0     0     FALSE        NA      NA
3  14      NA     0     FALSE        NA      NA
4   7      NA     0     FALSE        NA      NA
5  19    1500     0     FALSE        NA      NA
6  62   42600     2      TRUE        55       7
```

```
> newTestDF2[,c("age", "incwage", "sploc", "hasSpouse" ,"spouseAge",
"ageDiff")]
  age incwage sploc hasSpouse spouseAge ageDiff
1  43  150000     2      TRUE        46      -3
2  46    1000     1      TRUE        43       3
3  16       0     0     FALSE        NA      NA
4  14      NA     0     FALSE        NA      NA
5   7      NA     0     FALSE        NA      NA
6  19    1500     0     FALSE        NA      NA
7  62   42600     2      TRUE        55       7
8  55       0     1      TRUE        62      -7
```

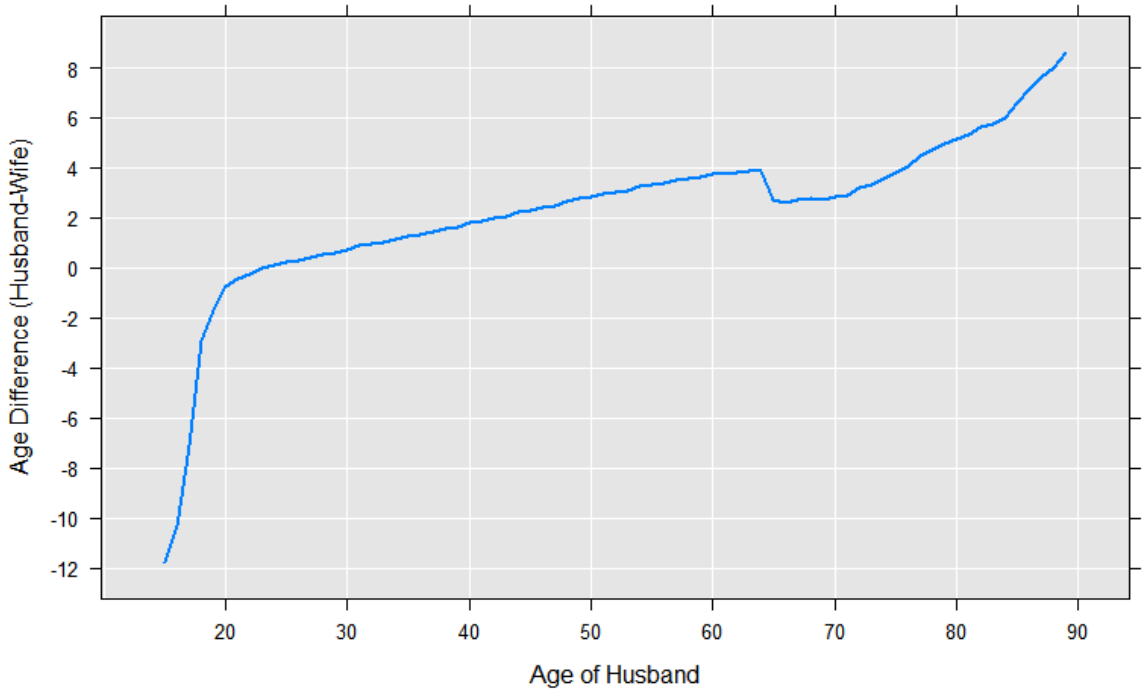
To create the new data set, we'll use the transformation function with *rxDataStep*. Observations for males living with female spouses will be written to a new data .xdf file named *spouseCensus2000.xdf*. It will include information about the age of their spouse.

```
spouseCensusXdf <- "spouseCensus2000"
rxDataStep(inData = bigCensusData, outFile=spouseCensusXdf,
      varsToKeep=c("age", "region", "incwage", "racwht", "nchild", "perwt"),
      transformFunc = spouseAgeTransform,
      transformVars = c("age", "incwage","sploc", "pernum", "sex"),
      rowSelection = sex == 'Male' & hasSpouse == 1 & sameSex == FALSE &
         age <= 90,
      blocksPerRead = 15, overwrite=TRUE)
```

Now for each husband age we can compute the distribution of spouse age. Then, after converting age back to an integer, we can plot the age difference by age of husband:

```
ageDiffData <- rxCube(ageDiff~F(age) , pweights="perwt", data = spouseCensusXdf,
      returnDataFrame = TRUE, blocksPerRead = 15)
ageDiffData$ownAge <- factoi(ageDiffData$F_age)
rxLinePlot(ageDiff~ownAge,  data = ageDiffData,
      xlab="Age of Husband", ylab = "Age Difference (Husband-Wife)",
main="Figure 5: Age Difference of Spouses Living Together, U.S. 2000 5% Census")
```

Figure 5: Age Difference of Spouses Living Together, U.S. 2000 5% Census



Beginning at ages in the early 20's, men tend to be married to younger women. The age difference increases as men get older. But beginning at age 65, our smooth trend stops and we see more erratic behavior, suggesting that our data has misinformation about ages of spouses within households at age 65 and above.

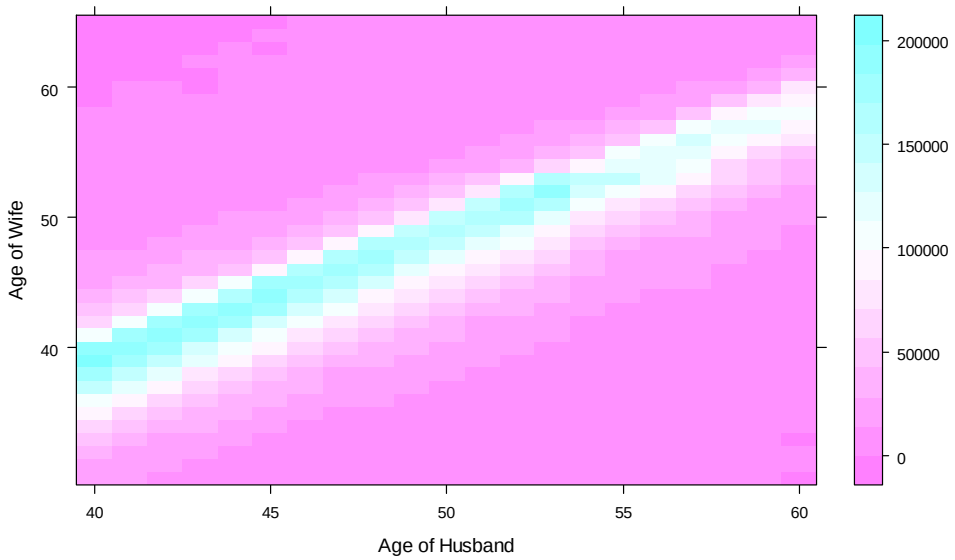
With our new data set we can also calculate the counts for each combination of husband's age and wife's age:

```
aa <- rxCube(~F(age):F(spouseAge), pweights = "perwt", data = spouseCensusXdf,
     returnDataFrame = TRUE, blocksPerRead = 7)
```

A level plot is a good way to visualize the results, where the color indicates the count of each category of combination of husband's and wife's age.

```
# Convert factors to integers
aa$age <- factoi(aa$F_age)
aa$spouseAge <- factoi(aa$F_spouseAge)

# Do a level plot showing the counts for husbands aged 40 to 60
ageCompareSubset <- subset(aa, age >= 40 & age <= 60 & spouseAge >= 30 &
spouseAge <= 65)
levelplot(Counts~age*spouseAge, data=ageCompareSubset,
     xlab="Age of Husband", ylab = "Age of Wife",
main="Figure 6: Counts by Age (40-60) and Spouse Age, U.S. 2000 5% Census")
```

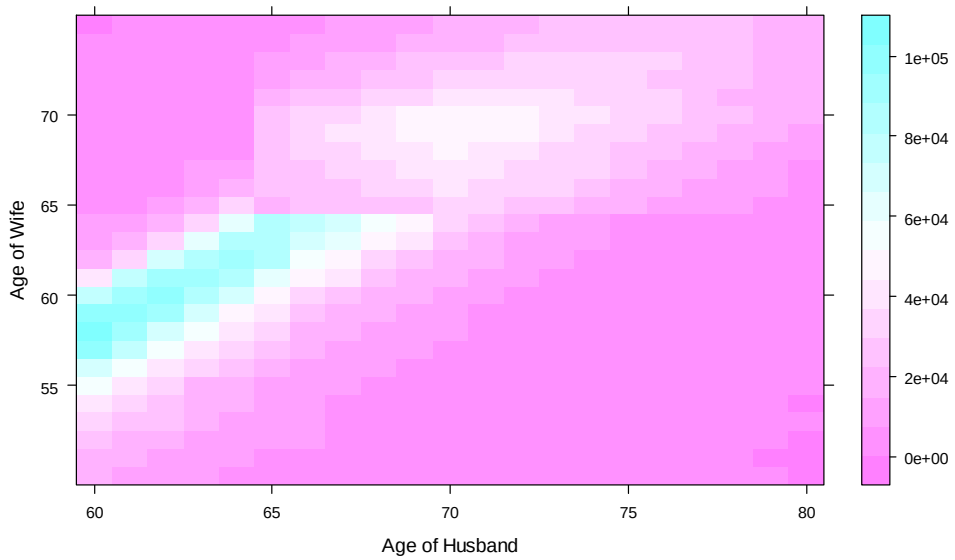
Figure 6: Counts by Age (40-60) and Spouse Age, U.S. 2000 5% Census



In the level plot, there is a very clear pattern with the mode of the relative age of wife dropping gradually as the age of husband increases. Now, repeat with husbands aged 60 to 80.

```
ageCompareSubset <- subset(aa, age >= 60 & age <= 80 & spouseAge >= 50 &
spouseAge <= 75)
levelplot(Counts~age*spouseAge, data = ageCompareSubset,
     xlab = "Age of Husband", ylab = "Age of Wife",
     main ="Figure 7: Counts by Age(60-80)and Spouse Age , U.S. 2000 5% Census")
```

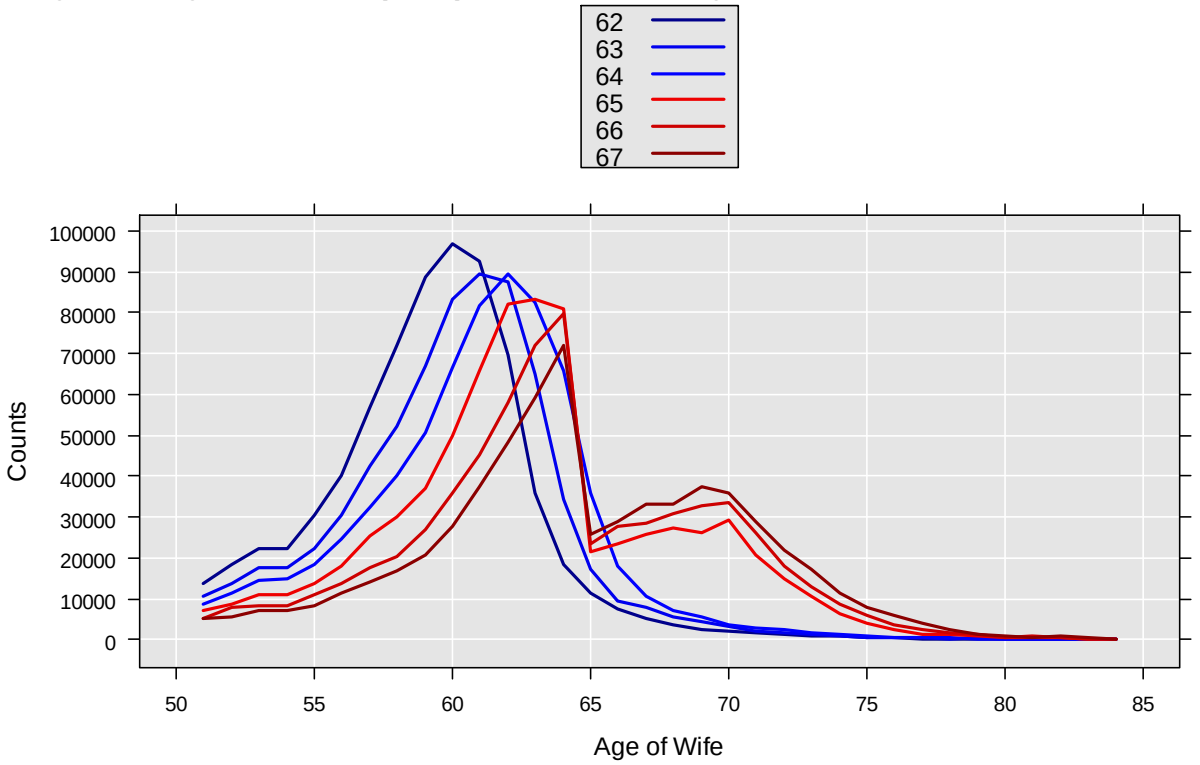
Figure 7: Counts by Age(60-80)and Spouse Age , U.S. 2000 5% Census



This shows a different story. Notice that there are very few men in the 60 to 80 age range married to 65 year-old women, and in particular, there are very few 65-year-old men married to 65-year-old women. To examine this further, we can look at line plots of the distributions of wife's ages for men ages 62 to 67:

```
ageCompareSubset <- subset(aa, age > 61 & age < 68 & spouseAge > 50 &
     spouseAge < 85)
rxLinePlot(Counts~spouseAge, groups = age, data = ageCompareSubset,
     xlab = "Age of Wife", ylab = "Counts",
     lineColor = c("Blue4", "Blue2", "Blue1", "Red2", "Red3", "Red4"),
main = "Figure 8: Ages of Wives (> 45) for Husband's Ages 62 to 67, U.S. 2000 5%
Census")
```

Figure 8: Ages of Wives (> 45) for Husband's Ages 62 to 67, U.S. 2000 5% Census



The blue lines show husbands ages 62 through 64. The mode of the wife's age is a couple of years younger than the husband, and we have a reasonable looking distribution in both tails. But starting at age 65, with the red lines, we have a very different pattern. It appears that when husbands reach the age of 65 they begin to leave (or lose) their 65-year-old wives in droves – and marry older women. This certainly makes one suspicious of the data. In fact, it turns out the aberration in the data was introduced by disclosure avoidance techniques applied to the data by the census bureau.[2]

[2] . For information on the inconsistent ratios, see (U.S. Bureau of the Census, April 2009) and (Alexander, Davern, & Stevenson, 2009).

Bibliography

Alexander, J. T., Davern, M., & Stevenson, B. (2009). *Inaccurate Age and Sex Data in the Census PUMS Files: Evidence and Implications.* http://bpp.wharton.upenn.edu/betseys/papers/Inaccurate%20Age%20and%20Sex%20Data%20in%20Census%20PUMS%20Files.pdf.

Ben-Haim, Y., & Tom-Tov, E. (2010). A streaming parallel decision tree algorithm. *Journal of Machine Learning Research*, 849-872.

Chambers, J. M., & Hastie, T. J. (1992). *Statistical Models in S.* Pacific Grove, CA: Wadsworth & Brooks/Cole.

Fox, J. (2002). *An R and S-PLUS Companion to Applied Regression.* Los Angeles: Sage Publications.

Fox, J. (2008). *Applied Regression Analysis and Generalized Linear Models, Second Edition.* Los Angeles: Sage Publications.

Frank, A., & Asuncion, A. (2010). (University of California, Irvine, School of Information and Computer Science) Retrieved August 2012, from UCI Machine Learning Repository: http://archive.ics.uci.edu/ml

Kabacoff, R. I. (2011). *R In Action.* Shelter Island, NY: Manning.

Kohavi, R. (1996). Scaling Up the Accuracy of Naive-Bayes Classifiers: a Decision-Tree Hybrid. *Proceedings of the Second International Conference on Knowledge Discovery and Data Mining.*

Lloyd, S. P. (1982). Least squares quantization in PCM. *IEEE Transactions on Information Theory*(28), 128-137.

Moore, D. S., & McCabe, G. P. (2006). *Introduction to the Practice of Statistics* (Fifth ed.). New York: Freeman.

Ruggles, S., Sobek, M., Alexander, T., Fitch, C. A., Goeken, R., Hall, P. K., et al. (2006). *Integrated Public Use Microdata Series: Version 3.0. [Machine-readable database]. Available at: http://usa.ipums.org .* Minneapolis, MN:: Minnesota Population Center [producer and distributor].

Therneau, T., & Atkinson, E. (1997). *An Introduction to Recursive Partitioning Using the RPART Routines.* Rochester, MN: Mayo Clinic.

U.S. Bureau of the Census. (April 2009). *How to Use the Data: Errata, User Note 47. Available at: http://www.census.gov/acs/www/UseData/Errata.htm.*

Venables, W. N., & Ripley, B. R. (2002). *Modern Applied Statistics with S, Fourth Edition.* New York: Springer.

Wilkinson, G. N., & Rogers, C. E. (1973). Symbolic Description of Factorial Models for Analysis of Variance. *Applied Statistics, 22*, 392-399.