Econometrics in R

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[*]This paper was originally written as part of a teaching assistantship and has subsequently become a personal reference. I learned most of this stuff by trial and error, so it may contain inefficiencies, inaccuracies, or incomplete explanations. If you find something here suboptimal or have suggestions, please let me know. Until at least 2008 I can be contacted at `g-farnsworth@kellogg.northwestern.edu`.

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1 Are You Ready for R?

1.1 What is R?

R is an implementation of the object-oriented mathematical programming language S. It is developed by statisticians around the world and is free software, covered by the GNU General Public License. Syntactically and functionally it is very similar (if not identical) to S+, the popular statistics package.

1.2 How is R Better Than Other Packages?

R is much more more flexible than most software used by econometricians because it is a modern mathematical programming language, not just a program that does regressions and tests. This means our analysis need not be restricted to the functions included in the default package. There is an extensive and constantly expanding collection of libraries online for use in many disciplines. As researchers develop new algorithms and processes, the corresponding libraries get posted on the R website. In this sense R is always at the forefront of statistical knowledge. Because of the ease and flexibility of programming in R it is easy to extend.

The S language is the *de facto* standard for statistical science. Reading the statistical literature, we find that examples and even pseudo-code are written in R-compatible syntax. Since most users have a statistical background, the jargon used by R experts sometimes differs from what an econometrician (especially a beginning econometrician) may expect. A primary purpose of this document is to eliminate this language barrier and allow the econometrician to tap into the work of these innovative statisticians.

Code written for R can be run on many computational platforms with or without a graphical user interface, and R comes standard with some of the most flexible and powerful graphics routines available anywhere.

And of course, R is completely free for any use.

1.3 Obtaining R

The R installation program can be downloaded free of charge from `http://www.r-project.org`. Because R is a programming language and not just an econometrics program, most of the functions we will be interested in are available through libraries (sometimes called packages) obtained from the R website. To obtain a library that does not come with the standard installation follow the *CRAN* link on the above website. Under *contrib* you will find is a list of compressed libraries ready for download. Click on the one you need and save it somewhere you can find it later. If you are using a gui, start R and click *install package from local directory* under the *package* menu. Then select the file that you downloaded. Now the package will be available for use in the future. If you are using R under linux, install new libraries by issuing the following command at the command prompt: "`R CMD INSTALL` *packagename*"

Alternately you can download and install packages at once from inside R by issuing a command like

```
> install.packages(c("car","systemfit"),repo="http://cran.stat.ucla.edu",dep=TRUE)
```

which installs the *car* and *systemfit* libraries. The `repo` parameter is usually auto-configured, so there is normally no need to specify it. The `dependencies` or `dep` parameter indicates that R should download packages that these depend on as well, and is recommended. Note: you must have administrator (or root) privileges to your computer to install the program and packages.

Contributed Packages Mentioned in this Paper and Why
(indicates package is included by default)*

car	Regression tests and robust standard errors
sem	Two stage least squares
MASS	Robust regression, ordered logit/probit
lmtest	Breusch-Pagan and Breusch-Godfrey tests
sandwich (and zoo)	Heteroskedasticity and autocorrelation robust covariance
tseries	Garch, ARIMA, and other time series functions
MNP	Multinomial probit via MCMC
Hmisc	LaTeX export
xtable	Alternative LaTeX export
systemfit	SUR and 2SLS on systems of equations
fracdiff	Fractionally integrated ARIMA models
survival	Tobit and censored regression
nlme	Nonlinear fixed and random effects models
nnet	Multinomial logit/probit
ts*	Time series manipulation functions
nls*	Nonlinear least squares
foreign*	Loading and saving data from other programs
zoo	required in order to have the sandwich package

1.4 Using R Interactively and Writing Scripts

We can interact directly with R through its command prompt. Under windows the prompt and what we type are in blue and the output it returns is red. Pressing the up arrow will generally cycle through commands from the history. Notice that R is case sensitive and that every function call has parentheses at the end. Instead of issuing commands directly we can load script files that we have previously written, which may include new function definitions.

Script files generally have the extension ".R". These files contain commands as you would enter them at the prompt, and they are recommended for any project of more than a few lines. In order to load a script file named "mcmc.R" we would use the command

```
> source("mcmc.R")
```

One way to run R is to have a script file open in an external text editor and run periodically from the R window. Commands executed from a script file may not print as much output to the screen as they do when run interactively. If we want interactive-level verbosity, we can use the `echo` argument

```
> source("mcmc.R",echo=TRUE)
```

If no path is specified to the script file, R assumes that the file is located in the current working directory. The working directory can be viewed or changed via R commands

```
> getwd()
[1] "/home/gvfarns/r"
> setwd("/home/gvfarns")
> getwd()
[1] "/home/gvfarns"
```

or under windows by using the menu item *change working directory*. Also note that under windows the slashes should be replaced with double backslashes.

```
> getwd()
[1] "C:\\Program Files\\R\\rw1051\\bin"
> setwd("C:\\Program Files\\R\\scripts")
> getwd()
[1] "C:\\Program Files\\R\\scripts"
```

We can also run R in batch (noninteractive) mode under linux by issuing the command:"R CMD BATCH *scriptname*.R" The output will be saved in a file named *scriptname*.Rout. Batch mode is also available under windows using Rcmd.exe instead of Rgui.exe.

Since every command we will use is a function that is stored in one of the libraries, we will often have to load libraries before working. Many of the common functions are in the library *base*, which is loaded by default. For access to any other function, however, we have to load the appropriate library.

```
> library(foreign)
```

will load the library that contains the functions for reading and writing data that is formatted for other programs, such as SAS and Stata. Alternately (under windows), we can pull down the *package* menu and select *library*

1.5 Getting Help

There are several methods of obtaining help in R

```
> ?qt
> help(qt)
> help.start()
> help.search("covariance")
```

Preceding the command with a question mark or giving it as an argument to `help()` gives a description of its usage and functionality. The `help.start()` function brings up a menu of help options and `help.search()` searches the help files for the word or phrase given as an argument. Many times, though, the best help available can be found by a search online. Remember as you search that the syntax and functionality of R is almost identical to that of the proprietary statistical package S+.

2 Working with Data

2.1 Basic Data Manipulation

R allows you to create many types of data storage objects, such as numbers, vectors, matrices, strings, and dataframes. The command `ls()` gives a list of all data objects currently available. The command `rm()` removes the data object given it as an argument. Typing the name of the object typically echos its data to the screen. In fact, a function is just another data member in R. We can see the function's code by typing its name without parenthesis.

The command for creating and/or assigning a value to a data object is the less-than sign followed by the minus sign.

```
> g <- 7.5
```

creates a numeric object called g, which contains the value 7.5.

```
> f <- c(7.5,6,5)
> F <- t(f)
```

uses the `c()` (concatenate) command to create a COLUMN vector with values 7.5, 6, and 5. `c()` is a generic function that can be used on multiple types of data. The `t()` command transposes f to make a row vector. The two data objects `f` and `F` are separate because of the case sensitivity of R. The command `cbind()` concatenates the objects given it side by side: into an array if they are vectors, and into a single dataframe if they are columns of named data.

```
> dat <- cbind(c(7.5,6,5),c(1,2,3))
```

Similarly, `rbind()` concatenates objects by rows (one above the other).

Elements in vectors and similar data types are indexed using square brackets. R uses one-based indexing.

```
> f
 [1] 7.5 6.0 5.0
> f[2]
 [1] 6
```

Notice that for multidimensional data types, such as matrices and dataframes, leaving an index blank refers to the whole column or row corresponding to that index. Thus if `foo` is a 4x5 array of numbers,

```
> foo
```

will print the whole array to the screen,

```
> foo[1,]
```

will print the first row,

```
> foo[,3]
```

will print the third column, etc. We can get summary statistics on the data in `goo` using the `summary()` and we can determine its dimensionality using the `NROW()`, and `NCOL()` commands. More generally, we can use the `dim()` command to know the dimensions of an R object.

If we wish to extract or print only certain rows or columns, we can use the concatenation operator.

```
> oddfoo <- foo[c(1,3,5),]
```

makes a 4x3 array out of columns 1,3, and 5 of foo and saves it in oddfoo. By prepending the subtraction operator, we can remove certain rows

```
> nooddfoo <- foo[-c(1,3,5),]
```

makes a 4x2 array out of columns 2 and 4 of foo (i.e., it removes columns 1,3, and 5). We can also use comparison operators to extract certain columns or rows.

```
> smallfoo <- foo[ foo[,1]<1 ,]
```

compares each entry in the first column of foo to one and inserts the row corresponding to each match into smallfoo. We can also reorder data. If wealth is a dataframe with columns `year`,`gdp`, and `gnp`, we could sort the data by year using `order()` or extract a period of years using the colon operator

```
> wealth <- wealth[ order(wealth$year),]
> firstten <- wealth[1:10,]
> eighty <- wealth[wealth$year==1980,]
```

This sorts by year and puts the first ten years of data in firstten. All rows from year 1980 are stored in eighty (notice the double equals sign).

Using double instead of single brackets for indexing changes the behavior slightly. Basically it doesn't allow referencing multiple objects using a vector of indices, as the single bracket case does. For example,

```
> w[[1:10]]
```

does not return a vector of the first ten elements of w, as it would in the single bracket case. Also, it strips off attributes and types. If the variable is a list, indexing it with single brackets yields a list containing the data, double brackets return the (vector of) data itself.

Occasionally we have data in the incorrect form (i.e., as a dataframe when we would prefer to have a matrix). In this case we can use the `as.` functionality. If all the values in `goo` are numeric, we could put them into a matrix named `mgoo` with the command

```
> mgoo <- as.matrix(goo)
```

Other data manipulation operations can be found in the standard R manual and online. There are a lot of them.

2.2 Important Data Types

2.2.1 Arrays, Matrices

In R, homogeneous (all elements are of the same type) multivariate data may be stored as an array or a matrix. A matrix is a two-dimensional object, whereas an array may be of many dimensions. These data types do not have special attributes giving names to columns or rows and can hold only numeric data. Note that one cannot make a matrix, array, or vector of two different types of data (numeric and character, for example). Either they will be coerced into the same type or an error will occur.

2.2.2 Dataframes

Most econometric data will be in the form of a dataframe. A dataframe is a collection of columns containing data, which need not all be of the same type, but each column must have the same number of elements. Each column has a title by which the whole column may be addressed. If `goo` is a 3x4 data frame with titles `age`, `gender`,`education`, and `salary`, then we can print the `salary` column with the command

```
> goo$salary
```

or view the names of the columns in goo

```
> names(goo)
```

Most mathematical operations affect multidimensional data elementwise. From the previous example,

```
> salarysq <- (goo$salary)^2
```

creates a dataframe with one column entitled `salary` with entries equal to the square of the corresponding entries in `goo$salary`. Most mathematical operations behave as one would expect.

Output from actions can also be saved in the original variable, for example,

```
> salarysq <- sqrt(salarysq)
```

replaces each of the entries in salarysq with its square root.

```
> goo$lnsalary <- log(salarysq)
```

adds a column named lnsalary to `goo`, containing the log of the salary.

2.2.3 Lists

A list is more general than a dataframe. It is essentially a bunch of data objects bound together, optionally with a name given to each. These data objects may be scalars, strings, dataframes, or any other type. Functions that return many elements of data (like `summary()`) generally bind the returned data together as a list, since functions return only one data object. As with dataframes, we can see what objects are in a list (by name if they have them) using the `names()` command.

2.3 Opening a Data File

R is able to read data from many formats. The most common format is a text file with data separated into columns and with a header above each column describing the data. If blah.dat is a text file of this type and is located on the windows desktop we could read it using the command

```
> mydata <- read.table("C:/WINDOWS/Desktop/blah.dat",header=TRUE)
```

Now mydata is a dataframe with named columns, ready for analysis. Note that R assumes that there are no labels on the columns, and gives them default values, if you omit the `header=TRUE` argument. Now let's suppose that instead of blah.dat we have blah.dta, a stata file.

```
> library(foreign)
> mydata <- read.dta("C:/WINDOWS/Desktop/blah.dta")
```

Stata files automatically have headers.

Another data format we may read is .csv comma-delimited files (such as those exported by spreadsheets). These files are very similar to those mentioned above, but use punctuation to delimit columns and rows. instead of `read.table()`, we use `read.csv()`.

3 Cross Sectional Regression

3.1 Ordinary Least Squares

Let's consider the simplest case. Suppose we have a data frame called `byu` containing columns for `age`, `salary`, and `exper`. We want to regress various forms of `age` and `exper` on `salary`. A simple linear regression might be

```
> lm(byu$salary ~ byu$age + byu$exper)
```

or alternately:

```
> lm(salary ~ age + exper,data=byu)
```

as a third alternative, we could "attach" the dataframe, which makes its columns available as regular variables

```
> attach(byu)
> lm(salary ~ age + exper)
```

Notice the syntax of the model argument (using the tilde). The above command would correspond to the linear model

$$salary = \beta_0 + \beta_1 age + \beta_2 exper + \epsilon \tag{1}$$

Using `lm()` results in an abbreviated summary being sent to the screen, giving only the β coefficient estimates. For more exhaustive analysis, we can save the results in as a data member or "fitted model"

```
> result <- lm(salary ~ age + exper + age*exper,data=byu)
> summary(result)
> myresid <- result$resid
> vcov(result)
```

The `summary()` command, run on raw data, such as `byu$age`, gives statistics, such as the mean and median (these are also available through their own functions, mean and median). When run on an ols object, summary gives important statistics about the regression, such as p-values and the R^2.

The residuals and several other pieces of data can also be extracted from result, for use in other computations. The variance-covariance matrix (of the beta coefficients) is accessible through the `vcov()` command.

Notice that more complex formulae are allowed, including interaction terms (specified by multiplying two data members) and functions such as `log()` and `sqrt()`. Unfortunately, in order to include a power term, such as `age` squared, we must either first compute the values, then run the regression, or use the `I()` operator, which forces computation of its argument before evaluation of the formula

```
> salary$agesq <- (salary$age)^2
> result <- lm(salary ~ age + agesq + log(exper) + age*log(exper),data=byu)
```

or

```
> result <- lm(salary ~ age + I(age^2) + log(exper) + age*log(exper),data=byu)
```

In order to run a regression without an intercept, we simply specify the intercept explicitly, traditionally with a zero.

```
> result <- lm(smokes ~ 0 + male + female ,data=smokerdata)
```

3.2 Extracting Statistics from the Regression

The most important statistics and parameters of a regression are stored in the lm object or the summary object. Consider the smoking example above

```
> output <- summary(result)
> SSR <- deviance(result)
> LL <- logLik(result)
> DegreesOfFreedom <- result$df
> Yhat <- result$fitted.values
> Coef <- result$coefficients
> Resid <- result$residuals
> s <- output$sigma
> RSquared <- output$r.squared
> CovMatrix <- s^2*output$cov
```

Where `SSR` is the residual sum of squares, `LL` is the log likelihood statistic, `Yhat` is the vector of fitted values, `Resid` is the vector of residuals, `s` is the estimated standard deviation of the errors (assuming homoskedasticity), `CovMatrix` is the variance-covariance matrix of the coefficients (also available via `vcov()`), and other statistics are as named.

3.3 Heteroskedasticity and Friends

3.3.1 Breusch-Pagan Test for Heteroskedasticity

In order to test for the presence of heteroskedasticity, we can use the Breusch-Pagan test from the *lmtest* package. Alternately we can use the the `ncv.test()` function from the *car* package. They work pretty much the same way. After running the regression, we call the `bptest()` function with the fitted regression.

```
> unrestricted <- lm(z~x)
> bptest(unrestricted)

        Breusch-Pagan test

data:  unrestricted
BP = 44.5465, df = 1, p-value = 2.484e-11
```

This performs the "studentized" version of the test. In order to be consistent with some other software (including `ncv.test()`) we can specify `studentize=FALSE`.

3.3.2 Heteroskedasticity (Autocorrelation) Robust Covariance Matrix

In the presence of heteroskedasticity, the ols estimates remain unbiased, but the ols estimates of the variance of the beta coefficients are no longer correct. In order to compute the heteroskedasticity consistent covariance matrix[1] we use the `hccm()` function (from the *car* library) instead of `vcov()`. The diagonal entries are variances and off diagonals are covariance terms.

This functionality is also available via the `vcovHC()` command in the *sandwich* package. Also in that package is the heteroskedasticity and autocorrelation robust Newey-West estimator, available in the function `vcovHAC()` or the function `NeweyWest()`.

3.4 Linear Hypothesis Testing (Wald and F)

The *car* package provides a function that automatically performs linear hypothesis tests. It does either an F or a Wald test using either the regular or adjusted covariance matrix, depending on our specifications. In order to test hypotheses, we must construct a hypothesis matrix and a right hand side vector. For example, if we have a model with five parameters, including the intercept and we want to test against

$$H_0 : \beta_0 = 0, \beta_3 + \beta_4 = 1$$

The hypothesis matrix and right hand side vector would be

$$\begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 \end{bmatrix} \beta = \begin{pmatrix} 0 \\ 1 \end{pmatrix}$$

and we could implement this as follows

[1]obtaining the White standard errors, or rather, their squares.

```
> unrestricted <- lm(y~x1+x2+x3+x4)
> rhs <- c(0,1)
> hm <- rbind(c(1,0,0,0,0),c(0,0,1,1,0))
> linear.hypothesis(unrestricted,hm,rhs)
```

Notice that if `unrestricted` is an *lm* object, an F test is performed by default, if it is a *glm* object, a Wald χ^2 test is done instead. The type of test can be modified through the `type` argument.

Also, if we want to perform the test using heteroskedasticity or autocorrelation robust standard errors, we can either specify `white.adjust=TRUE` to use white standard errors, or we can supply our own covariance matrix using the `vcov` parameter. For example, if we had wished to use the Newey-West corrected covariance matrix above, we could have specified

```
> linear.hypothesis(unrestricted,hm,rhs,vcov=NeweyWest(unrestricted))
```

See the section on heteroskedasticity robust covariance matrices for information about the `NeweyWest()` function. We should remember that the specification `white.adjust=TRUE` corrects for heteroskedasticity using an improvement to the white estimator. To use the classic white estimator, we can specify `white.adjust="hc0"`.

3.5 Weighted and Generalized Least Squares

You can do weighted least squares by passing a vector containing the weights to `lm()`.

```
> result <- lm(smokes ~ 0 + male + female ,data=smokerdata,weights=myweights)
```

Generalized least squares is available through the `lm.gls()` command in the *MASS* library. It takes a formula, weighting matrix, and (optionally) a dataframe from which to get the data as arguments.

The `glm()` command provides access to a plethora of other advanced linear regression methods. See the help file for more details.

4 Special Regressions

4.1 Models With Factors/Groups

There is a separate datatype for qualitative factors in R. When a variable included in a regression is of type factor, the requisite dummy variables are automatically created. For example, if we wanted to regress the adoption of personal computers (pc) on the number of employees in the firm (emple) and include a dummy for each state (where `state` is a vector of two letter abbreviations), we could simply run the regression

```
> summary(lm(pc~emple+state))

Call:
lm(formula = pc ~ emple + state)

Residuals:
    Min      1Q  Median      3Q     Max
-1.7543 -0.5505  0.3512  0.4272  0.5904

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  5.572e-01  6.769e-02   8.232   <2e-16 ***
```

```
emple        1.459e-04  1.083e-05  13.475   <2e-16 ***
stateAL     -4.774e-03  7.382e-02  -0.065    0.948
stateAR      2.249e-02  8.004e-02   0.281    0.779
stateAZ     -7.023e-02  7.580e-02  -0.926    0.354
stateDE      1.521e-01  1.107e-01   1.375    0.169

 ...

stateFL     -4.573e-02  7.136e-02  -0.641    0.522
stateWY      1.200e-01  1.041e-01   1.153    0.249
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.4877 on 9948 degrees of freedom
Multiple R-Squared: 0.02451,    Adjusted R-squared: 0.01951
F-statistic: 4.902 on 51 and 9948 DF,  p-value: < 2.2e-16
```

The three dots indicate that some of the coefficients have been removed for the sake of brevity.

In order to convert data (either of type string or numeric) to a factor, simply use the `factor()` command. It can even be used inside the regression. For example, if we wanted to do the same regression, but by a numeric code specifying an area, we could use the command

```
> myout <- lm(pc~emple+factor(naics6))
```

which converts naics6 into a factor, generates the appropriate dummies, and runs a standard regression.

The package *nlme* contains functions for doing fixed and random effects models in a linear or nonlinear framework.

4.2 Logit/Probit

There are several ways to do logit and probit regressions in R. The simplest way may be to use the `glm()` command with the family option.

```
> h <- glm(c~y, family=binomial(link="logit"))
```

or replace `logit` with `probit` for a probit regression. The `glm()` function produces an object similar to the `lm()` function, so it can be analyzed using the `summary()` command. In order to extract the log likelihood statistic, use the `logLik()` command.

```
> logLik(h)
‘log Lik.’ -337.2659 (df=1)
```

There is also a special package for binary dependent variable regressions called *boolean*. The *boolean* framework generally requires that a boolean data object be prepared using `boolprep()` and passed to `boolean()`. It also includes functions to plot and do tests.

4.2.1 Multinomial Logit

There is a great function for performing a multinomial logit calculation in the *nnet* library called `multinom()`. To use it, simply transform our dependent variable to a vector of factors (including all cases) and use syntax like a normal regression. If our factors are stored as vectors of dummy variables, we can use the properties of decimal numbers to create unique factors for all combinations. Suppose my factors are pc, inetacc, and iapp, then

```
> g <- pc*1 + inetacc*10 + iapp*100
> multinom(factor(g)~pc.subsidy+inet.subsidy+iapp.subsidy+emple+msamissing)
```

and we get a multinomial logit using all combinations of factors.

Multinomial probit is characteristically ill conditioned. A method that uses markov chain monte carlo simulations, `mnp()`, is available in the *MNP* library.

4.2.2 Ordered Logit/Probit

The *MASS* library has a function to perform ordered logit or probit regressions, called `polr()`. If `Sat` is an ordered factor vector, then

```
> house.plr <- polr(Sat ~ Infl + Type + Cont, method="probit")
```

4.3 Tobit and Censored Regression

In order to estimate a model in which the values of some of the data have been censored, we use the *survival* library. The function `survreg()` performs this type of regression, and takes as its dependent variable a *Surv* object. The best way to see how to do this type of regression is by example. Suppose we want to regress y on x and z, but a number of y observations were censored on the left and set to zero.

```
result <- survreg(Surv(y,y>0,type='left') ~ x + z, dist='gaussian')
```

The second argument to the `Surv()` function specifies whether each observation has been censored or not (one indicating that it was observed and zero that it was censored). The third argument indicates on which side the data was censored. Since it was the lower tail of this distribution that got censored, we specify `left`. The `dist` option passed to the survreg is necessary in order to get a classical Tobit model.

4.4 Robust Regression - M Estimators

For some datasets, outliers influence the least squares regression line more than we would like them to. One solution is to use a minimization approach using something besides the sum of squared residuals (which corresponds to minimizing the L_2 norm) as our objective function. Common choices are the sum of absolute deviations (L_1) and the Huber method, which is something of a mix between the L_1 and L_2 methods. R implements this robust regression functionality through the `rlm()` command in the MASS library. The syntax is the same as that of the `lm()` command except that it allows the choice of objective function to minimize. That choice is specified by the `psi` parameter. Possible implemented choices are `psi.huber`, `psi.hampel`, and `psi.bisquare`.

In order to specify a custom psi function, we write a function that returns $\psi(x)/x$ if `deriv=0` and $\psi'(x)$ for `deriv=1`. This function than then be passed to `rlm()` using the `psi` parameter.

4.5 Nonlinear Least Squares

Sometimes the economic model just isn't linear. R has the capability of solving for the coefficients a generalized least squares model that can be expressed

$$Y = F(X;\beta) + \epsilon \tag{2}$$

Notice that the error term must be additive in the functional form. If it is not, transform the model equation so that it is. The R function for nonlinear least squares is `nls()` and has a syntax similar to `lm()`. Consider the following nonlinear example.

$$Y = \frac{\epsilon}{1+e^{\beta_1 X_1 + \beta_2 X_2}} \tag{3}$$

$$\log(Y) = -\log(1+e^{\beta_1 X_1 + \beta_2 X_2}) + \log(\epsilon) \tag{4}$$

The second equation is the transformed version that we will use for the estimation. `nls()` takes the formula as its first argument and also requires starting estimates for the parameters. The entire formula should be specified, including the parameters. R looks at the starting values to see which parameters it will estimate.

```
> result <- nls(log(Y)~-log(1+exp(a*X1+b*X2)),start=list(a=1,b=1),data=mydata)
```

stores estimates of `a` and `b` in an nls object called `result`. Estimates can be viewed using the `summary()` command. In the most recent versions of R, the `nls()` command is part of the base package, but in older versions, we may have to load the nls library.

4.6 Two Stage Least Squares on a Single Structural Equation

For single equation two stage least squares, the easiest function is probably `tsls()` from the *sem* library. If we want to find the effect of education on wage while controlling for marital status but think `educ` is endogenous, we could use `motheduc` and `fatheduc` as instruments by running

```
> library(sem)
> outputof2sls <- tsls(lwage~educ+married,~married+motheduc+fatheduc)
```

The first argument is the structural equation we want to estimate and the second is a tilde followed by all the instruments and exogenous variables from the structural equation (everything we need for the Z matrix in the 2sls estimator $\tilde{\beta} = \{X'Z(Z'Z)^{-1}Z'X\}^{-1}X'Z(Z'Z)^{-1}Z'y$).

The resulting output can be analyzed using `summary()` and other ols analysis functions. Note that since this command produces a two stage least squares object, the summary statistics, including standard errors, will be correct. Recall that if we were to do this using an actual two stage approach, the resulting standard errors would be bogus.

4.7 Systems of Equations

The commands for working with systems of equations (including instrumental variables, two stage least squares, seemingly unrelated regression and variations) are contained in the *systemfit* library. In general these functions take as an argument a list of regression models. Note that in R an equation model (which must include the tilde) is just another data type. Thus we could create a list of equation models and a corresponding list of labels using the normal assignment operator

```
> demand <- q ~ p + d
> supply <- q ~ p + f + a
> system <- list(demand,supply)
> labels <- list("demand","supply")
```

4.7.1 Seemingly Unrelated Regression

Once we have the system and labels set up, we can use `systemfit()` with the `SUR` option to specify that the system describes a seemingly unrelated regression.

```
> resultsur <- systemfit("SUR",system,labels)
```

4.7.2 Two Stage Least Squares on a System

Instruments can be used as well in order to do a two stage least squares on the above system. We create a model object (with no left side) to specify the instruments that we will use and specify the 2SLS option

```
> inst <- ~ d + f + a
> result2sls <- systemfit("2SLS",system,labels,inst)
```

There are also routines for three stage least squares, weighted two stage least squares, and a host of others.

5 Time Series Regression

R has a special datatype, *ts*, for use in time series regressions. Vectors, arrays, and dataframes can be coerced into this type using the `ts()` command for use in time series functions.

```
> datats <- ts(data)
```

Most time-series related functions automatically coerce the data into *ts* format, so this command is often not necessary.

5.1 Differences and Lags

We can compute differences of a time series object using the `diff()` operator, which takes as optional arguments which difference to use and how much lag should be used in computing that difference. For example, to take the first difference with a lag of two, so that $w_t = v_t - v_{t-3}$ we would use

```
> w <- diff(v,lag=2,difference=1)
```

By default, `diff()` returns the simple first difference of its argument.

There are two general ways of generating lagged data. If we want to lag the data directly (without necessarily converting to a time series object), one way to do it is to omit the first few observations using the minus operator for indices. We can then remove the last few rows of un-lagged data in order to achieve conformity. The commands

```
> lagy <- y[-NROW(y)]
> ysmall <- y[-1]
```

produce a once lagged version of `y` relative to `ysmall`. This way of generating lags can get awkward if we are trying combinations of lags in regressions because for each lagged version of the variable, conformability requires that we have a corresponding version of the original data that has the first few observations removed.

Another way to lag data is to convert it to a time series object and use the `lag()` function. It is very important to remember that this function does not actually change the data, it changes an attribute of a time series object that indicates where the series starts. This allows for more flexibility with time series functions, but it can cause confusion for general functions such as `lm()` that do not understand time series attributes. Notice that `lag()` **only works usefully on time series objects**. For example, the code snippet

```
> d <- a - lag(a,-1)
```

creates a vector of zeros named `d` if `a` is a normal vector, but returns a *ts* object with the first difference of the series if `a` is a *ts* object. There is no warning issued if `lag()` is used on regular data, so care should be exercised.

In order to use lagged data in a regression, we can use time series functions to generate a dataframe with various lags of the data and NA characters stuck in the requisite leading and trailing positions. In order to do this, we use the `ts.union()` function. Suppose `X` and `Y` are vectors of ordinary data and we want to include a three times lagged version of `X` in the regression, then

```
> y <- ts(Y)
> x <- ts(X)
> x3 <- lag(x,-3)
> d <- ts.union(y,x,x3)
```

converts the vectors to *ts* data and forms a multivariate time series object with columns $\mathtt{y_t}$, $\mathtt{x_t}$, and $\mathtt{x_{t-3}}$. Again, remember that data must be converted to time series format **before** lagging or binding together with the union operator in order to get the desired offset. The `ts.union()` function automatically decides on a title for each column, must as the `data.frame()` command does. We can also do the lagging inside the union and assign our own titles

```
> y <- ts(Y)
> x <- ts(X)
> d <- ts.union(y,x,x1=lag(xt,-1),x2=lag(xt,-2),x3=lag(xt,-3))
```

It is critical to note that **the lag operator works in the opposite direction of what one might expect**: positive lag values result in leads and negative lag values result in lags.

When the resulting multivariate time series object is converted to a data frame (as it is read by `ls()` for example), the offset will be preserved. Then

```
> lm(y~x3,data=d)
```

will then regress $\mathtt{y_t}$ on $\mathtt{x_{t-3}}$.

Also note that by default observations that have a missing value (NA) are omitted. This is what we want. If the default setting has somehow been changed, we should include the argument `na.action=na.omit` in the `lm()` call. In order to get the right omission behavior, it is generally necessary to bind all the data we want to use (dependent and independent variables) together in a single union.

In summary, in order to use time series data, convert all data to type *ts*, lag it appropriately (using the strange convention that positive lags are leads), and bind it all together using `ts.union()`. Then proceed with the regressions and other operations.

5.2 Filters

5.2.1 Canned AR and MA filters

One can pass data through filters constructed by polynomials in the lag operator using the `filter()` command. It handles two main types of filters: autoregressive or "recursive" filters and moving average or "convolution" filters. The first type is of the form

$$y = (1 + a_1 L + a_2 L^2 + \ldots + a_p L^p)x$$

and the second has the same form except that it does not include the implied unit coefficient on the zero lag. Further, for recursive filters, if we specify `sides=2` the filter coefficients will be centered about zero (including as many leads as lags) unless there is an even number of coefficients, in which case one more lead than lag is included.

When we use the `filter()` command, we supply the `a` vector as follows

```
> y <- filter(x,c(.2,-.35,.1),method="recursive")
```

The data vector `x` may be a time series object or a normal vector of data, and the output `y` will be a *ts* object.

5.2.2 Manual Filtration

If the `filter()` command is not flexible enough for our application—a situation easily encountered—we can manually generate the lags and compute the result. The following imitates the filter command above

```
> x <- ts(x)
> y <- x+.2*lag(x,-1)-.35*lag(x,-2)+.1*lag(x,-3)
```

except that the `filter()` command by default inserts zeros (or a pre-specified vector) for missing beginning data, whereas the manual filter omits the observations for which lagged data is unavailable. Notice that the above command will only work if `x` is a *ts* object.

5.2.3 Hodrick Prescott Filter

Data may be passed through the Hodrick-Prescott filter a couple of ways, neither of which require the data to be a time series vector. First, we can filter manually using the function defined below (included without prompts so it may be copied and pasted into R)

```
hpfilter <- function(x,lambda=1600){
  eye <- diag(length(x))
  result <- solve(eye+lambda*crossprod(diff(eye,lag=1,d=2)),x)
  return(result)
}
```

where `lambda` is the standard tuning parameter, often set to 1600 for macroeconomic data. Passing a series to this function will return the smoothed series.

This filter is also a special case of the `smooth.spline()` function in which the parameter tt all.knots=TRUE has been passed. Unfortunately, the tuning parameter for the `smooth.spline()` function, `spar` is different from the `lambda` above and we have not figured out how to convert from `spar` to `lambda`. If we knew the appropriate value of `spar` to use, the filter would be

```
>  z <- smooth.spline( y , all.knots=TRUE, spar=myspar )
```

5.2.4 Kalman Filter

R has functions for smoothing, forecasting, or finding a likelihood function using the Kalman filter. In order to use these routines, we must generate an object of type *list* that represents the state-space version of our model. If we have an ARIMA model, the state space representation is returned as `model` by default. For example

```
>  mymodel <- arima(x,c(2,1,0))$model
```

Otherwise we could generate this list manually. Recall that a state space model can be written

$$y = Z'a + \eta$$
$$a = Ta + Re$$

Where η and e are normally distributed disturbances, a is the unobserved state vector, and y is the observed data vector. The elements of the list represent the coefficients here. For more information on generating a state-space model, see help on `KalmanLike`.

Once we have the state-space list, we can use `KalmanLike`, `KalmanSmooth`, and `KalmanPredict` to get estimated likelihoods, state estimates, and predicted values, respectively.

5.3 ARIMA/ARFIMA

The `arima()` command from the `ts()` library can fit time series data using an autoregressive integrated moving average model.

$$\Delta^d y_t = \mu + \gamma_1 \Delta^d y_{t-1} + ... + \gamma_p \Delta^d y_{t-p} + \epsilon_t + \theta_1 \epsilon_{t-1} + ... + \theta_q \epsilon_{t-q} \tag{5}$$

where

$$\Delta y_t = y_t - y_{t-1} \tag{6}$$

The parameters `p`, `d`, and `q` specify the order of the arima model. These values are passed as a vector `c(p,d,q)` to `arima()`. Notice that the model used by R makes no assumption about the sign of the θ terms, so the sign of the corresponding coefficients may differ from those of other software packages (such as S+).

```
> ar1 <- arima(y,order=c(1,0,0))
> ma1 <- arima(y,order=c(0,0,1))
```

Data-members `ar1` and `ma1` contain estimated coefficients obtained by fitting y with an AR(1) and MA(1) model, respectively. They also contain the log likelihood statistic and estimated standard errors.

If we are modeling a simple autoregressive model, we could also use the `ar()` command, from the *ts* package, which either takes as an argument the order of the model or picks a reasonable default order.

```
> ar3 <- ar(y,order.max=3)
```

fits an AR(3) model, for example.

The function `fracdiff()`, from the *fracdiff* library fits a specified ARMA(p,q) model to our data and finds the optimal fractional value of d for an ARFIMA(p,d,q). Its syntax differs somewhat from the `arima()` command.

```
> library(fracdiff)
> fracdiff(y,nar=2,nma=1)
```

finds the optimal d value using p=2 and q=1.

5.4 ARCH/GARCH

R can numerically fit data using a generalized autoregressive conditional heteroskedasticity model GARCH(p,q), written

$$\sigma_t^2 = \alpha_0 + \delta_1 \sigma_{t-1}^2 + ... + \delta_p \sigma_{t-p}^2 + \alpha_1 \epsilon_t^2 + ... + \alpha_q \epsilon_{t-q}^2 \tag{7}$$

setting $p = 0$ we obtain the ARCH(q) model. The R command `garch()` comes from the *tseries* library. It's syntax is

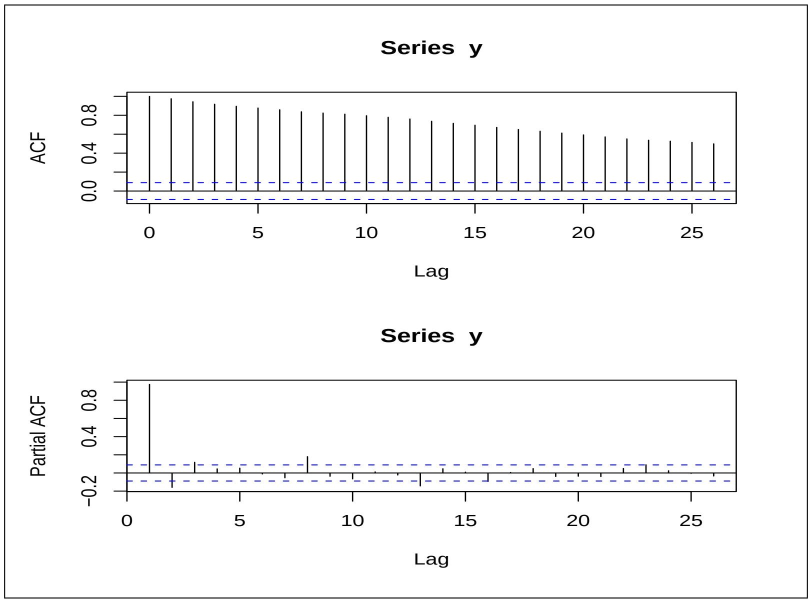
```
> archoutput <- garch(y,order=c(0,3))
> garchoutput <- garch(y,order=c(2,3))
```

so that `archoutput` is the result of modeling an ARCH(3) model and `garchoutput` is the result of modeling a GARCH(2,3). Notice that the first value in the `order` argument is p, the number of alphas, and the second argument is the number of delta parameters. The resulting coefficient estimates will be named `a0`, `a1`, etc. for the alpha and `b1`, `b2`, etc. for the delta parameters.

5.5 Correlograms

It is common practice when analyzing time series data to plot the autocorrelation and partial autocorrelation functions in order to try to guess the functional form of the data. To plot the autocorrelation and partial autocorrelation functions, use the *ts* library functions `acf()` and `pacf()`, respectively. The following commands plot the ACF and PACF on the same graph, one above (not on top of) the other. See section on plotting for more details.

```
> par(mfrow=c(2,1))
> acf(y)
> pacf(y)
```



5.6 Predicted Values

The `predict()` command takes as its input an lm, glm, arima, or other regression object and some options and returns corresponding predicted values. For time series regressions, such as `arima()` the argument is the number of periods into the future to predict.

```
> a <- arima(y,order=c(1,1,2))
> predict(a,5)
```

returns predictions on five periods following the data in `y`, along with corresponding standard error estimates.

5.7 Time Series Tests

5.7.1 Durbin-Watson Test for Autocorrelation

The Durbin-Watson test for autocorrelation can be administered using the `durbin.watson()` function from the *car* library. It takes as its argument an *lm* object (the output from an `lm()` command) and returns the autocorrelation, DW statistic, and an estimated p-value. The number of lags can be specified using the `max.lag` argument. See help file for more details.

```
> library(car)
> results <- lm(Y ~ x1 + x2)
> durbin.watson(results,max.lag=2)
```

5.7.2 Box-Pierce and Breusch-Godfrey Tests for Autocorrelation

In order to test the residuals (or some other dataset) for autocorrelation, we can use the Box-Pierce test from the *ts* library.

```
> library(ts)
> a <- arima(y,order=c(1,1,0))
> Box.test(a$resid)

        Box-Pierce test

data:  a$resid
X-squared = 18.5114, df = 1, p-value = 1.689e-05
```

would lead us to believe that the model may not be correctly specified, since we soundly reject the Box-Pierce null. If we want to the Ljung-Box test instead, we include the parameter `type="Ljung-Box"`.

For an appropriate model, this test is asymptotically equivalent to the Breusch-Godfrey test, which is available in the `lmtest()` library as `bgtest()`. It takes a fitted *lm* object instead of a vector of data as an argument.

5.7.3 Dickey-Fuller Test for Unit Root

The augmented Dickey-Fuller test checks whether a series has a unit root. The default null hypothesis is that the series does have a unit root. Use the `adf.test()` command from the *tseries* library for this test.

```
> library(tseries)
> adf.test(y)

        Augmented Dickey-Fuller Test

data:  y
Dickey-Fuller = -2.0135, Lag order = 7, p-value = 0.5724
alternative hypothesis: stationary
```

5.8 Vector Autoregressions (VAR)

There is a package (*mAr*) especially designed to do multivariate autoregressions and analysis, but the standard `ar()` routine can do the estimation part. In order to do a vector autoregression, one need only bind the vectors together as a dataframe and give that dataframe as an argument to `ar()`. Notice that `ar()` by default uses AIC to determine how many lags to use, so it may be necessary to specifiy `aic=FALSE` and/or an `order.max` parameter. Remember that if `aic` is `TRUE` (the default), the function uses AIC to choose a model using up to the number of lags specified by `order.max`.

```
> y <- ts.union(Y1,Y2,Y3)
> var6 <- ar(y,aic=FALSE,order=6)
```

6 Plotting

One of R's strongest points is its graphical ability. It provides both high level plotting commands and the ability to edit even the smallest details of the plots.

The `plot()` command opens a new window and plots the the series of data given it. By default a single vector is plotted as a time series line. If two vectors are given to `plot()`, the values are plotted in the x-y place using small circles. The type of plot (scatter, lines, histogram, etc.) can be determined using the `type` argument. Strings for the main, x, and y labels can also be passed to plot.

```
> plot(x,y,type="l", main="X and Y example",ylab="y values",xlab="x values")
```

plots a line in the x-y plane, for example. Colors, symbols, and many other options can be passed to `plot()`. For more detailed information, see the help system entries for `plot()` and `par()`.

After a plotting window is open, if we wish to superimpose another plot on top of what we already have, we use the `lines()` command or the `points()` command, which draw connected lines and scatter plots, respectively. Many of the same options that apply to `plot()` apply to `lines()` and a host of other graphical functions.

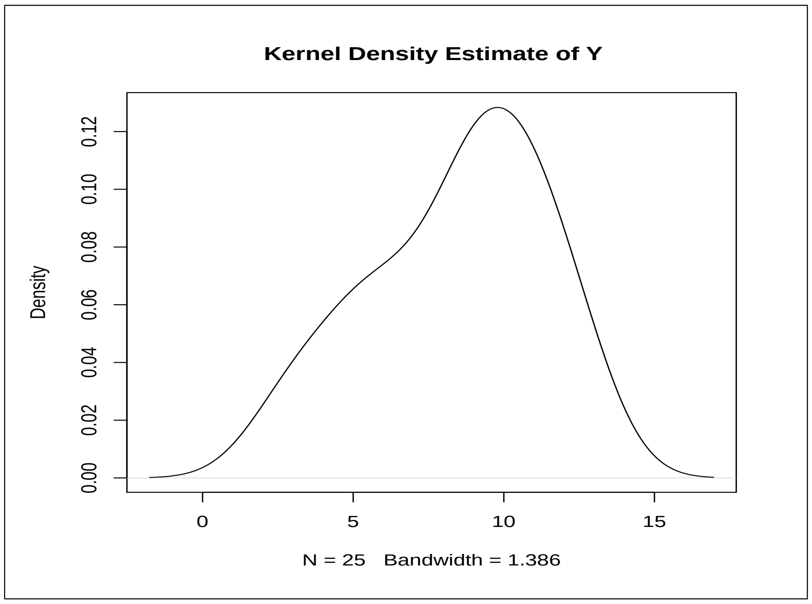
We can plot a line, given its coefficients, using the `abline()` command. This is often useful in visualizing the placement of a regression line after a bivariate regression

```
> results <- lm(y ~ x)
> plot(x,y)
> abline(results$coef)
```

6.1 Plotting Empirical Distributions

We typically illustrate the distribution of a vector of data by separating it into bins and plotting it as a histogram. This functionality is available via the `hist()` command. Histograms can often hide true trends in the distribution because they depend heavily on the choice of bin width. A more reliable way of visualizing univariate data is the use of a kernel density estimator, which gives an actual empirical estimate of the PDF of the data. The `density()` function computes a kernel estimator and can be plotted using the `plot()` command.

```
> d <- density(y)
> plot(d,main="Kernel Density Estimate of Y")
```



We can also plot the empirical CDF of a set of data using the `ecdf()` command from the *stepfun* library, which is included in the default distribution. We could then plot the estimated CDF using `plot()`.

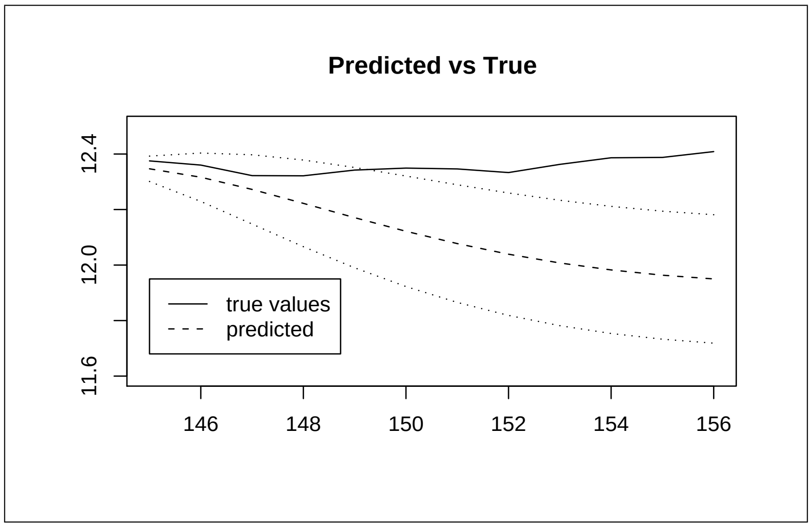
```
> library(stepfun)
> d <- ecdf(y)
> plot(d,main="Empirical CDF of Y")
```

6.2 Adding Legends and Stuff

After plotting we often wish to add annotations or other graphics that should really be placed manually. Functions like `text()` and `legend()` take as their first two arguments coordinates on the graph where the resulting objects should be placed. In order to manually determine the location of a point on the graph, use the `locator()` function. The location of one or several right clicks on the graph will be returned by this function after a left click. Those coordinates can then be used to place text, legends, or other add-ons to the graph.

An example of a time series, with a predicted curve and standard error lines around it

```
> plot(a.true,type="l",lty=1,ylim=c(11.6,12.5),main="Predicted vs True",xlab="",ylab="")
> lines(a.predict$pred,lty=2,type="l")
> lines(a.predict$pred+a.predict$se,lty=3,type="l")
> lines(a.predict$pred-a.predict$se,lty=3,type="l")
> legend(145,11.95,c("true values","predicted"),lty=c(1,2))
```



6.3 Multiple Plots

We can partition the drawing canvas to hold several plots. There are several functions that can be used to do this, including `split.screen()`, `layout()`, and `par()`. The simplest and most important is probably `par()`, so we will examine only it for now. The `par()` function sets many types of defaults about the plots, including margins, tick marks, and layout. The simplest way arrange several plots is by modifying the `mfrow` attribute. It is a vector whose first entry specifies the number of rows of figures we will be plotting and the second, the number of columns. Sometimes when plotting several figures, the default spacing may not be pleasing to the eye. In this case we can modify the default margin (for each plot) using the `mar` attribute. This is a four entry vector specifying the default margins in the form (bottom, left, top, right). The default setting is $\mathtt{c}(5, 4, 4, 2) + 0.1$. For a top/bottom plot, we may be inclined to decrease the top and bottom margins somewhat. In order to plot a time series with a seasonally adjusted version of it below, we could use

```
> op <- par(no.readonly=TRUE)
> par(mfrow=c(2,1),mar=c(3,4,2,2)+.1)
> plot(d[,1],main="Seasonally Adjusted",ylab=NULL)
> plot(d[,2],main="Unadjusted", ylab=NULL)
> par(op)
```

Notice that we saved the current settings in `op` before plotting so that we could restore them after our plotting and that we must set the `no.readonly` attribute while doing this.

6.4 Saving Plots

In order to save plots to files we change the graphics device via the `png()`, `jpg()`, or `postscript()` commands, then we plot what we want and close the special graphics device using `dev.off()`. For example,

```
> png("myplot.png")
> plot(x,y,main="A Graph Worth Saving")
> dev.off()
```

creates a png file of the plot of `x` and `y`. In the case of the postscript file, if we intend to include the graphics in another file (like in a LaTeX document), we could modify the default postscript settings controlling the paper size and orientation. Notice that when the `special` paper size is used, the width and height must be specified. Actually with LaTeX we often resize the image explicitly, so the resizing may not be that important.

```
> postscript("myplot.eps",paper="special",width=4,height=4,horizontal=FALSE)
> plot(x,y,main="A Graph Worth Including in LaTeX")
> dev.off()
```

One more thing to notice is that the default paper size is a4, which is the European standard. For 8.5x11 paper, we use `paper="letter"`. When using images that have been generated as a postscript, then converted to pdf, incorrect paper specifications are a common problem.

There is also a `pdf()` command that works the same way the `postscript` command does, except that by default its paper size is `special` with a height and width of 6 inches.

7 Statistics

R has extensive statistical functionality. The functions `mean()`, `sd()`, `min()`, `max()`, and `var()` operate on data as we would expect[2].

7.1 Working with Common Statistical Distributions

R can also generate and analyze realizations of random variables from the standard distributions. Commands that generate random realizations begin with the letter 'r' and take as their first argument the number of observations to generate; commands that return the value of the pdf at a particular observation begin with 'd'; commands that return the cdf value of a particular observation begin with 'p'; commands that return the number corresponding to a cdf value begin with q. Note that the 'p' and 'q' functions are inverses of each other.

```
> rnorm(1,mean=2,sd=3)
[1] 2.418665
> pnorm(2.418665,mean=2,sd=3)
[1] 0.5554942
> dnorm(2.418665,mean=2,sd=3)
[1] 0.1316921
> qnorm(.5554942,mean=2,sd=3)
[1] 2.418665
```

These functions generate a random number from the N(2,9) distribution, calculate its cdf and pdf value, and then verify that the cdf value corresponds to the original observation. If we had not specified the mean and standard deviation, R would have assumed standard normal. Note that we could replace `norm` with `binom` , `nbinom` , `chisq` ,`t` ,`f` or other distribution names if appropriate.

Command	**Meaning**
rX()	Generate random vector from distribution X
dX()	Return the value of the PDF of distribution X
pX()	Return the value of the CDF of distribution X
qX()	Return the number at which the CDF hits input value [0,1]

[2]note: the functions `pmax()` and `pmin()` function like max and min but elementwise on vectors or matrices.

7.2 P-Values

By way of example, in order to calculate the p-value of 3.6 using an $f(4,43)$ distribution, we would use the command

```
> 1-pf(3.6,4,43)
[1] 0.01284459
```

and find that we fail to reject at the 1% level, but we would be able to reject at the 5% level. Remember, if the p-value is smaller than the alpha value, we are able to reject. Also recall that the p-value should be multiplied by two if it we are doing a two tailed test. For example, the one and two tailed tests of a t statistic of 2.8 with 21 degrees of freedom would be, respectively

```
> 1-pt(2.8,21)
[1] 0.005364828
> 2*(1-pt(2.8,21))
[1] 0.01072966
```

So that we would reject the null hypothesis of insignificance at the 10% level if it were a one tailed test (remember, small p-value, more evidence in favor of rejection), but we would fail to reject in the sign-agnostic case.

8 Math in R

8.1 Matrix Operations

8.1.1 Matrix Algebra and Inversion

Most R commands work with multiple types of data. Most standard mathematical functions and operators (including multiplication, division, and powers) operate on each component of multidimensional objects. Thus the operation `A*B`, where `A` and `B` are matrices, multiplies corresponding components. In order to do matrix multiplication or inner products, use the `%*%` operator. Notice that in the case of matrix-vector multiplication, R will automatically make the vector a row or column vector, whichever is conformable. Matrix inversion is obtained via the `solve()` function. (Note: if `solve()` is passed a matrix and a vector, it solves the corresponding linear problem) The `t()` function transposes its argument. Thus

$$\beta = (X'X)^{-1}X'Y \tag{8}$$

would correspond to the command

```
> beta <- solve(t(X)%*%X)%*%t(X)%*%Y
```

or more efficiently

```
> beta <- solve(t(X)%*%X,t(X)%*%Y)
```

The Kronecker product is also supported and is specified by the the `%x%` operator.

```
> bigG <- g%x%h
```

calculates the Kronecker product of g with h.

The trace of a square matrix is calculated by the function `tr()`.

8.1.2 Factorizations

R can compute the standard matrix factorizations. The Cholesky factorization of a symmetric positive definite matrix is available via `chol()`. It should be noted that `chol()` does not check for symmetry in its argument, so the user must be careful.

We can also extract the eigenvalue decomposition of a symmetric matrix using `eigen()`. By default this routine checks the input matrix for symmetry, but the parameter `symmetric=FALSE` may be specified in order to skip this test if we know the matrix is symmetric by construction.

```
> J <- cbind(c(20,3),c(3,18))
> j <- eigen(J)
> t(j$vec)%*%diag(j$val)%*%j$vec
     [,1] [,2]
[1,]   20    3
[2,]    3   18
```

If the more general singular value decomposition is desired, we use instead `svd()`.

8.2 Writing Functions

A function can be treated as any other object in R. It is created with the assignment operator and `function()`, which is passed an argument list (use the equal sign to denote default arguments; all other arguments will be required at runtime). The code that will operate on the arguments follows, surrounded by curly brackets if it comprises more than one line.

If an expression or variable is evaluated within a function, it will not echo to the screen. However, if it is the last evaluation within the function, it will act as the return value. This means the following functions are equivalent

```
> g <- function(x,Alpha=1,B=0) sin(x[1])-sin(x[2]-Alpha)+x[3]^2+B
> f <- function(x,Alpha=1,B=0){
+ out <- sin(x[1])-sin(x[2]-Alpha)+x[3]^2+B
+ return(out)
+ }
```

Notice that R changes the prompt to a "+" sign to remind us that we are inside brackets.

Because R does not distinguish what kind of data object a variable in the parameter list is, we should be careful how we write our functions. If `x` is a vector, the above functions would return a vector of the same dimension. Also, notice that if an argument has a long name, it can be abbreviated as long as the abbreviation is unique. Thus the following two statements are equivalent

```
> f(c(2,4,1),Al=3)
> f(c(2,4,1),Alpha=3)
```

Variables that are not passed in as arguments are not available within functions and variables defined within functions are unavailable outside of the function. Changing the value of a passed-in argument within a function does not change its value outside of the function. In other words, R passes arguments by value and variable scoping applies.

8.3 Numerical Optimization

R can numerically minimize an arbitrary function using the command `nlm()`, which takes as its argument a function and a starting vector at which to evaluate the function. The fist argument of the user-defined function should be the parameter(s) over which R will minimize the function, additional arguments to the function (constants) should be specified by name in the nlm call. In order to maximize a function, multiply the function by -1 and minimize it.

```
> g <- function(x,A,B){
+ out <- sin(x[1])-sin(x[2]-A)+x[3]^2+B
+ out
+ }
> results <- nlm(g,c(1,2,3),A=4,B=2)
> results$min
[1] 6.497025e-13
> results$est
[1] -1.570797e+00 -7.123895e-01 -4.990333e-07
```

This function uses a matrix-secant method that numerically approximates the gradient, but if the return value of the function contains an attribute called `gradient`, it will use a quasi-newton method. The gradient based optimization corresponding to the above would be

```
> g <- function(x,A,B){
+ out <- sin(x[1])-sin(x[2]-A)+x[3]^2+B
+ grad <- function(x,A){
+   c(cos(x[1]),-cos(x[2]-A),2*x[3])
+ }
+ attr(out,"gradient") <- grad(x,A)
+ return(out)
+ }
> results <- nlm(g,c(1,2,3),A=4,B=2)
```

Other optimization functions which may be of interest are `optimize()` for one-dimensional minimization, `uniroot()` for root finding, and `deriv()` for calculating numerical derivatives.

9 Programming

9.1 Looping

Looping is performed using the `for` command. It's syntax is as follows

```
> for (i in 1:20){
+ cat(i)
> }
```

Where `cat()` may be replaced with the block of code we wish to repeat. Instead of `1:20`, a vector or matrix of values can be used. The index variable will take on each value in the vector or matrix and run the code contained in curly brackets.

If we simply want a loop to run until something happens to stop it, we could use the `repeat` loop and a `break`

```
> repeat {
+ g <- rnorm(1)
+ if (g > 2.0) break
+ cat(g);cat("\n")
> }
```

Notice the second `cat` command issues a newline character, so the output is not squashed onto one line. The semicolon acts to let R know where the end of our command is, when we put several commands on a line. For example, the above is equivalent to

```
> repeat {g <- rnorm(1);if (g>2.0) break;cat(g);cat("\n");}
```

9.2 Conditionals

9.2.1 Binary Operators

Conditionals, like the rest of R, are highly vectorized. The comparison

```
> x < 3
```

returns a vector of TRUE/FALSE values, if x is a vector. This vector can then be used in computations. For example. We could set all x values that are less that 3 to zero with one command

```
> x[x<3] <- 0
```

The conditional within the brackets evaluates to a TRUE/FALSE vector. Wherever the value is TRUE, the assignment is made. Of course, the same computation could be done using a `for` loop and the `if` command.

```
> for (i in 1:NROW(x)){
+ if (x[i] < 3) {
+  x[i] <- 0
+ }
+ }
```

Because R is highly vectorized, the latter code works much more slowly than the former. It is good programming practice to avoid loops and `if` statements whenever possible when writing in any scripting language.

The Boolean Operators

`! x`	NOT x
`x & y`	x and y elementwise
`x && y`	x and y total object
`x | y`	x or y elementwise
`x || y`	x or y total object
`xor(x, y)`	x xor y (true if one and only one argument is true)

9.3 The Ternary Operator

Since code segments of the form

```
> if (x) {
+ y } else {
+ z }
```

come up very often in programming, R includes a ternary operator that performs this in one line

```
> ifelse(x,y,z)
```

If `x` evaluates to `TRUE`, then `y` is returned. Otherwise `z` is returned. This turns out to be helpful because of the vectorized nature of R programming. For example, `x` could be a vector of `TRUE/FALSE` values, whereas the long form would have to be in a loop or use a roundabout coding method to achieve the same result.

10 Changing Configurations

10.1 Default Options

A number of runtime options relating to R's behavior are governed by the `options()` function. Running this function with no arguments returns a list of the current options. One can change the value of a single option by passing the option name and a new value. For temporary changes, the option list may be saved and then reused.

```
> oldops <- options()
> options(verbose=true)
...
> options(oldops)
```

10.1.1 Significant Digits

Mathematical operations in R are generally done to full possible precision, but the format in which, for example, numbers are saved to a file when using a write command depends on the option `digits`.

```
> options(digits=10)
```

increases this from the default 7 to 10.

10.1.2 What to do with NAs

The behavior of most R functions when they run across missing values is governed by the option `na.action`. By default it is set to `na.omit`, meaning that the corresponding observation will be ignored. Other possibilities are `na.fail`, `na.exclude`, and `na.pass`. The value `na.exclude` differs from `na.omit` only in the type of data it returns, so they can usually be used interchangeably.

10.1.3 How to Handle Errors

When an error occurs in a function or script more information may be needed than the type of error that occurs. In this case, we can change the default behavior of error handling. This is set via the `error` option, which is by default set to `NULL` or `stop`. Setting this option to `recover` we enter debug mode on error. First R gives a list of "frames" or program locations to start from. After selecting one, the user can type commands as if in interactive mode there. In the example below, one of the indices in my loop was beyond the dimension of the matrix it was referencing. First I check `i`, then `j`.

```
> options(error=recover)
> source("log.R")
Error: subscript out of bounds

Enter a frame number, or 0 to exit

1: source("log.R")
2: eval.with.vis(ei, envir)
3: eval.with.vis(expr, envir, enclos)
4: mypredict(v12, newdata = newdata)

Selection: 4
```

```
Called from: eval(expr, envir, enclos)
Browse[1]> i
[1] 1
Browse[1]> j
[1] 301
```

Pressing enter while in browse mode takes the user back to the menu. After debugging, we can set `error` to `NULL` again.

10.1.4 Suppressing Warnings

Sometimes non-fatal warnings issued by code annoyingly uglifies output. In order to suppress these warnings, we use `options()` to set `warn` to a negative number. If `warn` is one, warnings are printed are printed as they are issued by the code. By default warnings are saved until function completion `warn=0`. Higher numbers cause warnings to be treated as errors.

11 Saving Your Work

11.1 Saving the Data

When we choose to exit, R asks whether we would like to save our workspace image. This saves our variables, history, and environment. You manually can save R's state at any time using the command

```
> save.image()
```

You can save one or several data objects to a specified file using the `save()` command.

```
> save(BYU,x,y,file="BYUINFO.Rdata")
```

saves the variables `BYU`, `x`, and `y` in the default R format in a file named "BYUINFO.Rdata". They can be loaded again using the command

```
> load("BYUINFO.Rdata")
```

R can save to a number of other formats as well. Use `write.table()` to write a data frame as a space-delimited text file with headers, for example.

11.2 Saving the Session Output

We may also wish to write the output of our commands to a file. This is done using the `sink()` command.

```
> sink("myoutput.txt")
> a
> sink()
```

The output of executing the command `a` (that is, echoing whatever a is) is written to "myoutput.txt". Using `sink()` with no arguments starts output echoing to the screen again. Of course, `sink()` hides the output from us as we are interacting with R, so many times the easiest way to get a transcript of our session is to copy and paste using the mouse.

If we are using a script file, a nice way to get a transcript of our work and output is to use `sink()` in connection with `source()`.

```
> sink("myoutput.txt")
> source("rcode.R",echo=T)
> sink()
```

R can save plots and graphs as image files as well. Under windows, simply click once on the graph so that it is in the foreground and then go to *file/Save as* and save it as jpeg or png. There are also ways to save as an image or postscript file from the command line, as described in the plotting section.

11.3 Saving as LaTeX

R objects can also be saved as LaTeX tables using the `latex()` command from the *Hmisc* library. The most common use we have had for this command is to save a table of the coefficients and estimates of a regression.

```
> reg <- lm(educ~exper+south,data=d)
> latex(summary(reg)$coef)
```

produces a file named "summary.tex" that produces the following when included in a LaTeX source file[3]

summary	Estimate	Std. Error	t value	Pr(¿—t—)
(Intercept)	17.2043926	0.088618337	194.140323	$0.00000e + 00$
exper	-0.4126387	0.008851445	-46.618227	$0.00000e + 00$
south	-0.7098870	0.074707431	-9.502228	$4.05227e - 21$

which we see is pretty much what we want. The table lacks a title and the math symbols in the p-value column are not contained in $ characters. Fixing these by hand we get

OLS regression of `educ` on `exper` and `south`

summary	Estimate	Std. Error	t value	$\Pr(> \lvert t \rvert)$
(Intercept)	17.2043926	0.088618337	194.140323	$0.00000e + 00$
exper	-0.4126387	0.008851445	-46.618227	$0.00000e + 00$
south	-0.7098870	0.074707431	-9.502228	$4.05227e - 21$

Notice that the `latex()` command takes matrices, summaries, regression output, dataframes, and many other data types. Another option, which may be more flexible, is the `xtable()` function from the *xtable* library.

12 Conclusion

R provides an effective platform for econometric computation and research. It has built in functionality sufficiently advanced for professional research and has a reasonably steep learning curve (if you put knowledge on the y axis and effort on the x). Because R is a programming language as well as an econometrics program, it allows for more complex, tailored computations and simulations than one would get in a prepackaged system. On the other hand, it takes some time to become familiar with the syntax and reasoning of the language. I hope that this guide eases the burden of learning to program and do standard data analysis in the finest statistical environment available. Don't forget to let me know if you feel like I didn't do this or have a suggestion about how I could do it better.

[3]Under linux, at least, the `latex()` command also pops up a window showing how the output will look.

13 Appendix: Code Examples

13.1 Monte Carlo Simulation

The following block of code creates a vector of randomly distributed data X with 25 members. It then creates a y vector that is conditionally distributed as

$$y = 2 + 3x + \epsilon. \tag{9}$$

It then does a regression of x on y and stores the slope coefficient. The generation of y and calculation of the slope coefficient are repeated 500 times. The mean and sample variance of the slope coefficient are then calculated. A comparison of the sample variance of the estimated coefficient with the analytic solution for the variance of the slope coefficient is then possible.

```
>A <- array(0, dim=c(500,1))
>x <- rnorm(25,mean=2,sd=1)
>for(i in 1:500){
+ y <- rnorm(25, mean=(3*x+2), sd=1)
+ beta <- lm(y~x)
+ A[i] <- beta$coef[2]
+ }
>Abar <- mean(A)
>varA <- var(A)
```

13.2 The Haar Wavelet

The following code defines a function that returns the value of the Haar wavelet, defined by

$$\psi^{(H)}(u) = \begin{cases} -1/\sqrt{2} & -1 < u \leq 0 \\ 1/\sqrt{2} & 0 < u \leq 1 \\ 0 & \text{otherwise} \end{cases} \tag{10}$$

of the scalar or vector passed to it. Notice that a better version of this code would use a vectorized comparison, but this is an example of conditionals, including the `else` statement. The interested student could rewrite this function without using a loop.

```
> haar <- function(x){
+ y <- x*0
+ for(i in 1:NROW(y)){
+   if(x[i]<0 && x[i]>-1){
+      y[i]=-1/sqrt(2)
+   } else if (x[i]>0 && x[i]<1){
+      y[i]=1/sqrt(2)
+   }
+ }
+ y
+ }
```

Notice also the use of the logical 'and' operator, &&, in the `if` statement. The logical 'or' operator is the double vertical bar, ||. These logical operators compare the entire object before and after them. For example, two vectors that differ in only one place will return FALSE under the && operator. For elementwise comparisons, use the single & and | operators.

13.3 Maximum Likelihood Estimation

Now we consider code to find the likelihood estimator of the coefficients in a nonlinear model. Let us assume a normal distribution on the additive errors

$$y = aL^bK^c + \epsilon \tag{11}$$

Notice that the best way to solve this problem is a nonlinear least squares regression using `nls()`. We do the maximum likelihood estimation anyway. First we write a function that returns the log likelihood value (actually the negative of it, since minimization is more convenient) then we optimize using `nlm()`. Notice that `Y`, `L`, and `K` are vectors of data and `a`, `b`, and `c` are the parameters we wish to estimate.

```
> mloglik <- function(beta,Y,L,K){
+  n <- length(Y)
+  sum( (log(Y)-beta[1]-beta[2]*log(L)-beta[3]*log(K))^2 )/(2*beta[4]^2) + \
+  n/2*log(2*pi) + n*log(beta[4])
+ }
> mlem <- nlm(mloglik,c(1,.75,.25,.03),Y=Y,L=L,K=K)
```