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L E C T U R E N O T E S

For the course

Numerical Methods for Economists

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Chapter 1

Introduction to R

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1.1 Getting help

You can find R on the official web site http://www.r-project.org/. It is available for Windows, Mac and Linux. As for any open source software, there are several manuals on R that can be downloaded from the internet for free. On the web site (http://cran.r-project.org/manuals.html), you will find detailed manuals for both users and developers. I recommend going through sections 1 to 9 of "An Introduction to R", which will give you what you need to get started. The manual "R Data Import/Export" is a complete reference on how to deal with data from different sources (Stata, Matlab, Excel, etc.). There are also manuals specialized in econometrics. I suggest downloading http://cran.r-project.org/doc/contrib/Farnsworth-EconometricsInR.pdf. Finally, there are several books published by Springer for any area of econometrics which are not too expensive.

There are also tools integrated in R which are helpful when we are looking for a particular function or when we want to know how to use it. Suppose we want to know how to generate random numbers, but we don't know the name of the function. We can search using key words :

```
> help.search("Normal Distribution")
```

which gives a list of functions for which "Normal Distribution" is in the description. For example, one of the results is "stats::Normal The Normal Distribution", which means that the function "Normal" can be found in the package "stats". The latter is included in R and therefore do not need to be added. However, the result "mnormt::dmnorm Multivariate normal distribution" refers to the function dmnorm() which belongs to the package "mvtnorm" of [Genz *et al.* 2011]. This is one of the many packages that can be found on CRAN (see the list here: http://probability.ca/cran/web/packages/) and which can be installed using:

```
> install.packages("mvtnorm")
```

Once we have found the function we are looking for, we use the help() function in order to learn the syntax. For example, if we are interested by the above result "Normal", we type:

```
> help("Normal")
```

Notice that R is case sensitive. If you type help("normal"), you will get an error message. There are four functions associated with the term "Normal". The help file starts with the syntax of these functions:

dnorm(x, mean = 0, sd = 1, log = FALSE)
pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
qnorm(p, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
rnorm(n, mean = 0, sd = 1)

Some arguments such as "mean" have default values and others such as "x" or "q" require a value. Here is some examples:

- The density of a N(0,1) evaluated at 0.5:

  ```
  > dnorm(0.5)

  [1] 0.3520653
  ```

- The logarithm of the density of a N(0,1) evaluated at 0.5:

  ```
  > dnorm(0.5,log=TRUE)

  [1] -1.043939
  ```

- The density of a N(5,10) evaluated at 2:

  ```
  > dnorm(2,mean=5,sd=sqrt(10))
  ```

```
[1] 0.08044102
```

- 5 pseudo random numbers from a N(0,1) using the seed 123:

```
> set.seed(123)
> rnorm(5)

[1] -0.56047565 -0.23017749  1.55870831  0.07050839  0.12928774
```

There are no secret tricks to learn a computer language. You need to sit down and work hard. The best way is to think about a numerical project and try to do it. And remember that if you have a problem, someone must have gone through the same. The answer is probably somewhere in a newsgroup. Internet search engines such as Google are therefore endless sources of information. You can even participate and ask a question. But remember that the persons who answer are usually very friendly and work for free. Therefore, show them that you have made an effort before asking a question otherwise you could get the answer rtfm (read the f... manual).

Exercise 1.1. *Using the help() or help.search(), try to find a function that: (i) solves the system $Ax = b$, (ii) estimates a linear model by OLS, (iii) gives you the number of characters in a string such as "hello" and (iv) computes the mean of each column of a matrix.*

1.2 The basic concepts

1.2.1 Understanding the structure

R is an object-oriented language. The only difference between an object-oriented language and one which is not object-oriented is the organization of functions and elements. For example, the following

```
> x <- 1
> print(x)

[1] 1
```

means that the new object "x" receives all the attributes of the right-hand side. In that case, the operators "=" and "<-" are identical. However, it is often suggested to always use the latter when defining an object. The former is used when we set the options in a function:

```
> y <- matrix(1,nrow=1, ncol = 1)
> print(y)
```

```
     [,1]
[1,]    1
```

To see the difference, the two-line code above can be written in one single line as:

```
> print(y <- matrix(1,nrow=1, ncol = 1))

     [,1]
[1,]    1
```

It defines the object "y" and then print it. In that case, the operator "=" cannot be used; try

```
> print(y = matrix(1,nrow=1, ncol = 1))
```

An object is defined by its attributes and classes. Objects of some classes don't have any attributes and some have many. For example, x and y, defined above, look identical. But they are different objects. We can obtain the classes associated with an object by using the function "is()":

```
> is(x)

[1] "numeric" "vector"

> is(y)

[1] "matrix"    "array"     "structure" "vector"
```

and the attributes with "attributes()":

```
> attributes(x)

NULL

> attributes(y)

$dim
[1] 1 1
```

The difference between these two objects is that x does not have the attribute "dim" which gives the dimension of an array. Therefore we could make x identical to y simply by adding the attribute "dim" to it as follows:

```
> attributes(x) <- list(dim=c(1,1))
> is(x)
```

```
[1] "matrix"    "array"     "structure" "vector"
```

However, this is not the most efficient way to transform the object x. We would obtain the same result with the command "x <- as.matrix(x)". It is very important to understand the difference between vectors with and without the attribute "dim". The usual matrix operations can be performed only if the objects have the attribute "dim". If they don't, the operations can produce unexpected results. To see that, let A be a 2×2 matrix and x be a simple vector (without "dim") containing two elements.

```
> A <- matrix(c(1,2,3,4),2,2)
> A

     [,1] [,2]
[1,]    1    3
[2,]    2    4

> x <- c(1,2)
> x

[1] 1 2
```

Additions of two matrices are allowed only if the dimensions coincide. Because x does not have any dimension, the operation $A + x$ is allowed. But we have to be careful with how R treats such operations. In fact, a matrix of the same dimension as A is constructed by repeating the vector x until the total number of elements is equal to the number of elements of A. Therefore, the number of elements of A should be a multiple of the number of elements of x. A warning message is printed otherwise (try to experiment as much cases as possible to make sure you understand). The result is:

```
> A+x

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

However, if x is a 2×1 matrix, R returns an error message (Here I use the function try() which returns the result if the operation is allowed and an error message otherwise):

```
> x <- as.matrix(x)
> try(x+A)[1]

[1] "Error in x + A : non-conformable arrays\n"
```

This way of treating operations may seem confusing at first, but it happens to be very useful in some cases. Suppose you have a $T \times N$ matrix R of asset returns. Each column represents a different time series of returns. You also have a time series of returns on the three-month US treasury bill (R_f) that you want to use as proxy for the risk-free rate. To compute a time series of excess returns of each asset ($Z_{it} = R_{it} - R_{ft}$), you can simply define the vector of risk-free rates as a simple vector and do

```
> Z<- R-Rf
```

There are also different kinds of vector. We can create a vector of messages:

```
> W <- c("hello!", "Bonjour!", "Ohayogozaimasu!")
> is(W)
```

```
[1] "character"           "vector"              "data.frameRowLabels"
[4] "SuperClassMethod"
```

It is a vector, which means that it is a collection of elements, but we don't see the class "numeric". Therefore, mathematical operations are not allowed on that kind of objects. In C++, which is probably the most popular object-oriented language for software developers, you can redefine the operator "+" for vectors of characters. It would, for example, construct a new vector by combining the characters of each vector. The operator "+" would react differently whether the vector is numeric or not. There is no point of having such operators in R, but it shows how it works. Many functions are built in such a way that they react differently depending on the type of objects. We call them "methods". A method is a function that adapts itself to the class of the object. An example of method is "summary()". We can see the type of objects that this method deals with:

```
> methods(summary)
```

```
 [1] summary.aov             summary.aovlist         summary.aspell*
 [4] summary.connection      summary.data.frame      summary.Date
 [7] summary.default         summary.ecdf*           summary.factor
[10] summary.glm             summary.infl            summary.lm
[13] summary.loess*          summary.manova          summary.matrix
[16] summary.mlm             summary.nls*            summary.packageStatus*
[19] summary.PDF_Dictionary* summary.PDF_Stream*     summary.POSIXct
[22] summary.POSIXlt         summary.ppr*            summary.prcomp*
[25] summary.princomp*       summary.srcfile         summary.srcref
[28] summary.stepfun         summary.stl*            summary.table
[31] summary.tukeysmooth*

   Non-visible functions are asterisked
```

The class of the object appears after the dot. So, summary() will treat objects of class "matrix " differently from objects of class, say, "data.frame". Other classes not listed are treated by "summary.default". For example, let X be a data.frame, than summary produces:

```
> set.seed(123)
> X <- matrix(runif(24),4,3)
> X <-  data.frame(Consumption=X[,1],Income= X[,2], Wealth=X[,3])
> summary(X)
```

```
  Consumption         Income            Wealth
 Min.   :0.2876   Min.   :0.04556   Min.   :0.4533
 1st Qu.:0.3786   1st Qu.:0.40747   1st Qu.:0.4558
 Median :0.5986   Median :0.71026   Median :0.5040
 Mean   :0.5920   Mean   :0.60164   Mean   :0.6046
 3rd Qu.:0.8120   3rd Qu.:0.90443   3rd Qu.:0.6528
 Max.   :0.8830   Max.   :0.94047   Max.   :0.9568
```

If we create an object of class "lm" which is create by the OLS procedure "lm()", the summary() method produces very different results:

```
> res <- lm(Income~Consumption,data=X)
> summary(res)
```

```
Call:
lm(formula = Income ~ Consumption, data = X)

Residuals:
      1       2       3       4
 0.1994 -0.4662 -0.1573  0.4241

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   0.8728     0.6181   1.412    0.293
Consumption  -0.4580     0.9621  -0.476    0.681

Residual standard error: 0.4805 on 2 degrees of freedom
Multiple R-squared: 0.1018,        Adjusted R-squared: -0.3473
F-statistic: 0.2266 on 1 and 2 DF,  p-value: 0.681
```

In fact, every function produces an object of some kind. Even summary() does:

```
> is(summary(X))
```

```
[1] "table"    "oldClass"
```

It is very useful because you can store all your results in different variables and save it in a file. For Example, if we estimate two models and want to save the properties of the data only, we would proceed this way:

```
> res1 <-   lm(Income~Consumption,data=X)
> res2 <- lm(Wealth~Consumption,data=X)
> sum_stat <- summary(X)
> save(res1,res2,sum_stat,file="data/all_result.rda")
> rm(list=ls())
```

(the last line deletes all objects from the workspace) Then, you can reload later and analyze the results:

```
> load("data/all_result.rda")
> anova(res1)

Analysis of Variance Table

Response: Income
            Df  Sum Sq  Mean Sq F value Pr(>F)
Consumption  1 0.05232 0.052319  0.2266  0.681
Residuals    2 0.46167 0.230837
```

There are two categories of classes: S3 and S4. Functions that produce S3/class objects, like lm(), are lists of elements. An element of a list can be extracted using $. You can obtain the names of each element with the names(). For example, objects produced by lm() contain the following elements:

```
> names(res1)

 [1] "coefficients"  "residuals"     "effects"       "rank"
 [5] "fitted.values" "assign"        "qr"            "df.residual"
 [9] "xlevels"       "call"          "terms"         "model"
```

If there is no conflict with other elements, you can only use the first letters:

```
> res1$coefficients

(Intercept) Consumption
  0.8727695  -0.4580178

> res1$coef
```

```
(Intercept) Consumption
  0.8727695  -0.4580178
```

```
> res1$co
```

```
(Intercept) Consumption
  0.8727695  -0.4580178
```

For S4/class objects, the elements are called slots which may themself be S3/class objects. The unit root test procedure *adfTest*() from the package "fUnitRoots" of [Wuertz *et al.* 2009] is an example of functions producing S4/class objects. Let us first create it:

```
> x <- as.ts(rnorm(200))
> library(fUnitRoots)
> res <- adfTest(x,lags=2, type="ct")
```

The elements of S4/class objects can be extracted using @. We can obtain the names of the slots as follows:

```
> slotNames(res)
```

```
[1] "call"        "data"        "test"        "title"       "description"
```

The slot "test" is a list as we can see:

```
> res_test <- res@test
> names(res_test)
```

```
[1] "data.name" "statistic" "p.value"   "parameter" "lm"
```

Some elements are just values, as for "statistic" and "p.value":

```
> res_test$statistic
```

```
Dickey-Fuller
    -7.904307
```

```
> res_test$p.value
```

```
0.01
```

Others are S3/class objects like "lm" which contains the results of the OLS estimation:

```
> summary(res_test$lm)
```

```
Call:
lm(formula = y.diff ~ y.lag.1 + 1 + tt + y.diff.lag)

Residuals:
     Min       1Q   Median       3Q      Max
-2.25260 -0.65132 -0.08469  0.62403  2.96349

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.0150866  0.1382080  -0.109    0.913
y.lag.1     -1.0628340  0.1344626  -7.904 2.05e-13 ***
tt           0.0001167  0.0011923   0.098    0.922
y.diff.lag1 -0.0097415  0.1055491  -0.092    0.927
y.diff.lag2 -0.0921900  0.0717865  -1.284    0.201
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.9516 on 192 degrees of freedom
Multiple R-squared: 0.5451,        Adjusted R-squared: 0.5356
F-statistic: 57.52 on 4 and 192 DF,  p-value: < 2.2e-16
```

Don't get scared with all this terminology. Once we get used to it, it really makes things easier.

The following gives you all that you need to play with matrices and vectors. First, we create the following matrix and vector:

$$A = \begin{pmatrix} 1 & 4 & 7 \\ 2 & 5 & 8 \\ 3 & 6 & 9 \end{pmatrix} \quad , \quad x = \{5\ ,\ 6\ ,\ 7\},$$

using the following code (# means comment. R does not execute what comes after)

```
> A <- matrix(1:9,3,3)
> x <- 5:7 # or c(5,6,7)
```

- Extracting elements from a matrix. I let you figure out what the following codes mean:

  ```
  > A[1,2]

  [1] 4

  > x[1]
  ```

```
[1] 5

> A[1,]

[1] 1 4 7

> A[,3]

[1] 7 8 9

> diag(A)

[1] 1 5 9

> A[c(1,3),c(2,3)]

     [,1] [,2]
[1,]    4    7
[2,]    6    9
```

- Ax (matrix multiplication): Notice that x does not need to be a column vector. If it is a simple vector without dimension, R will do the only operation that is allowed.

```
> A%*%x

     [,1]
[1,]   78
[2,]   96
[3,]  114
```

- $x'Ax$: Again, we don't need to transpose x because it is the only logical way to do the operation with a simple vector. The following two ways are identical:

```
> t(x)%*%A%*%x

     [,1]
[1,] 1764

> x%*%A%*%x

     [,1]
[1,] 1764
```

- Adding x to each column of A:

```
> A+x

     [,1] [,2] [,3]
[1,]    6    9   12
[2,]    8   11   14
[3,]   10   13   16
```

- Adding x to each row of A: 2 ways: The sweep() function is useful but somehow confusing. In the code bellow, the 2 means that we want the operation $+x_i$ to be applied to each element of the second dimension of A, the column, for each row.

```
> t(t(A)+x)

     [,1] [,2] [,3]
[1,]    6   10   14
[2,]    7   11   15
[3,]    8   12   16

> sweep(A,2,x,FUN="+")

     [,1] [,2] [,3]
[1,]    6   10   14
[2,]    7   11   15
[3,]    8   12   16
```

- Subtracting the mean of each column:

```
> t(t(A)-colMeans(A))
> sweep(A,2,colMeans(A),FUN="-")
```

- Computing $x'x$

```
> crossprod(x)

     [,1]
[1,]  110

> t(x)%*%x

     [,1]
[1,]  110
```

```
> x%*%x

     [,1]
[1,]  110
```

- computing the outer product xx': It must be done explicitly if the oprator %*% is used. Doing x%*%x will not work as it computes the inner product. The outer product operator is %o%. The following are identical:

```
> xx <- x%*%t(x)
> xx <- outer(x,x)
> xx <- x%o%x
> xx

     [,1] [,2] [,3]
[1,]   25   30   35
[2,]   30   36   42
[3,]   35   42   49
```

- Element by element operation. The operators +,*,/ are element by element operators. As mentioned above, if x is a vector without dimension and we run $A * x$, $A + x$ or A/x, R constructs a matrix of the same dimension as A by stacking the vector x until the number of elements are equal and then apply the operator element by element. If we apply the operators on two matrices, they must have the same dimension. If not, R with return an error message. The variable xx computed above has the same dimensions and therefore can be used to run:

```
> A+xx
> A*xx
> A/xx
```

- Stacking two vector or matrices one beside the other (cbind for column-bind) or one under the other (rbind for row-bind):

```
> xc <- cbind(x,x)
> xr <- rbind(x,x)
```

  Notice that the columns of the new matrix in the first case and the rows in the second case have names. It is a new attribute of the object that it automatically added when cbind and rbind are used. The attribute is called dimnames. It is a list which gives the name with as many element as the number of dimension. Look at the difference between the two objects:

```
> attributes(xc)

$dim
[1] 3 2

$dimnames
$dimnames[[1]]
NULL

$dimnames[[2]]
[1] "x" "x"

> attributes(xr)

$dim
[1] 2 3

$dimnames
$dimnames[[1]]
[1] "x" "x"

$dimnames[[2]]
NULL
```

xc has no row names and xr has no column names.

- Adding or modifying names: matrix or data.frame?. This has nothing to do with matrix operation but since we just saw that rows and columns can have names, it is a good place to start. First, why would we be interested in giving names to rows and columns? In economics, each number we are playing with are associated with something. For example, suppose the matrix B stores the information about the consumption habits of individuals. Suppose we have three individuals and 2 goods. Here is one way to create it:

```
> B <- matrix(c(200,100,150,150,100,200),2,3)
> dimnames(B) <- list(c("Book","Beer"),c("John","James","Bill"))
> B

     John James Bill
Book  200   150  100
Beer  100   150  200
```

A data.frame is another class of objects that is used to store data. It has different attributes than matrices which implies that some operators or methods may work with matrices and not with data.frame and vice versa. Since data.frame objects are also lists, we start by introducing that particular object. A list is a collection of almost everything you can think of. Here is an example:

```
> Pierre = list(address = "UofW Waterloo",
+          Inventory=c("Computer", "Coffee Maker","Books"),
+          LuckyNumbers = c(2,5,6,733,44))
```

You can extract the element of a list with $ as seen above or with [[i]] for the value of the i^{th} element of the list or [1] for the element with the name:

```
> Pierre[1] # This is still a list

$address
[1] "UofW Waterloo"

> Pierre[[1]] # this if the object of the list

[1] "UofW Waterloo"

> Pierre$addr

[1] "UofW Waterloo"
```

You can add things to the list like:

```
> Pierre$Mydata <- B
> Pierre$Mydata

     John James Bill
Book  200   150  100
Beer  100   150  200
```

A data.frame is more restrictive because it requires the elements to be vectors with the same number of elements. In the following example, I generate data randomly and store them in a data.frame object:

```
> set.seed(100)
> X1 <- rnorm(100,mean=200,sd=50)
> X2 <- rnorm(100,mean=500,sd=25)
> Data <- data.frame(Consumption=X1, Income=X2)
> is(Data)
```

```
[1] "data.frame" "list"       "oldClass"   "vector"
```

The is() function shows the inheritance of the object. The "list" means that we can treat the object as a list. We can then extract the Income using Data$Income or Data[[2]]. The is() also tells us that the data.frame can be treated as a vector. We can then do operation on a data.frame. For example, we can rescale the Data as follows:

```
> Data <- Data/100
```

However, we cannot do matrix operations because the inheritance does not include "matrix". If we want, we can transform a data.frame to a matrix:

```
> Data <- as.matrix(Data)
```

We can also change it back to a data.frame:

```
> Data <- as.data.frame(Data)
```

- Time series object: We can create a time series object with ts(). That object has an attribute called tsp that gives information about the first and last dates and the frequency of the data. For example, we can define the above Data as a quarterly time series starting the first quarter of 1970:

```
> tsData <- ts(Data,start=c(1970,1),freq=4)
> is(tsData)
```

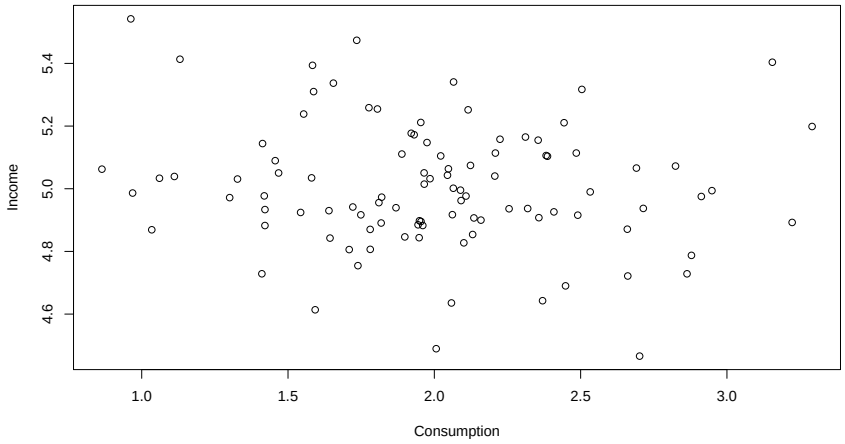
```
[1] "mts"         "matrix"      "ts"          "array"       "structure"
[6] "oldClass"    "vector"      "otherornull"
```

The "mts" means multivariate time series. Is is no longer a data.frame. The plot() function will react differently with matrix, data.frame or ts objects. With ts objects, the plot knows that the x axis is time:

```
> plot(tsData)
```

which is different from the case in which the object is a matrix:

```
> Data <- as.matrix(Data)
> plot(Data)
```



- Higher dimensional arrays: It may sometimes be useful to store information in a matrix with more than 2 dimensions. If we consider the matrix B above, we could be interested to store the consumption habits of the individuals for two different periods. Suppose B was the consumption in 1990 and B2, defined bellow is the consumption in 2000. We can define a new matrix containing all the two matrices.

```
> B2 <- matrix(c(250,75,300,250,500,20),2,3)
> dimnames(B2) <- dimnames(B2)
```

```
> allB <- array(0,c(2,3,2))
> allB[,,1] <- B
> allB[,,2] <- B2
> dimnames(allB)[[1]] <- dimnames(B)[[1]]
> dimnames(allB)[[2]] <- dimnames(B)[[2]]
> dimnames(allB)[[3]]<- c("1990","2000")
> allB

, , 1990

     John James Bill
Book  200   150  100
Beer  100   150  200

, , 2000

     John James Bill
Book  250   300  500
Beer   75   250   20
```

Exercise 1.2. *In order to do the exercise, you will need to load the data file "PriceIndex.rda", in which you'll find seven vectors of price index: all, Car, Clothing, Electricity, Food, NatGas and Gasoline. All vectors are monthly time series going from January 1949 to September 2011. This exercise makes you use what we have covered above and more. You may need to use Google, help() or help.search(). That is where the fun begins*

1. *Collect the data in a matrix of class "ts" with the correct starting date and frequency. You can then plot the data and compare the inflation of different items.*
2. *Build a table in which you have for each item, the average annual inflation, its standard deviation, its kurtosis and its skewness.*
3. *Create a matrix of annual data from your monthly series. An annual index is defined as the average monthly index.*
4. *Using the annual series, plot on the same graph the annual inflation series of all component of CPI and include a legend. Do you see a difference between the different items?*

Exercise 1.3. *In the next section, we will see how to organize our programs. It is often a good practice to create our own objects with their associated methods. We will learn how to use them later. For now, create the following objects:*

1. *An object of class "consumer". We consider a world in which only two goods are produced, x_1 and x_2, and the consumers have a Cobb-Douglas utility function. The object must therefore inform us about the parameters of the utility function, the income of the consumer, his name, address, occupation, and so on. Here is an example of an object I created (notice that you need a print method for this kind of object in order to obtain that result. We'll cover that in the next section)*

```
> print(cons1)

Pierre
##############
Address :  U of Waterloo
Occupation :  Professor
Income =  2000

Utility function : U(x1, x2) == 1 * X1^0.4 * X2^0.6
```

2. *Create now an object of class "producer". The object will include the name of the firm, what kind of good it produces, its location, the parameter of its production function and so on. You can assume that the production function is a constant elasticity of substitution (CES) function.*

3. *Create an object of class "market". In that object, we have all the information about the goods produced, taxes, the kind of competition, and any other factor that you consider to be important.*

Usually, we do not create objects without knowing what we'll be doing with them. For example, we may want to have a method, choice(), that computes the optimal choice of a consumer given that he lives in market "mark1". The method could look like:

```
> res <- choice(cons1, market1)

> print(res)

[1] "Pierre chooses to consume 1 unit if x1 and 5 units of x2"
```

This is the subject of next section. For now, you are free to create the objects the way you like it. Use your imagination.

1.3 Organizing our programs

The main goal of object-oriented programming is mainly to be organized. It is not essential to know how to do it, but it makes life much easier once you get to know how

to do it. Just take for example the comment at the end of Exercise 1.3. For solving the consumer problem, you could write a program like the following which I would consider the least organized approach (keep in mind that many things I write here are a matter of opinion or taste. If you don't agree, speak up!):

```
> # We consider the consumer "cons1" created in the
> # previous section
> p1 <- 5
> p2 <- 10
> a1 <- .4
> a2 <- .6
> Y <- 2000
> x1 <- a1*Y/p1
> x2 <- a2*Y/p2
> print(x1)

[1] 160

> print(x2)

[1] 120
```

There are several problem with that approach. If you want to do it for another consumer, you need to rewrite all the lines with different parameter values. Remember that one way to minimize the risk of errors is to have a shorter programs. It is simple arithmetics. Also, you need to know the solution of the utility maximization in order to compute the solution. What if you have a totally new utility function?

I am going to the extreme here because I believe it is the best way to learn. Or course, it is not always optimal to spend time being organized for everything we compute. For example, if you only have to do it once for an assignment and you will never solve another consumer problem in the future because you hate microeconomics, then it is probably the best way to compute it. However, it is a good practice to be more organized especially when the complexity of the problem we are trying to solve increases. I am presenting you my way of programming. It is not the only way. You are free to choose your own way.

The first improvement would be to write a function that computes the solution given the parameter values:

```
solveCobb <- function(name, a1, a2, Y, p1,
    p2, print = TRUE) {
    x1 <- a1 * Y/p1
    x2 <- a2 * Y/p2
```

```
    if (print)
        cat(name, " chooses to consume ", x1, " x1 and ",
            x2, " x2\n")
    choice <- list(x1 = x1, x2 = x2)
}
```

It can then be called for different consumers:

```
> solveCobb("Pierre", .4,.6,2000,p1,p2)

Pierre  chooses to consume  160  x1 and  120  x2

> solveCobb("Luc", .4,.6,1000,p1,p2)

Luc  chooses to consume  80  x1 and  60  x2

> solveCobb("Bill", .2,.8,1000,p1,p2)

Bill  chooses to consume  40  x1 and  80  x2
```

Notice that I chose to build a function that prints the results (when the option print is TRUE) in a nice way using the command cat(). It is not necessary. Also, the function does not end with return(). In that case, you can recover the last object created as follows:

```
> choice <- solveCobb("Pierre", .4,.6,2000,p1,p2,print=FALSE)
> print(choice)

$x1
[1] 160

$x2
[1] 120
```

It is often suggested to avoid using return() when it is possible (not everyone agrees with that though). But it is not always possible. Also, you have to make sure when you do not include return() at the end of the function that it returns what you want. For example, the following function is a good illustration:

```
f <- function(x) {
    ft <- x^2
    class(ft) <- "A new Class"
    pretty.print(f)
}
```

```
$text.tidy
[1] "f <- function(x) {\n    ft <- x^2\n    class(ft) <- \"A new Class\"\n    pretty.print(

$text.mask
[1] "f <- function(x) {\n    ft <- x^2\n    class(ft) <- \"A new Class\"\n    pretty.print(

$begin.comment
[1] ".BeGiN_TiDy_IdEnTiFiEr_HaHaHa"

$end.comment
[1] ".HaHaHa_EnD_TiDy_IdEnTiFiEr"
```

So it returns the class of the object instead of the object itself. In that case, you have to end the function with return(r). Another improvement would be to store the information of a particular consumer in a variable (like in Exercise 1.3) and use that variable as argument for solveCobb(). Let us first create the consumer:

```
> pierre <- list(a1=.4,a2=.6,Y=2000,name="Pierre")
> luc <- list(a1=.2,a2=.8,Y=1000,name="Luc")
```

Then, we have to adapt the function solveCobb():

```
solveCobb <- function(cons, p1, p2, print = TRUE) {
    x1 <- cons$a1 * cons$Y/p1
    x2 <- cons$a2 * cons$Y/p2
    if (print)
        cat(cons$name, " chooses to consume ", x1,
            " x1 and ", x2, " x2\n")
    choice <- list(x1 = x1, x2 = x2)
}
```

```
> solveCobb(pierre,p1,p2)

Pierre  chooses to consume  160  x1 and  120  x2

> solveCobb(luc,p1,p2)

Luc  chooses to consume  40  x1 and  80  x2
```

I am still not satisfied with the above. Creating the consumers using a list() used by solveCobb may not work if we misspell the name of the variables or if we forget to define one. In general, when you want to use an object inside a function which respects a certain structure, it is better to have another function that creates that object. In C

or C++, we call these kind of functions the constructors. I like things to be as general as possible when I write programs so that it can easily be adapted to other realities. Here is a consumer constructor that I propose:

```
consumer <- function(name = NULL, para,
    Y, utility = c("Cobb", "Linear", "Leontief", "Subsistence")) {
    utility <- match.arg(utility)
    if (utility == "Subsistence") {
        x01 = para[3]
        x02 = para[4]
    } else {
        x01 = NULL
        x02 = NULL
    }
    # Cobb = x1^a1*x2^a2, Linear = a1*x1 + a2*x2
    # Leontief = min(a1*x2, a2*x2), Subsistence =
    #   (x1-x01)^a1(x2-x02)^a2
    # para = c(a1, a2, x10, x20)
    list(name = name, a1 = para[1], a2 = para[2], x01 = x01,
        x02 = x02, Y = Y, utility = utility)
}
```

Notice that utility can take more than one values. The first line in the function is to make sure that what we write is among the choices. It also allow us to use the first letters when there is no ambiguity. For example, we can write utility=”C” or utility=”Li”, but not utility=”L”. The first choice in the list is the default value. We can then proceed as follows:

```
> pierre <- consumer("pierre",c(.4,.6),2000)
> solveCobb(pierre,p1,p1)

pierre  chooses to consume  160  x1 and  240  x2
```

Exercise 1.4. *Write three functions for the last three utility functions in the list of consumer() that solves the consumer problem. You can call them solveLinear(), solveLeontief() and solveSubsistence().*

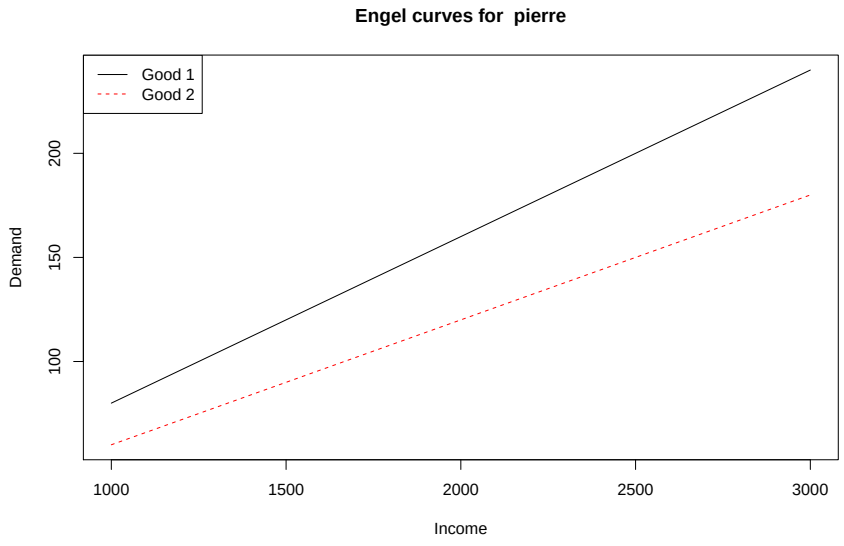
Exercise 1.5. *Write a function that creates an object ”market” that includes the price of the two goods and the taxe imposed on each one ($t1$ and $t2$). Then adapt the solve functions so that they only take the market and consumer objects as arguments (ex. solveCobb(cons1, market1, print=T))*

What is nice with this structure is that you can create other functions that can be applied to the consumer object. For example, you can plot the Engel's curve of a particular consumer:

```
engelCobb <- function(cons, p1, p2) {
    if (is.null(cons$name))
        cons$name <- "anonymous"
    Yr <- seq(0.5 * cons$Y, 1.5 * cons$Y, len = 50)
    E1 <- Yr * cons$a1/p1
    E2 <- Yr * cons$a2/p2
    ylim <- range(c(E1, E2))
    plot(Yr, E1, ylim = ylim, xlab = "Income", ylab = "Demand",
        type = "l")
    lines(Yr, E2, col = 2, lty = 2)
    legend("topleft", c("Good 1", "Good 2"), col = 1:2,
        lty = 1:2)
    title(paste("Engel curves for ", cons$name))
}
```

Then we can easily plot the Engel curve for any consumer created with consumer():

```
> engelCobb(pierre,p1,p2)
```

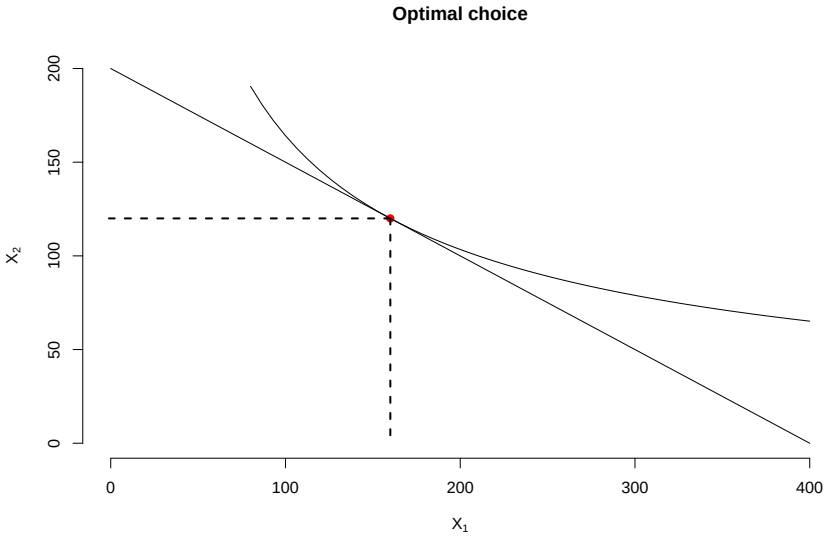


Exercise 1.6. *Write the Engel function for the three other utility functions.*

A last nice function we can add is the graphical representation of the solution:

```
plotSolveCobb <- function(cons, p1, p2) {
    choice <- solveCobb(cons, p1, p2, F)
    xr <- seq(choice$x1 * 0.5, cons$Y/p1, len = 50)
    U <- choice$x1^cons$a1 * choice$x2^cons$a2
    indif <- (U * xr^(-cons$a1))^(1/cons$a2)
    budg <- curve(cons$Y/p2 - p1 * x/p2, 0, cons$Y/p1,
        xlab = expression(X[1]), ylab = expression(X[2]),
        bty = "n")
    points(choice$x1, choice$x2, pch = 21, bg = 2,
        col = 2)
    lines(xr, indif)
    segments(choice$x1, choice$x2, -1, choice$x2, lty = 2,
        lwd = 2)
    segments(choice$x1, choice$x2, choice$x1, -1, lty = 2,
        lwd = 2)
    title("Optimal choice")
}
```

```
> plotSolveCobb(pierre,p1,p2)
```



Exercise 1.7. *Do it for the three other utility functions.*

There is still a problem with the above structure. In order to solve the consumer problem or to plot the Engel's curve, we need to print the consumer's characteristics so that we use the right function. It would be nice if we could just write solve(pierre)

plot(pierre) or Engel(pierre). We can either write a function with things like "if (cons$utility=="Cobb") ... else if () ... else ..." or to use classes. I let the consumer problem to you as an exercise at the end of the chapter. But before we'll see how to create objects, classes and methods using a very simple example.

1.3.1 Classes and methods for second order polynomials

Classes are a way of identifying the type of objects. We saw several classes in the previous sections such as "ts", "vector", "numeric". We also saw that methods such as plot() react differently depending on the object. There is no magic here; just organization. Suppose for example that we have an object x of class "ts" and a simple vector y. The reason why plot(x) and plot(y) produce different graphs is that different functions are called. Because x is of class ts, plot(x) is in fact plot.ts(x). R looks for functions with names ending by .ts when applied to objects of class "ts". It produces a time series plot with the dates which are included inside the structure of x. Those dates exist because x was created using the constructor ts() which always creates dates. The type of plot is also automatically chosen to be "l". On the other hand, there is no specific plot() method for regular vector. In that case, it is the function plot.default() that is called for y. There are many plot() methods for all kind of objects. Imagine how messy it would be to put everything inside one function plot() with a collection of "if... else if" everywhere. The function plot.default() works fine. So why should we modify it? Every time we need to plot another object, we create a new function. That function can then be tested and bugs can easily be removed.

This is what we are going to do in this section for a simple object: a second order polynomial. A second order polynomial is defined by its 3 parameters: A, B and C:

$$f(x) = Ax^2 + Bx + C$$

We first write the constructor. It is like for the consumer constructor that we built in the previous section. The only difference is that we want that object to belong to a particular class that we will call "Quadra". This is simply done using the function class():

```
Quadra <- function(a, b, c) {
    if (a == 0)
        stop("It is not a quadratique function;\n'a' must be different from zero")
    obj <- list(a = a, b = b, c = c)
    class(obj) <- "Quadra"
    return(obj)
}
```

We can then create the polynomial $f(x) = 2x^2 - 4x + 10$ and print it.

```
> P1 <- Quadra(2,-4,10)
> P1

$a
[1] 2

$b
[1] -4

$c
[1] 10

attr(,"class")
[1] "Quadra"
```

We can see that the output from the print() method is not very nice. But because there is no print.Quadra() function, the print.default() is used. There is a print() method for a large number of objects. For example, if you estimate a model by OLS using lm(). The object created is of class "lm". There is a lot of information inside that object (residuals, fitted values, covariance matrix of the coefficients and so on) but we don't want print() to show everything. Therefore, print.lm() only prints the estimates and few other things. Let us do the same for our new object:

```
print.Quadra <- function(obj) {
    cat("\nSecond order polynomial\n\n")
    cat("F(x) = Ax^2 + Bx + C\n")
    cat("with: A=", obj$a, ", B=", obj$b, ", C=", obj$c,
        "\n\n")
}
```

Then we can try it on the object we created before (notice that just writing P1 is the same as writing print(P1)):

```
> P1

Second order polynomial

F(x) = Ax^2 + Bx + C
with: A= 2 , B= -4 , C= 10
```

Now that we are starting to understand the idea, lets create a bunch of other methods. The next one finds the zeros of the polynomial which could be real or complex. The

method I want to use is zeros(). However, that method does not exist in R like print(). Therefore we need to inform R of this new method (which could be use to find zeros of any kind of function $f(x)$ by other users):

```
zeros <- function(object, ...) {
    UseMethod("zeros")
}
```

The "..." are required because the zeros() method applied to other type of objects may required other arguments. We can now create our new method for the object of class "Quadra".

```
zeros.Quadra <- function(obj) {
    det <- obj$b^2 - 4 * obj$a * obj$c
    if (det > .Machine$double.eps) {
        r1 <- (-obj$b - sqrt(det))/(2 * obj$a)
        r2 <- (-obj$b + sqrt(det))/(2 * obj$a)
        r <- cbind(r1, r2)
        class(r) <- "zeros"
        attr(r, "type") = "Real and distinct"
    }
    if (abs(det) <= .Machine$double.eps) {
        r1 <- -obj$b/(2 * obj$a)
        r <- cbind(r1, r1)
        class(r) <- "zeros"
        attr(r, "type") = "Real and identical"
    }
    if (det < -.Machine$double.eps) {
        det <- sqrt(-det)/(2 * obj$a)
        r1 <- -obj$b/(2 * obj$a) - det * (0+1i)
        r2 <- -obj$b/(2 * obj$a) + det * (0+1i)
        r <- cbind(r1, r2)
        class(r) <- "zeros"
        attr(r, "type") = "Complexe"
    }
    return(r)
}
```

We will discuss the content of the function in class. Notice that the function produces objects of class "zeros". We can then create a print method for that class of objects.

```
print.zeros <- function(obj) {
    n <- length(obj)
```

```
    cat("\nType of zeros: ", attr(obj, "type"), "\n\n")
    for (i in 1:n) cat("Zero[", i, "] = ", obj[i],
        "\n")
    cat("\n")
}
```

We can then apply the method to the polynomial $P1$ and print it directly:

```
> zeros(P1)

Type of zeros:  Complexe

Zero[ 1 ] =  1-2i
Zero[ 2 ] =  1+2i
```

Lets create another polynomial with real zeros:

```
> P2 <- Quadra(-4,2,10)
> zeros(P2)

Type of zeros:  Real and distinct

Zero[ 1 ] =  1.850781
Zero[ 2 ] =  -1.350781
```

The next method computes the stationary point (max or min). For that, I use the existing method solve() and the object produced is of class "solve.Quadra". I then create a print method for that new object.

```
solve.Quadra <- function(obj) {
    x <- -obj$b/(2 * obj$a)
    f <- obj$a * x^2 + obj$b * x + obj$c
    if (obj$a > 0)
        what <- "min" else what <- "max"
    ans <- list(x = x, f = f, what = what)
    class(ans) <- "solve.Quadra"
    return(ans)
}

print.solve.Quadra <- function(obj) {
    if (obj$what == "min")
        mes <- "\nThe polynomial has a minimum at " else mes <- "\nThe polynomial has a m
    cat(mes, "x = ", obj$x, "\n")
    cat("At that point, f(x) = ", obj$f, "\n\n")
}
```

Lets try them:

```
> solve(P1)

The polynomial has a minimum at  x =  1
At that point, f(x) =  8

> solve(P2)

The polynomial has a maximum at  x =  0.25
At that point, f(x) =  10.25
```

Notice that I did not use the generic function solve() as it should be. If you look at help(solve), it says that it is a generic function for solving $Ax = b$ and the inputs are A and b. In the package numericalecon I created on RForge, I had to change the function name to solveP() (for solve polynomial) because we are not allowed to use existing generic functions with different inputs.

The following shows one nice thing we can do. We want to create a binary operator that will allow us to add two polynomials. First we need to create the function:

```
addQuadra <- function(Q1, Q2) {
    if (class(Q1) != "Quadra" | class(Q2) != "Quadra")
        stop("This operator can only be applied to\nobjects of class Quadra")
    a <- Q1$a + Q2$a
    b <- Q1$b + Q2$b
    c <- Q1$c + Q2$c
    Quadra(a, b, c)
}
```

Then we create the binary operator:

```
> "%+%" <- function(Q1,Q2) addQuadra(Q1,Q2)
```

We can then create a third polynomial which is the sum of the first two:

```
> P3 <- P1%+%P2
> solve(P3)

The polynomial has a maximum at  x =  -0.5
At that point, f(x) =  20.5

> zeros(P3)
```

```
Type of zeros:  Real and distinct

Zero[ 1 ] =  2.701562
Zero[ 2 ] =  -3.701562
```

I conclude this section with the following two methods. We'll discuss them in class if we have time.

```
plot.Quadra <- function(obj, from = NULL,
    to = NULL) {
    f <- function(x) obj$a * x^2 + obj$b * x + obj$c

    res <- solve(obj)

    if (is.null(from) | is.null(to)) {
        from <- res$x - 4
        to <- res$x + 4
    }
    if (res$what == "min") {
        d <- max(f(to), f(from)) - res$f
        mes <- paste("Min=(", round(res$x, 2), ", ",
            round(res$f, 2), ")", sep = "")
    }
    if (res$what == "max") {
        mes <- paste("Max=(", round(res$x, 2), ", ",
            round(res$f, 2), ")", sep = "")
        d <- res$f - min(f(to), f(from))
    }

    curve(f, from, to, xlab = "X", ylab = "f(X)")
    if (obj$b > 0 & obj$c > 0)
        title(substitute(f(X) == a * X^2 + b * X +
            c, obj))
    if (obj$b < 0 & obj$c > 0)
        title(substitute(f(X) == a * X^2 - b2 * X +
            c, c(obj, b2 = -obj$b)))
    if (obj$b > 0 & obj$c < 0)
        title(substitute(f(X) == a * X^2 + b * X -
            c2, c(obj, c2 = -obj$c)))
    if (obj$b == 0 & obj$c > 0)
        title(substitute(f(X) == a * X^2 + c, obj))
```

```
if (obj$b == 0 & obj$c < 0)
    title(substitute(f(X) == a * X^2 - c2, c(obj,
        c2 = -obj$c)))
if (obj$c == 0 & obj$b > 0)
    title(substitute(f(X) == a * X^2 + b * x, obj))
if (obj$c == 0 & obj$b < 0)
    title(substitute(f(X) == a * X^2 - b2 * x,
        c(obj, b2 = -obj$b)))

points(res$x, res$f, col = 3, cex = 0.8, pch = 21,
    bg = 3)
if (res$what == "min") {
    text(res$x, res$f + 0.2 * d, mes)
    arrows(res$x, res$f + 0.18 * d, res$x, res$f)
} else {
    text(res$x, res$f - 0.2 * d, mes)
    arrows(res$x, res$f - 0.18 * d, res$x, res$f)
}

z <- zeros(obj)
if (attr(z, "type") == "Real and distinct") {
    points(z[1], 0, col = 2, cex = 0.8, pch = 21,
        bg = 2)
    points(z[2], 0, col = 2, cex = 0.8, pch = 21,
        bg = 2)
    r1 <- paste(round(min(z), 2))
    r2 <- paste(round(max(z), 2))
    if (res$what == "min") {
        if (abs(res$f) > d/2)
            d2 <- -d else d2 <- d
        text(min(z), 0.25 * d2, r1)
        text(max(z), 0.25 * d2, r2)
        arrows(min(z), 0.23 * d2, min(z), 0)
        arrows(max(z), 0.23 * d2, max(z), 0)
    } else {
        if (abs(res$f) > d/2)
            d2 <- -d else d2 <- d
        text(min(z), -0.25 * d2, r1)
        text(max(z), -0.25 * d2, r2)
        arrows(min(z), -0.23 * d2, min(z), 0)
```

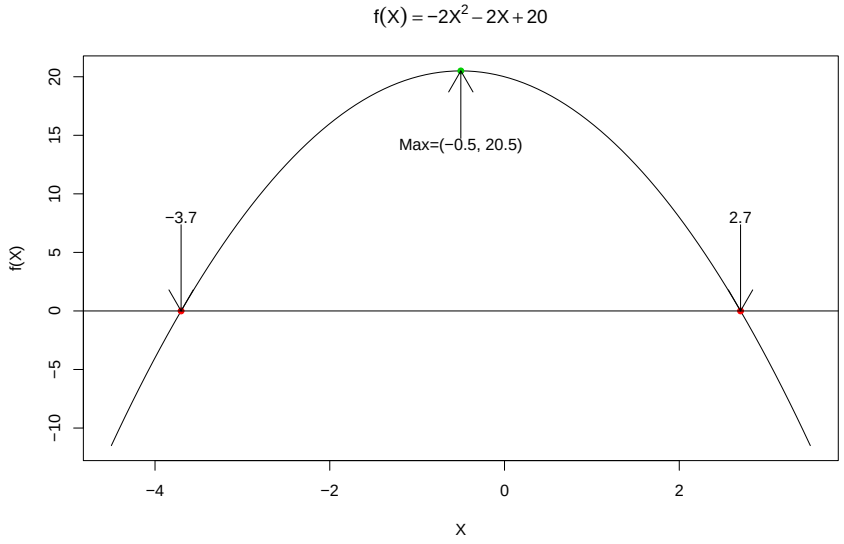
```
            arrows(max(z), -0.23 * d2, max(z), 0)
        }
    }
    if (attr(z, "type") != "Complexe" | attr(z, "type") ==
        "Real and identical")
        abline(h = 0)
}


summary.Quadra <- function(obj) {
    print(obj)
    print(zeros(obj))
    print(solve(obj))
}
```

Let us test them:

```
> summary(P1)
```

```
Second order polynomial

F(x) = Ax^2 + Bx + C
with: A= 2 , B= -4 , C= 10


Type of zeros:  Complexe

Zero[ 1 ] =  1-2i
Zero[ 2 ] =  1+2i


The polynomial has a minimum at  x =  1
At that point, f(x) =  8
```

```
> plot(P3)
```



Notice that the whole exercise that we just went through is meant to help you understand how to program. Of course, unless you are building your own package that will be used by other users, you don't really need to create a print method for every new object you create to make it look nice. However, when I program, I try as much as I can to take advantage of this object-oriented structure. For example, when I create a function to estimate a model, when it is possible, I try to keep the same structure as "lm" or "gmm" objects so that I can use for example the summary method or plot method that are already defined for these objects.

As another example, I presently work on a project in which I have to play with many macroeconomic series from many countries. I was not satisfied with the existing objects ("vector", "ts", "timeSeries", ...), so I created a object of class "macroData". Each object has an attribute "Country", "trend", "Interest rate" (because we have many possibilities for each), the plot method has many more options and the summary method returns some important moments that we often use to evaluate the performance of different models. All my estimation procedures are then based on that type of objects. When I simulate data, I create an object of the same class but with the attribute "country" being equal to "simulated". When we plan to work on a project for some time, it makes a lot of sense to use that approach.

Exercise 1.8. *You work for the Bank of Canada you are asked to create programs that will allow the economists to quickly simulate their models and, based on the results, make decisions related to the monetary policy. Try to think about a good structure for your set of programs. You can create new objects and methods. To make it clear, name each object you create, describe their structure and explain what the associated methods do.*

Exercise 1.9. *In the last exercise of the chapter, you are ask to construct a pseudo microeconomic package for solving the consumer problem. You will create a consumer objects and solve(), print(), plot() and any other methods. You are free to build you package the way you like it. The best package will be put on RForge so that it can be improved by the members (us). We'll talk about it in class.*

1.4 Programming efficiently

In the last section, we have seen how to be organized. Being organized is important, but we also need to write functions that do not take forever to compute our results. In this section we will learn few tips to write efficient functions. The term "efficiency" refers to the computational speed. In many cases, it won't make much difference whether your function is efficient or not. Why should we worry if it takes 1 second instead of .5 second? But if you learn immediately to be efficient for easy tasks, it will become natural to do it when you will need to solve more computationally demanding problems.

1.4.1 Loops versus matrix operations

In this section, we consider loops because they are the main source of inefficiency among new programers. To see that, we consider the following example. Suppose we want to write a function that sums the elements of a matrix, A (we suppose that there exists no such function in R). The first thing that comes to our mind is to write a loop that sums each element one at the time. The following function assumes that the input A is a matrix (not a vector):

```
mySum <- function(A) {
    S <- 0
    for (i in 1:ncol(A)) {
        for (j in 1:nrow(A)) S <- S + A[i, j]
    }
    return(S)
}
```

The function system.time() reports how much time was required to execute a certain task. Of course, the result depends on the computer. This document was produced on a computer equipped with an Intel i7-2600 at 3.4GHz CPU with 8 MB's of RAM. You can only obtain similar results if you have a comparable machine. The elapsed time also depends on other factors. In fact, depending on what other tasks are performed by your computer, system.time() may produce different result. In order to have a precise idea, we often execute the task several times and take the average. But we won't do it because we just want to have an approximated time.

In order to measure the performance of our function, we first create a $3,000 \times 3,000$ matrix randomly:

```
> set.seed(555)
> A <- matrix(rnorm(3000^2),ncol=3000)
> T1 <- system.time(SA <- mySum(A))
> T1

   user  system elapsed
  5.628   0.000   5.650
```

You will say that 6 seconds is not that bad if we consider that we are summing 9 million numbers. But suppose you write a function in which you have to compute that sum several times. Suppose also that you need to call the function several times. In that case, that small 6 seconds can quickly become several minutes. A loop in R, or in any high level language such as Matlab, STATA or Gauss, should be avoided in general. In lower level languages like C or C++, loops are much more efficient. The R function sum(), for example, is just a loop like the one we perform in our function mySum(), but written in C. The reason why loops in C are more efficient than loops in R requires to understand how computer works and is beyond the scope of this course. We can compare the efficiency of sum() by applying it to the same matrix A:

```
> T2 <- system.time(SA2 <- sum(A))
> T2

   user  system elapsed
  0.008   0.000   0.008
```

In our example, the sum() is about 706 times faster than mySum() and we can see that they both produce the same answer:

```
> SA

[1] 3012.563

> SA2

[1] 3012.563
```

The first general rule is therefore to use R function when it is possible and avoid using loops. Sometimes, it requires to do a little search on the Internet or using the R help tools to find out which function performs what you want to do. For example,

suppose you want to apply a moving average on a time series to remove high frequency fluctuations. Suppose the moving average is the following:

$$X_t = \frac{1}{3}Y_{t-1} + \frac{1}{3}Y_t + \frac{1}{3}Y_{t+1},$$

with $X_1 = Y_1$ and $X_n = Y_n$. Here X_t is the smoothed version of the series Y_t. At first, we may think that using a loop is unavoidable. Here is how we would proceed with a loop (notice that we loose two observations):

```
myMA <- function(y) {
    n <- length(y)
    x <- rep(0, n)
    x[1] <- y[1]
    x[n] <- x[n]
    for (i in 2:(n - 1)) x[i] <- (y[(i - 1)] + y[i] +
        y[(i + 1)])/3
    x <- as.ts(x)
    attr(x, "tsp") <- attr(y, "tsp")
    return(x)
}
```

However, this can be done using the function kernapply(). This function requires us to provide the weights, and the weights must be in an object of class "tskernel". The latter can easily be created with the function kernel(). For our example, we create the weights as follows:

```
> w <- kernel("daniell",m=1)
> w

Daniell(1)
coef[-1] = 0.3333
coef[ 0] = 0.3333
coef[ 1] = 0.3333
```

The following function produce the same result as myMA() but without using a loop:

```
myMA2 <- function(y) {
    n <- length(y)
    w <- kernel("daniell", m = 1)
    x <- kernapply(y, w)
    x <- as.ts(c(y[1], x, y[n]))
    attr(x, "tsp") <- attr(y, "tsp")
    return(x)
}
```

We can compare the relative performance of the two function using a simulated AR(1):

```
> y <- arima.sim(n=3000,model=list(ar=.9))
> T1 <- system.time(myMA(y))
> T2 <- system.time(myMA2(y))
> T1

   user  system elapsed
   0.08    0.00    0.08

> T2

   user  system elapsed
  0.004   0.000   0.001
```

Therefore, myMA2() is about 80 times faster than myMA(). Again, you will say that 0.08 second is not that bad. But, suppose your function has to be called hundreds of times. For example, some estimation procedures require the data to be smoothed before computing the objective function that we need to minimize. In that case, the optimizer calls the function several times to evaluate its value and to compute numerical derivatives. Then, improving the efficiency of the function will make a difference.

In other cases, relying on matrix algebra may be the solution to avoid loops. However, it sometimes requires some thinking and good understanding of matrix algebra. For example, we can show that the moving average of a series is just a matrix operation. In fact, the above moving average can be written as $X = AY$, with

$$A = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1/3 & 1/3 & 1/3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1/3 & 1/3 & 1/3 & 0 & 0 & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & 0 & 0 & 1/3 & 1/3 & 1/3 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1/3 & 1/3 & 1/3 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}$$

Exercise 1.10. *Construct the function that computes the moving average using the matrix approach and compare its performance with myMA() and myMA2(). Verify that they all produce the same result. The difficulty here is to find an efficient way to compute the matrix A. You do not want to create it using a loop.*

Exercise 1.11. *Write a function that simulates an AR(1) process. And AR(1) process is defined as:*

$$x_t = \rho x_{t-1} + \varepsilon_t$$

with, for the purpose of the simulation, $x_0 = 0$. We suppose that $\varepsilon_t \sim N(0, 1)$. The function must have as arguments the value of ρ, the sample size and the seed for generating ε_t. Call these arguments r, n and s respectively. The returned series must also be of class "ts". Usually, we create more observations than what is necessary and we drop the extra observations at the beginning of the series. It reduces the impact of the initial value (here $x_0 = 0$). Your function must produce $(n + 100)$ observations and return the last n.

a) Write the function using a loop.

b) Write the same function without loop (Hint: look at the function filter())

c) Compare the performance and verify that they both produce the same result (you will have to set the same seed before calling the functions if you want to compare the values).

In the moving average example using matrix form, we are required to create an $n \times n$ matrix. This matrix needs to be stored in memory, which could be a problem on certain computer if n is large and the size of the RAM is not big enough. When all the RAM is used, the CPU starts using SWAP memory. The SWAP memory uses space on your hard disk and is much slower than the RAM. When writing a function using matrices, you have to be aware of that problem. In some cases, loops, which avoid storing big matrices, may be more efficient. But this is less and and less of a problem with the computers that we have.

Beside the memory problem, we have to be careful about the general rule of using matrices instead of loops. You probably have noticed in Exercise 1.10 that the loop was more efficient than the matrix version of the moving average function. So, what is the problem? In fact, there are two big operations: the construction of A and the multiplication Ay. Beside the construction of A, which is itself a long process, there are too many useless operations that we perform. Each x_t is the result of the sum of n elements and each element is the product of 2 numbers. Therefore, there is a total of $2n$ operations per x_t or $2n^2$ operations for the whole vector. The problem is that most elements are zeros. We only need to do 6 operations per x_t. Counting the number of operations is also important when choosing a good method. It does not mean that we have to rely on loops. It only means that we have to find another vector/matrix approach. In the following function, we use a vector approach without using an $n \times n$ matrix:

```
myMA3 <- function(y) {
    n <- length(y)
    x <- (y[-c(n - 1, n)] + y[-c(1, n)] + y[-c(1, 2)])/3
    x <- ts(c(y[1], x, y[n]))
```

```
    attr(x, "tsp") <- attr(y, "tsp")
    return(x)
}
```

```
> system.time(myMA3(y))

   user  system elapsed
  0.000   0.000   0.001
```

It is even faster then myMA2(). We therefore modify the general rule to

Suggested Rule 1. *Avoid loops if possible and replace them with vector of matrix operations that minimize the number of operations. Constructing big matrices should also be avoided.*

Before going to the next section, you have to be aware that there are also built-in functions that are more efficient than others. For example, is you want to compute $A'B$, there are to ways to it in R: using the binary operator "%*%" with the transpose function t() or the crossprod() function. We can compare their relative efficiency using two 2000×2000 matrices:

```
> A <- matrix(rnorm(4e6,2000,2000))
> B <- matrix(rnorm(4e6,2000,2000))
> T1 <- system.time(t(A)%*%B)
> T2 <- system.time(crossprod(A,B))
> T1

   user  system elapsed
  0.044   0.000   0.037

> T2

   user  system elapsed
  0.012   0.000   0.006
```

Therefore, crossprod() is 6 times faster. Of course, we cannot enumerate all possible functions and discuss their relative efficiency. You can only learn that by experimenting them by yourself. User lists is also a good source of information.

Exercise 1.12. *Some covariance matrix are defined as*

$$V = (G'WG)^{-1}$$

where G is $n \times q$ and W is an $n \times n$ diagonal matrix with the i^{th} diagonal element being the squared residual ε_i^2.

a) Construct a function that computes the above operation with the argument of the function being the matrix G and the vector of residuals e. In your function, compute V exactly as it is written above.

b) Do the same, but without constructing the $n \times n$ matrix W.

c) Compare the relative efficiency of the two functions. To do so, generate a $n \times q$ matrix G and $n \times 1$ vector e randomly, with $n = 5000$ and $q = 20$.

1.4.2 Parallel programming

In this section, we briefly discuss some methods to improve efficiency by taking advantage of the fact that computers are now equipped with multiple core processors. For example, the Intel i7-2600 processor allows to send jobs to 8 cores simultaneously. If you are lucky enough to work on a computer equipped with a Tesla GPU 2075 (graphical processor unit), you can send up to 448 jobs simultaneously to your processor. It is like having 448 computers working simultaneously. Parallel programing is a way of write your program so that jobs are sent in blocks. For example, if you have 8 cores, and want to run a simulation of 1000 iterations, you can run a loop of size equal to 125. In each loop, you send a block of 8 jobs to the 8 cores. These jobs are then run simultaneously. You can then increase the speed of the simulation substantially.

Lets consider the following simulation. You want to measure the mean and variance of $\bar{x}$, where $x_i \sim N(3, 4)$. To do so, you generate 5000 samples of size equals to 500 and save each $\bar{x}$ in a vector. We know that the true mean and variance should be 3 and 4/500=0.008 respectively. The following function will do the job:

```
simXbar <- function(n, iter) {
    xbar <- vector()
    for (i in 1:iter) {
        x <- rnorm(n, mean = 3, sd = 2)
        xbar[i] <- mean(x)
    }
    return(list(mu = mean(xbar), sigma = var(xbar)))
}
```

We can then run the simulation:

```
> T1 <- system.time(sim1 <- simXbar(500,5000))
> T1

   user  system elapsed
  0.264   0.008   0.270
```

```
> sim1

$mu
[1] 2.998812

$sigma
[1] 0.008070684
```

The result is not too far from the theoretical one. The simulation is also quite fast because the task of computing the mean and variance is almost instantaneous. However, we can still improve it by writing our function differently. Here we only consider the parallel programing tool mclapply() from the package "multicore" of [Urbanek 2011]. There exists other packages in R that work as well but they are similar. mclapply() is the parallel version of lapply(). We will start by studying how lapply() works. Specifically, the function is lapply(X,FUN,...), where X is a list or a vector and FUN is a function. It runs FUN on each element of X and returns the values as a list. For example, if we want to compute the mean of 5000 500×1 vectors of $N(3, 4)$, we can proceed as follows:

```
> x <- lapply(rep(500,5000),rnorm,mean=3,sd=2)
> xbar <- lapply(x,mean)
```

In order to compute the mean and the variance of *xbar*, we first need to convert it to a vector because mean() does not work on lists. There are two ways to do it:

```
> xbarVec1 <- simplify2array(xbar)
> xbarVec2 <- unlist(xbar)
> cbind(mean(xbarVec1),var(xbarVec1))

         [,1]        [,2]
[1,] 3.002372 0.008128158

> cbind(mean(xbarVec2),var(xbarVec2))

         [,1]        [,2]
[1,] 3.002372 0.008128158
```

The first is preferred if each element are vectors or matrices. Another possibility would have been to use sapply() to produce xbar:

```
> xbar <- sapply(x,mean)
> cbind(mean(xbar),var(xbar))
```

```
         [,1]        [,2]
[1,] 3.002372 0.008128158
```

The function is like lapply() but it automatically runs simplify2array() after to convert the list to a vector. However, we do not want to use it here because there is no multi-core version of it. Any function of that type (lapply(), sapply(), vapply()) is just a more compact way to do a loop. Everything is computed sequentially. We first rewrite the simXbar() function using lapply() and measure its performance.

```
simXbar <- function(n, iter) {
    x <- lapply(rep(n, iter), rnorm, mean = 3, sd = 2)
    xbar <- lapply(x, mean)
    xbar <- simplify2array(xbar)
    return(list(mu = mean(xbar), sigma = var(xbar)))
}
```

```
> T2 <- system.time(sim2 <- simXbar(500,5000))
> T2

   user  system elapsed
  0.224   0.000   0.226

> sim2

$mu
[1] 3.001334

$sigma
[1] 0.007891793
```

The first version of the function took 0.27 second, which is not significantly different from the second version. It just confirms that lapply() is like a loop. mclapply() is like lapply() but it sends jobs simultaneously to several cores. The function has many options. The option mc.cores is the number of cores you want to send the jobs to. By default, it is the maximum number of cores that you have. The options mc.set.seed is a logical variable. If set to TRUE (the default) a different seed is used for each job. That's the value to choose if we want a different random vector x. In most of the time, we can use mclapply() like lapply() without modifying the options. The following function compute *xbar* using mclapply():

```
mcsimXbar <- function(n, iter) {
    xbar <- mclapply(rep(n, iter), function(n) mean(rnorm(n,
```

```
        mean = 3, sd = 2)))
    xbar <- simplify2array(xbar)
    return(list(mu = mean(xbar), sigma = var(xbar)))
}
```

```
> library(multicore)
> T3 <- system.time(mcsim <-mcsimXbar(500,5000))
> T3
```

```
   user  system elapsed
  0.340   0.092   0.100
```

```
> mcsim
```

```
$mu
[1] 3.001831


$sigma
[1] 0.007935995
```

Here we created a function inside the mclapply() that generates the vector x and computes its mean. The mcsimXbar() is 2 times faster than the simXbar() that uses lapply(). Of course, the relative efficiency will depend on your type of processor. Notice also that the document is created with Sweave which builds the document and execute the R codes simultaneously. The result is therefore different when the functions are compared in R directly. In R directly, McsimXbar() is 4.5 times faster than simXbar() (on a computer with an Intel i7-2600 processor running on Linux).

Exercise 1.13. *Show that if you write the mcsimXbar() function as the simXbar(), but with mclapply() instead of lapply(), you don't observe the same improvement.*

The previous exercise, shows that using mclapply() does not necessarily improve the performance. Therefore, we may have to try different approaches before being satisfied.

Exercise 1.14. *You want to simulate the following process:*

$$Y_i = 10 + 5X_i + \varepsilon_i$$

$$\varepsilon_i \sim N(0, 4),$$

5000 times, where the sample size is 500 and $X_i \sim N(4, 4)$ and fixed in repeated samples. In other words, you simulate X_i only once. At each iteration, you want to compute the OLS estimate of the coefficients and report at the end the sample mean and covariance matrix of the vector of estimates. Use the function lm() to obtain the OLS estimates.

1. *Do it using a loop*
2. *Find a way to improve the efficiency of the simulation by using mclapply()*

Chapter 2

Floating points arithmetic

Contents

This Chapter is only an introduction to floating-points arithmetic. The goal is only to make you realize that most numbers that we use in our numerical projects are only approximations. Our results are therefore subject to rounding errors that may accumulate if we are not careful. If you want a complete and detailed presentation of floating-point numbers, see [Goldberg 1991](http://neo.dmcs.p.lodz.pl/ak/IEEE754_article.pdf). As an example, the number 0.1 cannot be represented exactly by computers. We will see why in next section. We can verify that by the following small experiment:

```
> .1+.1+.1==.3
```

```
[1] FALSE
```

R tells us that 0.1+0.1+0.1 is not equal to 0.3. However, the difference is small as we can see:

```
> (.1+.1+.1)-.3
```

```
[1] 5.551115e-17
```

However, when we have to deal with thousands of operations, the error may become more substantial. In the next section, we explain briefly how a computer store numbers and why it cannot represent exactly simple numbers such as 0.1.

2.1 What is a floating-point number

A floating-point number is a real number that can be represented exactly by a computer. First, computers store information in binary format (0's and 1's). In order to have

software that are portable from one computer or operating system to another, we need a stable way or dealing with floating-point numbers. Different results obtain on different computers is enough to make a program crash. The most common standard used in computers is the IEEE 754 (Institute of Electrical and Electronics Engineers). It is a binary standard which means that numbers are represented in base 2. One of the reasons for using the base 2 is related to the tightness of the relative error that comes from the approximation of real numbers by floating-point numbers. Unless we want to build computers, we don't need to know more about the advantage of using that standard. In binary format, integers are exactly represented by computers:

$$\begin{aligned}
1 &= 1(2^0) =_2 1 \\
2 &= 1(2^1) + 0(2^0) =_2 10 \\
3 &= 1(2^1) + 1(2^0) =_2 11 \\
4 &= 1(2^2) + 0(2^1) + 0(2^0) =_2 100 \\
&\vdots =_2 \vdots \\
N &= \sum_{i=0}^{p} d_i(2^i) =_2 d_p d_{p-1} \cdots d_0
\end{aligned}$$

where $=_2$ means "equals in base 2" and d_i's are either 0 or 1. Of course, the number of bits restricts the number of integers that can be exactly represented. In general, a real floating-point number, x, is represented as follows:

$$x = \pm \left[d_0 + d_1(2^{-1}) + d_2(2^{-2}) + \cdots + d_{p-1}(2^{-(p-1)}) \right] 2^e,$$

or simply

$$x = \pm \left[d_0.d_1 d_2 \cdots d_{p-1} \right]_2 2^e,$$

where $[]_2$ means that the inside of the brackets is expressed in base 2, p is called the precision (or the number of digits) and e the exponent. The term $d_0.d_1...d_{p-1}$ is called the significant. For example:

$$4.5 = 2^2 + 2^{-1} = (1 + 2^{-3})2^2 = [1.001]_2 \times 2^2,$$

which implies that $d_0 = 1$, $d_3 = 1$ (or a significant equals to 1.001), $e = 2$ (or 10 in base 2) and all other d_i are equal to zero. Of course there are more than one ways to represent 4.5. Here is another one:

$$4.5 = (2^{-1} + 2^{-4})2^3,$$

which implies $d_1 = d_4 = 1$, $e = 3$ and all other d_i's equal to zero. However, the number is uniquely represented if we impose the normalization $d_0 = 1$. Furthermore,

the normalization saves us a bit because there is no need to store d_0 since it is always 1. The bits are allocated between the storage of the exponent, the $(p-1)$ d_i's and the sign (e.g. 1 if + and 0 if -). The exponent is store as an unsigned integer, which implies that the number of different exponents is $(e_{max} - e_{min})$. Therefore, the number of bits required to store a floating-point number is approximately:

$$Bits = \log_2 (e_{max} - e_{min}) + (p-1) + 1$$

In R the allocation is stored in the variable .Machine:

```
> print(p <- .Machine$double.digits)

[1] 53

> print(emax <- .Machine$double.max.exp)

[1] 1024

> print(emin <- .Machine$double.min.exp)

[1] -1022

> bits <- log(emax-emin,2)+(p-1)+1
> bits

[1] 63.99859
```

It gives 1 bit for the sign, 11 for the exponent and 52 for the significant. In fact, R follows the IEEE-754 standard for double precision floating-point numbers. Other important numbers are stored in .Machine. The first is the machine-epsilon (ε). It is usually defined as $\beta^{-p+1}/2$, where β is the base. It is the smallest positive floating-point number, x, such that $(1+x) \neq 1$:

```
> print(eps<-.Machine$double.eps)

[1] 2.220446e-16

> 1+eps==1

[1] FALSE
```

It is not the smallest number, which is rather equal to $2^{e_{min}}$, but the highest relative error that comes from approximating a real numbers by its nearest floating-point number. The accuracy of algorithms is often measured in terms of the machine-epsilon.

A bad algorithms may produce errors of size $n\varepsilon$ with $n >> 1$. We therefore want to choose algorithms that minimizes n. In the example we showed at the beginning of the chapter, R returned FALSE to the question: $0.1 + 0.1 + 0.1 = 0.3$? But, since 0.1 does not have an exact floating-point representation there is a rounding error that accumulates when summing them. If we want to compare the numbers we need to take into account these rounding errors. The function all.equal() compares numbers with a certain level of tolerance. So, they don't necessarily have to be exactly equal. If we go back to are first example:

```
> .1+.1+.1==.3

[1] FALSE

> all.equal(.1+.1+.1,.3,tolerance=eps)

[1] TRUE
```

The interpretation of the above result is that $(.1+.1+.1) \neq 0.3$ only because of rounding errors. The maximum and minimum floating-point numbers are:

```
> .Machine$double.xmax

[1] 1.797693e+308

> .Machine$double.xmin

[1] 2.225074e-308
```

Anything above the $xmax$ is considered to be equal to infinity an anything below $xmin$ is considered to be equal to 0:

```
> .Machine$double.xmax*2

[1] Inf
```

We conclude this section by looking at another important "number" that may appears when performing some operations. The "number" is NA or NaN, which means "Not a Number". It will result from operations that produced indeterminate results. It is not to be confused with operations that produce infinity. For example, $1/0 = \infty$ but $0/0 = NA$:

```
> 1/0

[1] Inf
```

```
> 0/0

[1] NaN
```

Here are other examples:

```
> Inf-Inf

[1] NaN

> log(-2)

[1] NaN

> sqrt(-1)

[1] NaN

> Inf/Inf

[1] NaN
```

Of course, we cannot compare NA numbers. NA, as it is called, is not a number. Therefore, we cannot use the logical operator "==" to verify if an operation produces an NA. In fact the result will also be an NA. There is a function in R that verify that:

```
> (0/0) == NA

[1] NA

> is.na(0/0)

[1] TRUE
```

However, we can use logical operators with infinity:

```
> (1/0)==Inf

[1] TRUE

> 1e400==Inf

[1] TRUE

> 1e200<Inf

[1] TRUE
```

2.2 Rounding errors

This section briefly covers the issue of rounding errors created by numerical computations. Again, we cannot cover it in details. In fact, it may be quite complicated to measure rounding errors from certain algorithms. But knowing how they are created may help us developing good programming habits. It will also help justifying some methods that will be presented in the next chapters.

In order to illustrate the problem related to rounding errors, consider the case of floating-point numbers represented in base 10 with the number of digits p equals to 3 (remember that the number of digits after the point is equal to $(p-1)$). In that case, π is approximated by the floating-point number 3.14×10^0. Suppose the true value is 3.1416. The term "last place" refers to the last decimal given by the floating-point representation (or 10^{-p+1}). The error is $0.0016 = 0.16 \times 10^{-2}$ or $0.16 ulps$ (units of the last place). An error smaller than $1 ulps$ means that the last digit is not contaminated. Error from approximating a real number is always less than $1 ulps$. However, we often get errors greater than $1 ulps$ when results come from mathematical operations. As an example, suppose the result of a computation is 3.12×10^0 and that the true answer is 3.14×10^0. The error is then equal to $2 ulps$. In the IEEE standard, where $p = 53$, the precision is up to about the 16^{th} decimal (the 53^{th} digit in base 2 refers to the $16th$ digit in base 10).

The error measure in *ulps* is affected by multiplications. Consider the approximated π above. Since it is represented by 3.14×10^0, if we multiply it by 2, the result will become 6.28×10^0. The true value is $2\pi = 6.2832$ which implies an error of $0.32 ulps$. Another measure of rounding error is the relative error defined as the error divided by the true value and it is often expressed in term of the machine-epsilon. The relative error for π is $0.0016/3.1416 = 0.0005$ and the one for the computation of 2π is $0.0032/6.2832 = 0.0005$. It is therefore unaffected by the operation. The relative error in terms of the machine-epsilon is $[error/(TRUE * \varepsilon)]\varepsilon$. In our example, the machine-epsilon is $10^{-2}/2 = 0.005$. The relative error for π or 2π is therefore 0.1ε.

There is a link between the error and the number of contaminated digits. If the error is n *ulps* the number of contaminated digits is $\log_\beta n$, if the relative error is $n\varepsilon$ the number of contaminated digits is $\log_\beta n$. Suppose we want to compute $(x - y)$. Suppose also that the base is 10, p=3 and the computer only keeps 2 decimal when performing operations. In the first case, $y = 2.15 \times 10^{12}$ and $x = 1,25 \times 10^{-5}$. The computer rewrites the numbers using the same exponent and keep only 2 digits:

$$y - x = 2.15 \times 10^{12} - 0.00 \times 10^{12} = 2.15 \times 10^{12}$$

The error is very small and no digits are contaminated. Consider the second case for which $y = 10.1$ and $x = 9.93$. Using the same rule, we obtain:

$$y - x = 1.01 \times 10^1 - 0.99 \times 10^1 = 2.00 \times 10^{-1}$$

The error is $30ulps$ which implies a relative error of $[0.03/(0.2 * 0.005)]\varepsilon = 30\varepsilon$. $\log_{10} 30 > 1$ meaning that the two digits are contaminated. The error from the last subtraction is called "Catastrophic cancellation", and it arises when x and y are very close to each other. Of course, we would not have obtained the same error with double precision floating-point numbers ($p = 53$ and $\beta = 2$). This example is meant to easily show what happens when we subtract numbers of similar values. In reality, computers are smarter than that. They usually have what we call "Guard Digits" which are extra digits used during floating-point operations. In our example, one Guard Digit would have been enough to have no error. However, "Catastrophic cancellation" exists even in double precision systems. The error is small in absolute term but quite big if we compare it with the error from other floating-point operations. To have an idea in double precision computations, consider the following example:

```
> x <- 332.2234
> y <- 332.223395
> s <- x-y
> error <- s-0.000005
> error

[1] 4.421963e-14
```

The error is therefore approximately $442ulps$ (if we consider that p=53 corresponds to the 16^{th} decimals). However, what we just computed is not really the error coming from $(y - x)$. In fact, rounding errors is hard to measure with a computer because we are not really subtracting the true solution (0.000005 does not have an exact floating-point representation). Catastrophic cancellation occurs in fact when we subtract numbers who are subject to rounding errors. In other words, numbers that come from floating-point operations (ex. $y^2 - x^2$). In that case, the rounding error is greater than the one from approximating a real number. If the numbers are close, the subtraction eliminates the good digits and we are left with the bad ones. Lets see what happens if y and x are not close:

```
> x <- 2.57
> y <- 0.13
> s <- x-y
> error <- s-2.44
> error

[1] 0
```

We don't really care in economics about an error at the 14^{th} decimal. We don't build bridges. Therefore, we won't worry when the number of floating-point operations is

small. But, these small errors can become huge if the operations are repeated hundreds or thousands of times. For example, when we work with big systems of matrices, solving the system requires many sums, products, subtractions and divisions. If we are not careful about how to minimize rounding errors, we may end up with a wrong solution. Even if we do use some accurate algorithms, there exists iterative procedures to reduce the rounding error further. We will cover that in the next section. Consider only the operation to compute the OLS estimate:

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

Suppose the sample size is 1000 and the number of coefficients is 10. Then, we need to compute 1000 sums and multiplications for each of the 100 elements of $(X'X)$ and each of the 10 elements of $(X'Y)$. But, that's not the end. We now have to invert $(X'X)$ (we don't really do that, as we'll see in the next chapter) and multiply the inverse by (X'Y). Fortunately, there exists a method that is less sensitive to rounding errors. We don't even have to compute $X'X$. We'll cover that in the next chapter.

The problem with floating-point arithmetic is that a method can be accurate most of the time but very bad in some cases, when our variables take some particular values. And because there is no error message that appears, we think that everything is fine. The purpose of this chapter is only to make sure that you are aware of that. It will also justify many numerical approaches that we will cover throughout the course.

We conclude this chapter with two examples. Suppose we want to compute the sum of the element of a vector. If the elements of the vector come from floating-point operations, the usual sum, $\sum_{i=1}^{n} x_i$, could produce large rounding errors. It would be even worse if some successive x_i's were close to each other in absolute value with different signs, because we would face multiple catastrophic cancellations. The first solution is to order the vector and to sum the element from the smallest to the largest. Adding a small number to a large number may make us loose the last digits of the small one. That's why sorting may improve the accuracy of the sum. The second is to use the following algorithm:

Exercise 2.1. *Write the R function mySum(x) of the Algorithm 2.1. Create a* $100,000 \times 1$ *vector with each element equals to 0.1. Compare the accuracy of your function with the R function sum().*

Algorithm 2.1 may seem to be an obscure way to improve accuracy. It is in fact quite hard to come up with such algorithms. Another way to minimize rounding errors is to minimize the number of operations when it is necessary. since it reduces the accumulation of errors. In fact, it kills two birds with the same stone because it also makes the algorithm faster. Suppose for example that we want to compute the following

Algorithm 2.1 Kahan Summation Formula

S=X[1]
C=0
for $i = 2 \rightarrow n$ **do**
  $Y = X[i] - C$
  $T = S + Y$
  $C = (T - S) - Y$
  $S = T$
end for
Return S

polynomial (see [Judd 1998] page 34):

$$S = \sum_{i=0}^{n} a_i x^i$$

The direct approach requires n multiplications, n additions and $(n-1)$ exponentiations for a total of $(3n-1)$ operations. By rewriting the sum as (for $n = 4$):

$$S = a_0 + x(a_1 + x(a_2 + x(a_3 + xa_4))),$$

we still have n additions and n multiplications but no exponentiation. The algorithm is called the Horner's method:

Algorithm 2.2 Horner Method

$\{A$ is $(n+1) \times 1$ vector of $a_i\}$
$\{x$ is a scalar$\}$
$S = A[n+1]$
for $i = n \rightarrow 1$ **do**
  $S = A[i] + S * x$
end for
Return S

Exercise 2.2. *[Judd 1998] Exercise 8 of Chapter 2*

a) Write a function to compute a n^{th} order polynomial using the Horner's method.

b) Modify the Horner's method to compute:

$$S = \sum_{i=0}^{n} \sum_{j=0}^{n} a_{ij} x^i y^j$$

c) Modify the Horner's method to compute:

$$S = \sum_{i=0}^{n} \sum_{j=0}^{n} \sum_{l=0}^{n} a_{ijl} x^i y^j z^l$$

Chapter 3

Linear Equations and Iterative Methods

Contents

3.1 Linear algebra

Suppose we want to compute the following problem:

$$Ax = y$$

The way we learn how to solve this system in basic textbooks is by inverting A and multiplying y by the inverse. In other words, the solution is:

$$x = A^{-1}y$$

This solution is right mathematically ans has a nice analytical form, but is not recommended numerically. Suppose you want to compute the inverse using textbook definition. The number of operations to compute the determinant for an $n \times n$ matrix is $O(n!)$. We want to minimize the number of operations and also the number of catastrophic cancellations. The LU decomposition with pivoting is an algorithm developed for that purpose. Pivoting is done to avoid unstable operations and LU decomposition to reduce the number of operations. Consider the following case:

```
> A <- matrix(c(5,4,7,8,6,3,2,9,1),3,3)
> y <- c(2,4,6)
> A
```

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

The package "Matrix" includes many algorithms for matrices. Most of the functions produce S4-class objects with information that can only be extracted using the appropriate method. Here is how we obtain L and U (Notice that is is A=PLU, not LU. P is a pivoting matrix):

```
> library(Matrix)
> res <- lu(A)
> U <- expand(res)$U
> L <- expand(res)$L
> P <- expand(res)$P
> U

3 x 3 Matrix of class "dtrMatrix"
     [,1]     [,2]     [,3]
[1,] 7.000000 3.000000 1.000000
[2,]        . 5.857143 1.285714
[3,]        .        . 7.487805

> P

3 x 3 sparse Matrix of class "pMatrix"

[1,] . | .
[2,] . . |
[3,] | . .

> L

3 x 3 Matrix of class "dtrMatrix" (unitriangular)
     [,1]      [,2]      [,3]
[1,] 1.0000000         .         .
[2,] 0.7142857 1.0000000         .
[3,] 0.5714286 0.7317073 1.0000000
```

The matrix P tells us that the the first line of A is the second line of LU, the second is the third and the third is the first as we can see:

```
> L%*%U
```

```
3 x 3 Matrix of class "dgeMatrix"
     [,1] [,2] [,3]
[1,]    7    3    1
[2,]    5    8    2
[3,]    4    6    9

> P%*%L%*%U

3 x 3 Matrix of class "dgeMatrix"
     [,1] [,2] [,3]
[1,]    5    8    2
[2,]    4    6    9
[3,]    7    3    1
```

An algorithm to solve the linear model using LU is: (i) first solve Lz=y by recursive substitution, (ii) then solve Ux=z also be recursive substitution. For an $n \times n$ matrix, the LU decomposition requires $n^3/3$ floating point operations. The 2 back-substitution algorithms require $O(n^2)$ operations. For large n, solving a system using LU decomposition is therefore of order $n^3/3$ (n^2 becomes negligible). We can estimate the order of an algorithm. If we suppose that the time per operation is constant, the estimated time of an algorithm applied to a system of dimension equals to n can be written as:

$$t_n = Cn^{\alpha},$$

where C is a constant (for the LU, $\alpha = 3$). By applying the algorithm to different n, we can estimate α using the following regression model:

$$\log(t_n) = \alpha_0 + \alpha \log(n) + \varepsilon_n$$

In the following, I estimate the α for the LU decomposition and Figure 3.1 shows that the relationship is indeed linear.

```
> n <- c(500,1000,1500,2000,2500,3000)
> t <- vector()
> A <- list()
> for (i in 1:length(n))
+         A[[i]] <- matrix(rnorm(n[i]^2),n[i],n[i])
> for (i in 1:length(n))
+         t[i] <- system.time(lu(A[[i]]))[[3]]
> ln <- log(n)
> lt <- log(t)
> print(res<-lm(lt~ln))
```

```
> plot(lt,ln,type="l",main="Computational time: LU decomposition",
+                 xlab=expression(log(n)),ylab=expression(log(t[n])))
```

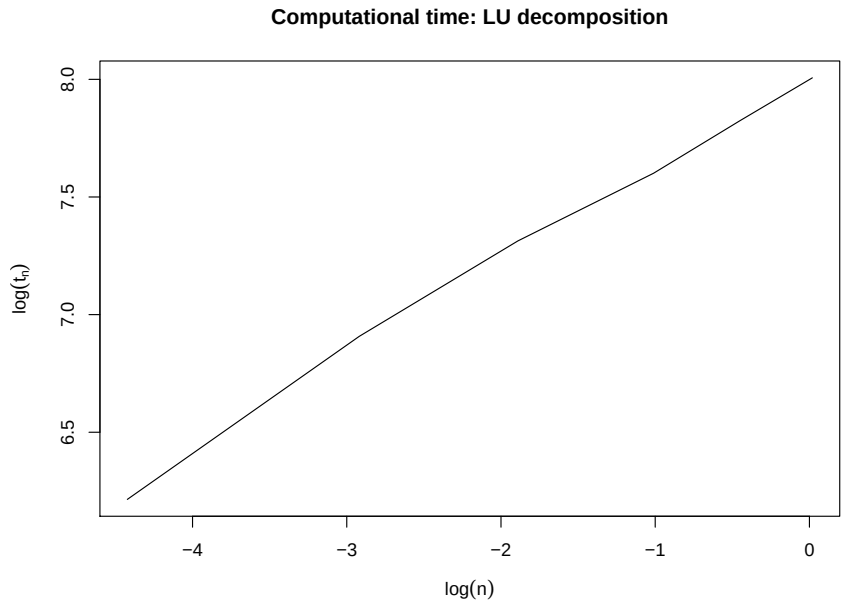


Figure 3.1: Estimated relationship between the dimension of a matrix and its LU decomposition

```
Call:
lm(formula = lt ~ ln)

Coefficients:
(Intercept)           ln
    -20.136        2.511
```

The estimated coefficient ($\hat{\alpha} = 2.51$), is not so far from its true value 3. Errors come from the small sample and the fact that time depends not only on oparations. Also, computational time may not be constant across operations. But it gives us a good idea. The constant term ($\hat{\alpha}$ =-20.14) is harder to interpret because it includes the time per operation and the factor of proportionality.

Exercise 3.1. *Suppose we want to solve $Ax = b$ using the following method: (i) invert A using solve(A), (ii) obtain the solution using $x = A^{-1}b$. If we suppose that the number of operation is of order $O(n^{\alpha})$, estimate α.*

When the matrix A is symmetric positive definite, there exist a more stable decomposition for which the number of operations is of order $n^3/6$ (half the number of operations of the LU). It is the Cholesky decomposition. It is a special case of the LU. The decomposition is $A = LL'$, where L is a lower triangular matrix. L' is therefore an upper triangular matrix like U. L is also called the square root of A. The function $chol()$ computes L':

```
> A <- matrix(c(5,4,7,8,6,3,2,9,1),3,3)
> A <- crossprod(A)
> A

     [,1] [,2] [,3]
[1,]   90   85   53
[2,]   85  109   73
[3,]   53   73   86

> chol(A)

         [,1]     [,2]     [,3]
[1,] 9.486833 8.959787 5.586691
[2,] 0.000000 5.359312 4.281230
[3,] 0.000000 0.000000 6.038208
```

This decomposition is useful when we work with covariance matrices. If for example the $n \times 1$ vector x is $\sim N(\mu, \Sigma)$, with $\Sigma = LL'$, x can be written as $x = \mu + Lz$, where $z \sim N(0, I)$. The generalized least square method (GLS) is based on the Cholesky decomposition: If $Var(\varepsilon) = \Sigma$ in $Y = X\beta + \varepsilon$, GSL is defined as the OLS applied on the following linear regression model:

$$[L^{-1}Y] = [L^{-1}X]\beta + [L^{-1}\varepsilon],$$

where again $\Sigma = LL'$.

The last decomposition is called the QR decomposition. It can be applied to any matrix, even if it is not square. Let A be an $n \times k$ matrix. The decomposition is $A = QR$, where Q is an $n \times k$ orthogonal matrix ($Q'Q = I$) and R is a $k \times k$ upper triangular matrix. The rank of R is equal to the rank of A. If A is singular, there will be zeros on the diagonal of R. The qr() function create an object of class "qr" from which Q and R can be extracted using qr.Q() and qr.R() respectively. Here is an example:

```
> A <- matrix(1:6,3,2)
> resqr <- qr(A)
> qr.Q(resqr)
```

```
           [,1]       [,2]
[1,] -0.2672612  0.8728716
[2,] -0.5345225  0.2182179
[3,] -0.8017837 -0.4364358
```

```
> qr.R(resqr)
```

```
          [,1]      [,2]
[1,] -3.741657 -8.552360
[2,]  0.000000  1.963961
```

There is a very useful result when it comes to compute the OLS estimate of $Y = X\beta+\varepsilon$. We can show that all we need is to solve $Y = X\beta$ using the QR decomposition. The problem to solve is $Y = QR\beta$, which implies $Q'Y = R\beta$. Since R is upper triangular, we can easily solve the problem using back substitutions. The analytical solution is $\hat{\beta} = R^{-1}Q'Y$. We can easily show that it is the OLS estimator $(X'X)^{-1}X'Y$, that the projection matrix is $P_x = QQ'$ and the residuals $(I - QQ')y$.

Exercise 3.2. *Write a function that computes the solution to $Ux = b$ where U is upper triangular. The function will be backSub(U,b). Make sure the function checks whether U is triangular of not. The solution must be done using the back substitutions. Loops may therefore be required in that case.*

Exercise 3.3. *Write the function myQrlm(Y,X), that returns the OLS estimators, the standard errors, the t-test and the p-values all in the same matrix with the appropriate names for the columns and the rows. You have to use the QR decomposition and the function you wrote in the previous exercise. You are not allowed to compute X'X, X'Y and to use the solve() function to compute inverses.*

In a problem in which we need to solve $f(x) = 0$, we want to measure the stability of the solution when the system is perturbed. In the linear system $Ax = b$, $f(x) = Ax - b$ and the solution is $x = A^{-1}b$. If b is subject to the rounding errors r, the solution to the perturbed system is $\tilde{x} = A^{-1}b + A^{-1}r$. The condition number is defined as:

$$Cond = \frac{\frac{\|x-\tilde{x}\|}{\|x\|}}{\frac{\|r\|}{\|b\|}} = \frac{\|A^{-1}r\|}{\|x\|}\frac{\|b\|}{\|r\|}$$

If we define the condition number of A as $Cond(A) = \|A\|\|A^{-1}\|$, the above condition number is bound above by $Cond(A)$ and bellow by $1/Cond(A)$. A condition number of C implies that the solution is subject to an error of approximately C times larger than the rounding error (in percentage). The condition number of a matrix can be approximated by the ratio of its largest eigenvalue (λ_{max}) to its smallest one (λ_{min}). In fact λ_{max} is an upper bound for $\|A\|$ and $1/\lambda_{min}$ an upper bound for $\|A^{-1}\|$ Consider the following OLS problem (here I use $(X'X)^{-1}X'Y$ to illustrate multicolinearity):

```
> set.seed(123)
> x <- cbind(1,2,rnorm(40))
> x[20,2] <- 2.0001
> XX <- t(x)%*%x
> XY <- c(1,2,3)
> ev <- eigen(XX)$value
> condNum <- max(ev)/min(ev)
> condNum

[1] 103520161082
```

The condition number of $X'X$ is huge. We can see that the impact of a small variation of $X'Y$ can have a large effect on $\hat{\beta}$:

```
> solve(XX,XY)

[1] -490.19784894  245.10898537    0.09440253

> XY <- c(1,2.00001,3)
> solve(XX,XY)

[1] -2.559598e+03  1.279808e+03  9.610748e-02
```

The problem of multicolinearity is a problem with the stability of the linear system $(X'X)\beta = (X'Y)$ caused by the near singularity of $X'X$. There is a way of stabilizing the solution. We can regularize the solution by adding a small positive number to the diagonal of $X'X$. In the OLS case, it is called "Ridge Regression". In a general problem $Ax = b$, it is called a regularized technique. We can see the impact of adding .01 to the diagonal of $X'X$ in our problem:

```
> XX2 <- XX+diag(3)*.01
> ev <- eigen(XX2)$value
> condNum2 <- max(ev)/min(ev)
> condNum2

[1] 20010.72

> XY <- c(1,2,3)
> solve(XX2,XY)

[1] 0.004055934 0.008348604 0.093968818

> XY <- c(1,2.00001,3)
> solve(XX2,XY)

[1] 0.003655954 0.008548644 0.093968813
```

The problem is of course to find the appropriate regularization parameter.

3.2 Iterative method

In this section, we give an introduction to iterative methods. In this section, it is only applied to the case of linear problems such as $Ax = b$. However, we will use similar methods in next chapters for solving nonlinear system of equations and to do numerical optimization. I only present here examples:

3.2.1 Stopping rules

Lets consider the computation of $e^x = \sum_{n=0}^{\infty} x^n/n!$. Obviously, we can not compute the exact value. We need to stop somewhere. What criterion should we use to consider our answer to be reasonably good? Table 3.1 gives us a measure of the error as a function of n:

```
> x <- 1
> n <- c(0:8)
> myExp <- cumsum((x^n)/factorial(n))
> Exp <- exp(x)
> er <- abs(myExp-Exp)
> err <- er/Exp
> ans <- cbind(n,myExp,Exp,er,err)
> colnames(ans) <- c("n","My Exp", "True Exp","Abs Error","Rel Error")

> library(xtable)
> xtable(ans,caption="Iterative procedure to compute exp(1)",label="tab3-1",digits=5)
```

	n	My Exp	True Exp	Abs Error	Rel Error
1	0.00000	1.00000	2.71828	1.71828	0.63212
2	1.00000	2.00000	2.71828	0.71828	0.26424
3	2.00000	2.50000	2.71828	0.21828	0.08030
4	3.00000	2.66667	2.71828	0.05162	0.01899
5	4.00000	2.70833	2.71828	0.00995	0.00366
6	5.00000	2.71667	2.71828	0.00162	0.00059
7	6.00000	2.71806	2.71828	0.00023	0.00008
8	7.00000	2.71825	2.71828	0.00003	0.00001
9	8.00000	2.71828	2.71828	0.00000	0.00000

Table 3.1: Iterative procedure to compute exp(1)

We can obtain the convergence rate by looking at the behavior of $\|x_{n+1} - x\|/\|x_n - x\|$ (see Figure 3.2):

```
> plot(n[-1],y,type="l",xlab="n",ylab="Conv. Ratio")
```

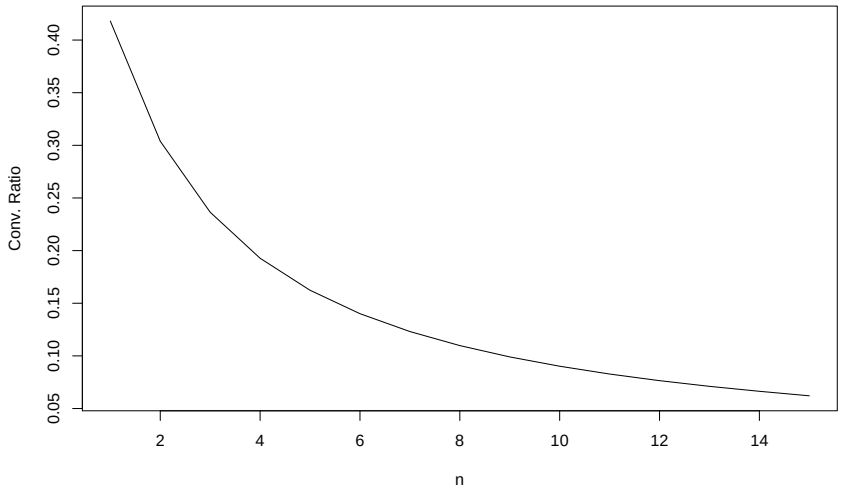


Figure 3.2: The convergence ratio $\|x_{n+1} - x\|/\|x_n - x\|$ as a function of n

```
> n <- c(0:15)
> myExp <- cumsum((x^n)/factorial(n))
> y <- abs(myExp[-1]-Exp)/abs(myExp[-length(n)]-Exp)
```

A sequence converge linearly if:

$$\lim_{n\to\infty} \frac{\|x_{n+1} - x\|}{\|x_n - x\|} \leq \beta < 1$$

and superlinearly (or at a rate $q > 1$) if $\beta = 0$. A general rule can be obtained by assuming that the above inequality is true which implies that:

$$\|x_{n+1} - x_n\| \geq \|x_n - x\|(1 - \beta)$$

Therefore, a rule that says: stops at x_{n+1} if $\|x_{n+1} - x_n\| < \varepsilon(1 - \beta)$ implies an error bounded by $\|x_n - x\| < \varepsilon$. For our case, it seems that the sequence to compute the exponential is superlinear (the ratio converges to zero) which implies that we can use the following function, which include the stopping rule. We can see that ε is just an upper bound for the error:

```
myExp <- function(x, eps) {
    y0 <- 1
```

```
    n <- 1
    crit <- 1000
    while (crit > eps) {
        y <- y0 + (x^n)/factorial(n)
        crit <- abs(y - y0)
        n <- n + 1
        y0 <- y
    }
    return(y)
}
```

```
> abs(myExp(2,1e-3)-exp(2))

[1] 6.138994e-05

> abs(myExp(2,1e-8)-exp(2))

[1] 4.142358e-10

> abs(myExp(2,1e-12)-exp(2))

[1] 4.618528e-14
```

Sometimes we also see rules based on the relative variation of the x_n. This rule is: stop at x_{n+1} if $\|x_{n+1} - x_n\|/(1 + \|x_n\|) \leq \varepsilon$. The value in the denominator is to allow convergence to zero. This rule however does not work well with sequences that converge linearly. We can see that using the sequence $x_n = \sum_{i=1}^{n}(1/i)$:

```
> N <- 100
> n <- 1:N
> x <- sum(1/n)
> xn <- cumsum(1/n[-N])
> y <- abs(xn[-1]-x)/abs(xn[-length(xn)]-x)
> beta <- max(y)
> beta

[1] 0.973315
```

In Figure 3.3 we can see that β as an upper bound around 1, which shows that there is no convergence. Using the first rule we would never conclude that the sequence converges.

```
> plot(n[-c(N-1,N)],y,xlab="n",ylab="Conv. Ratio",type="l")
```

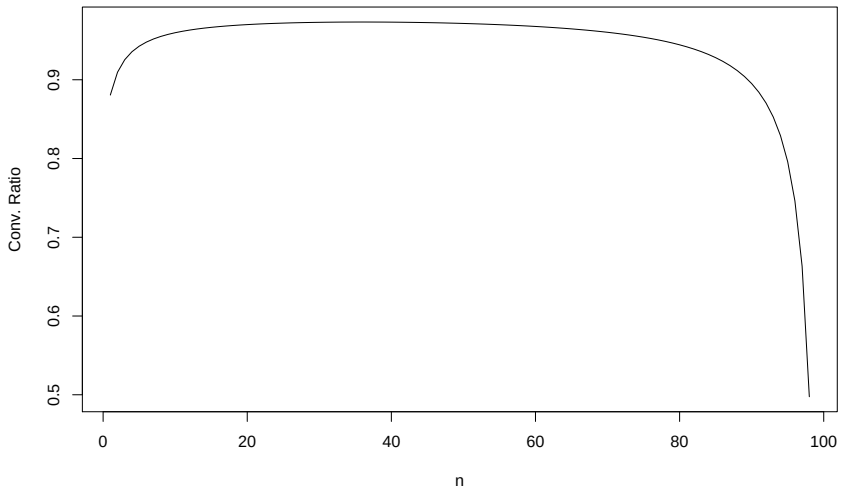


Figure 3.3: The convergence ratio $\|x_{n+1} - \hat{x}\|/\|x_n - \hat{x}\|$ as a function of n for $x_n = \sum_i (1/i)$

3.2.2 Fixed-Point Iteration

If we define $G(x) = Ax - b + x$, the solution to $Ax = b$ is the fixed-point $G(x) = x$. The following iteration, if it converges, will reach the solution:

$$x_{k+1} = G(x_k) = (A + I)x_k - b$$

Lets try it:

```
FP <- function(A, b, x0, eps, maxit = 1000, beta = 0) {
    crit <- 1000
    n <- 1
    while (crit > eps * (1 - beta)) {
        x <- (A + diag(ncol(A))) %*% x0 - b
        crit <- sqrt(crossprod(x - x0))
        x0 <- c(x)
        n <- n + 1
        if (n >= maxit | any(abs(x) == Inf)) {
            warning("No convergence")
            break
        }
    }
    return(x)
}
```

```
> A <- matrix(c(12,3,2,5,13,7,4,9,10),3,3)
> b <- c(4,5,6)
> trueX <- solve(A,b)
> FP(A,b,c(0,0,0),1e-6)

     [,1]
[1,] -Inf
[2,] -Inf
[3,] -Inf
```

No luck! It does not converge. This method is quite bad because we have convergence only if the modulus of the eigenvalues of $(A+I)$ are less than 1. The following example works.

```
> A <- matrix(c(-.2,.1,.1,.3,-.3,.3,.4,-.1,-.6),3,3)
> Tx <- solve(A,b)
> x <- FP(A,b,c(10,10,10),1e-5,maxit=5000)
> crossprod((Tx-x))^.5
```

```
           [,1]
[1,] 0.00101769

> x <- FP(A,b,c(10,10,10),1e-8,maxit=5000)
> crossprod((Tx-x))^.5

             [,1]
[1,] 1.017961e-06
```

The error is however higher than ε when $\beta = 0$. The convergence is therefore linear. We need a β close to 1 for the error to be bounded by ε:

```
> x <- FP(A,b,c(10,10,10),1e-5,maxit=5000,beta=.995)
> crossprod((Tx-x))^.5

            [,1]
[1,] 5.08009e-06

> x <- FP(A,b,c(10,10,10),1e-8,maxit=5000,beta=.995)
> crossprod((Tx-x))^.5

             [,1]
[1,] 5.078557e-09
```

3.2.3 Gauss-Jacobi and Gauss-Seidel

Here I reproduce Figure 3.2 of Judd. First I need to build few functions.

```
# Did I tell you I like small functions?

getXiGJ <- function(A, b, x) {
    a <- diag(A)
    diag(A) <- 0
    x <- (b - A %*% x)/a
    attr(x, "name") <- "Gauss-Jacobi"
    return(x)
}

getXiGS <- function(A, b, x) {
    xf <- rep(0, length(x))
    a <- diag(A)
    diag(A) <- 0
    for (i in 1:length(x)) x[i] <- (b[i] - crossprod(A[i, ],
```

```
        x))/a[i]
    attr(x, "name") <- "Gauss-Seidel"
    return(x)
}

# The function prepares A so that the diagonals are not zero

PrepA <- function(A, b) {
    bad <- which(abs(diag(A)) <= 1e-07)
    for (i in bad) {
        l <- which(abs(A[, i]) > 1e-07)
        if (length(l) == 0)
            return(list(A = NULL, b = NULL, fail = TRUE))
        A[i, ] <- A[i, ] + A[l[1], ]
        b[i] <- b[i] + b[l[1]]
    }
    return(list(A = A, b = b, fail = FALSE))
}

# This function works for both algorithm

IterSolve <- function(A, b, x0, algo, eps = 1e-08,
    maxit = 1000, ...) {
    res <- PrepA(A, b)
    if (res$fail)
        stop("The algorithm failed") else {
        A <- res$A
        b <- res$b
    }
    crit <- 1000
    AllX <- x0
    n <- 1
    while (crit > eps) {
        x <- c(algo(A, b, x0, ...))
        AllX <- rbind(AllX, x)
        if (any(abs(x) == Inf))
            stop("The algorithm diverges")
        crit <- crossprod(x - x0)^0.5
        if (n == maxit) {
            warning("Maxit reached")
            break
```

```
        }
        n <- n + 1
        x0 <- x
    }
    if (n < maxit)
        cat("\n", attr(x, "name"), "\nConverged after ", (n -
            1), "iterations\n")
    return(list(x = x, AllX = AllX))
}
```

We can try it with the previous matrix

```
> IterSolve(A,b,c(0,0,0),eps=1e-5,algo=getXiGJ)$x

Converged after  399 iterations
[1] -959.9998 -239.9999 -289.9999

> IterSolve(A,b,c(0,0,0),eps=1e-5,algo=getXiGS)$x

Converged after  169 iterations
[1] -959.9999 -240.0000 -290.0000
```

The second method is clearly faster than the first method, which is explained by the fact that it uses the new information as soon as it is available. The two methods are also much faster than the Fixed-point method. They also seem to converge better since they both can solve the first problem we tried above with the Fixed-Point algorithm. To see it, we even try very bad starting values:

```
> A <- matrix(c(12,3,2,5,13,7,4,9,10),3,3)
> b <- c(4,5,6)
> IterSolve(A,b,c(100,-100,50),eps=1e-5,algo=getXiGJ)$x

Converged after  104 iterations
[1]  0.16021871 -0.08840049  0.62983159

> IterSolve(A,b,c(100,-100,50),eps=1e-5,algo=getXiGS)$x

Converged after  22 iterations
[1]  0.16022332 -0.08840292  0.62983738
```

But there are examples in which the algorithms do not converge:

```
> set.seed(111)
> A <- matrix(rnorm(9),3,3)
> x1 <- try(IterSolve(A,b,c(100,-100,50),eps=1e-5,algo=getXiGS))
> cat(x1)

Error in IterSolve(A, b, c(100, -100, 50), eps = 1e-05, algo = getXiGS) :
  The algorithm diverges
```

We'll comeback to this convergence problem latter. We first want to see how we can use the algorithm to analyze the dynamics of market going from any point to the equilibrium. The model is:

$$p + q = 10 \quad \text{(demand)}$$

$$p - 2q = -2 \quad \text{(supply)}$$

or

$$\begin{pmatrix} 1 & 1 \\ 1 & -2 \end{pmatrix} \begin{pmatrix} p \\ q \end{pmatrix} = \begin{pmatrix} 10 \\ -2 \end{pmatrix}$$

First lets compare the two methods:

```
> A <- matrix(c(1,1,1,-2),2,2)
> b <- c(10,-2)
> res1 <- IterSolve(A,b,c(4,1),eps=1e-5,algo=getXiGS)
```

Converged after 21 iterations

```
> res2 <- IterSolve(A,b,c(4,1),eps=1e-5,algo=getXiGJ)
```

Converged after 40 iterations

```
> ans <- cbind(1:20,res1$AllX[1:20,],res2$AllX[1:20,])
> colnames(ans) <- c("n","p-(GS)","q-(GS)","p-(GJ)","q-(GJ)")
```

Table 3.2 shows some iteration results. We can see that the Gauss-Seidel method is faster. The function plotEqui() creates something similar to Figure 3.2 of Judd. The result is shown in Figure 3.4. The Gauss-Seidel method is slightly different because we solve for the price first while Judd does the opposite. Also, the path in the book shows movements between iteration while here we only show the final points.

```
plotEqui <- function(resGS, resGJ, A, b, n, Title = NULL,
    xlab = NULL, ylab = NULL) {
    x <- resGS$AllX[1:n, ]
    x2 <- resGJ$AllX[1:n, ]
    xsol <- solve(A, b)
```

	n	p-(GS)	q-(GS)	p-(GJ)	q-(GJ)
1	1.0000	4.0000	1.0000	4.0000	1.0000
2	2.0000	9.0000	5.5000	9.0000	3.0000
3	3.0000	4.5000	3.2500	7.0000	5.5000
4	4.0000	6.7500	4.3750	4.5000	4.5000
5	5.0000	5.6250	3.8125	5.5000	3.2500
6	6.0000	6.1875	4.0938	6.7500	3.7500
7	7.0000	5.9062	3.9531	6.2500	4.3750
8	8.0000	6.0469	4.0234	5.6250	4.1250
9	10.0000	6.0117	4.0059	6.1875	3.9375
10	15.0000	5.9996	3.9998	6.0156	4.0234
11	20.0000	6.0000	4.0000	5.9941	4.0020

Table 3.2: The convergence of the algorithm of Gauss-Jacobi versus Gauss-Seidel for a Demand-Supply example.

```
xlim <- c(0, 2 * xsol[2])
ylim <- c(0, 2 * xsol[1])
if (is.null(xlab))
    xlab <- "Q"
if (is.null(ylab))
    ylab <- "P"

curve((b[1] - A[1, 2] * x)/A[1, 1], 0, xlim[2], xlim = xlim,
    ylim = ylim, xlab = xlab, ylab = ylab, bty = "n")
abline(b[2]/A[2, 1], -A[2, 2]/A[2, 1])
if (is.null(Title))
    title("Dynamics of Demand and Supply Equilibrium") else title(Title)
for (i in 1:(n - 1)) {
    text(x[i, 2], x[i, 1], i, col = 2, lwd = 4)
    arrows(x[i, 2], x[i, 1], x[(i + 1), 2], x[(i + 1), 1],
        col = 2)
}
text(x[n, 2], x[n, 1], n, col = 2, lwd = 4)
for (i in 1:(n - 1)) {
    text(x2[i, 2], x2[i, 1], i, col = 4, lwd = 4)
    arrows(x2[i, 2], x2[i, 1], x2[(i + 1), 2], x2[(i + 1),
        1], lty = 2, col = 4)
}
```

```
> plotEqui(res1,res2,A,b,6)
```

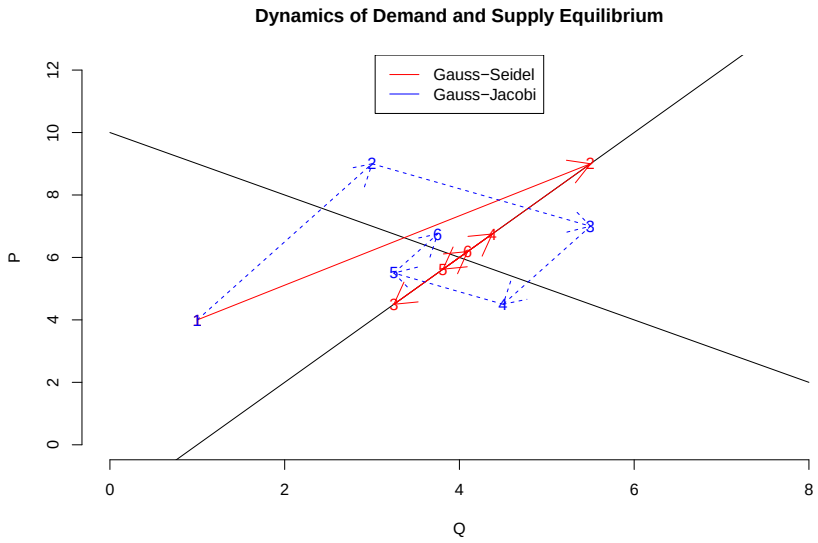


Figure 3.4: Dynamics of the market using two types of iterative methods

```
    text(x2[n, 2], x2[n, 1], n, col = 4, lwd = 4)
    legend("top", c("Gauss-Seidel", "Gauss-Jacobi"), lty = c(1,
        1), col = c(2, 4))
}
```

Using the dynamics of the model, we can see why in some cases, the iterative procedure does not converge. It is a nice example that uses the same argument as when we analyze movements in differential equation models graphically. The method converges because of the angle between the demand and the supply around the equilibrium. Figure 3.5 shows what happens if the slope of the demand becomes -2.1:

```
> A <- matrix(c(1,1,2.1,-2),2,2)
> b <- c(10,-2)
> res1 <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGS)
> res2 <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGJ)
```

We would get a perpetual cycle if the ratio was 1 in absolute value (try it). Here we are just solving a linear system. The non-convergence of the iterative methods does not imply tt we do not have a solution:

```
> solve(A,b)
```

```
> plotEqui(res1,res2,A,b,7)
```

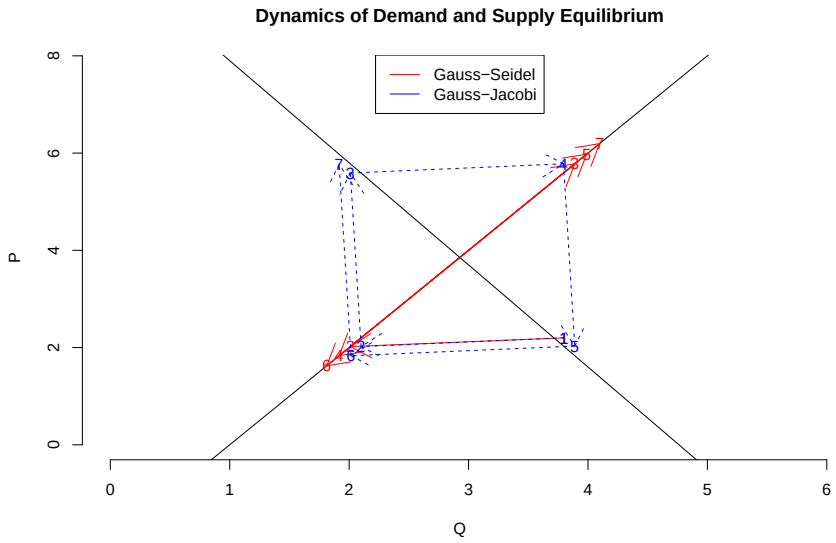


Figure 3.5: Dynamics of the market using two types of iterative methods

```
[1] 3.853659 2.926829
```

The problem comes from the algorithm not the system itself. However, if we had a dynamic system, the system would be considered unstable. We'll cover that later.

There is a general rule for the convergence of both algorithms. If A is diagonally dominant ($|a_{ii}| > \sum_{j \neq i} |a_{ij}|$) , the method works. We can construct diagonally dominant matrices from one that is not diagonally dominant. For example, if the first row of A is replaced by the sum of the first and the second we get (we have to do the same transformation to b):

```
> A[1,] <- A[1,]+A[2,]
> b[1] <- b[1]+b[2]
> A
```

```
     [,1] [,2]
[1,]    2  0.1
[2,]    1 -2.0
```

The matrix becomes diagonally dominant. The system can therefore be solved:

```
> IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGS)$x
```

```
Converged after  5 iterations
[1] 3.853659 2.926829

> IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGJ)$x

Converged after  9 iterations
[1] 3.853659 2.926829
```

Of course it make no sense economically to replace the demand by the sum of the demand and the supply. It is just a numerical trick to make the algorithm works.

Exercise 3.4. *Rewrite the function PrepA() so that (if possible) all rows of A becomes diagonally dominant.*

3.2.4 Acceleration and Stabilization Methods

We first rewrite the function getXiGJ() and getXiGS() to include the parameter ω of the altered iterative scheme, with default value of 1.

```
getXiGJ <- function(A, b, x, omega = 1) {
    a <- diag(A)
    diag(A) <- 0
    x <- omega * (b - A %*% x)/a + (1 - omega) * x
    attr(x, "name") <- "Gauss-Jacobi"
    return(x)
}

getXiGS <- function(A, b, x, omega = 1) {
    xf <- rep(0, length(x))
    a <- diag(A)
    diag(A) <- 0
    for (i in 1:length(x)) x[i] <- omega * (b[i] - crossprod(A[i,
        ], x))/a[i] + (1 - omega) * x[i]
    attr(x, "name") <- "Gauss-Seidel"
    return(x)
}
```

Lets try to solve our previous unstable system using this modified iterative scheme:

```
> A <- matrix(c(1,1,2.1,-2),2,2)
> b <- c(10,-2)
> resGS <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGS,omega=.7)
```

```
> plotEqui(resGS,resGJ,A,b,7)
```

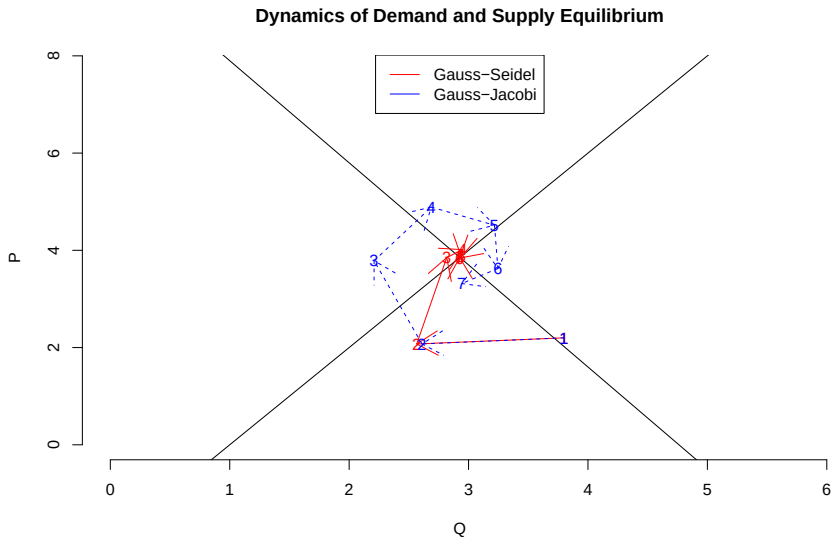


Figure 3.6: Gauss-Seidel and Gauss-Jacobi using an altered scheme

```
Converged after  12 iterations
```

```
> resGJ <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGJ,omega=.7)
```

```
Converged after  49 iterations
```

Figure 3.6 shows what happens. The problem was that the steps were to large. By reducing them, we obtain convergence. In the case of a slow convergence, we can also use ω to accelerate convergence. The following system is an example in which convergence is very slow:

$$p = -1.95q + 10$$

$$q = 2q - 2$$

Figure 3.7 shows the convergence when $\omega = 1$ and Figure 3.8 shows what happens if we set ω to 0.6.

```
> A <- matrix(c(1,1,1.95,-2),2,2)
> resGS <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGS)

Converged after  504 iterations

> resGJ <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGJ)

Converged after  955 iterations

> plotEqui(resGS,resGJ,A,b,27)
```

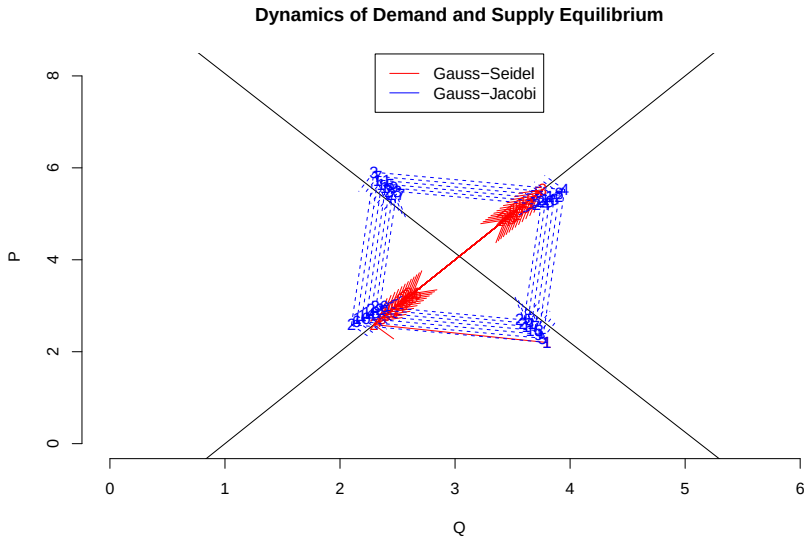


Figure 3.7: Gauss-Seidel and Gauss-Jacobi using an altered scheme (Slow convergence with $\omega = 1$

```
> A <- matrix(c(1,1,1.95,-2),2,2)
> resGS <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGS,omega=0.6)

Converged after  14 iterations

> resGJ <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGJ,omega=0.6)

Converged after  36 iterations

> plotEqui(resGS,resGJ,A,b,7)
```

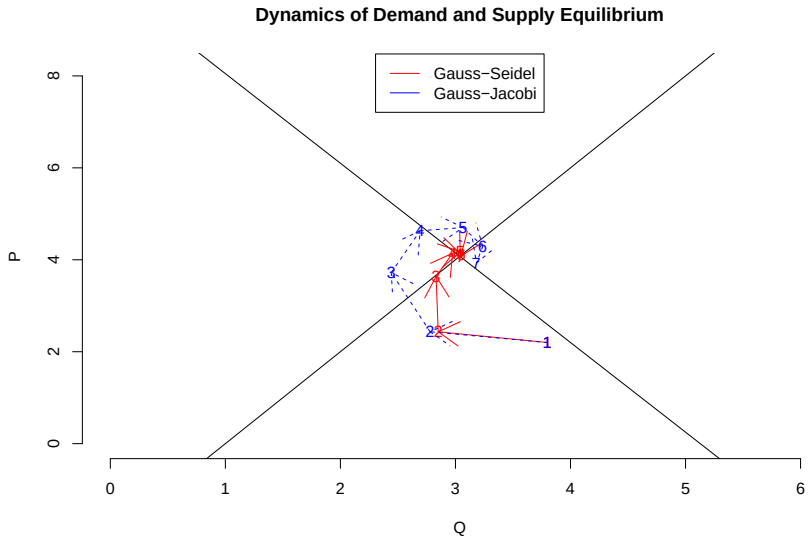


Figure 3.8: Gauss-Seidel and Gauss-Jacobi using an altered scheme (Slow convergence with $\omega = 0.6$

For Gauss-Seidel, we can obtain an optimal ω. If we write the iteration in matrix form, we have:

$$x_{k+1} = M_\omega^{-1} N_\omega x_k + \omega M_\omega^{-1} b$$

where $M_\omega = (D + \omega L)$, $M_\omega = (1 - \omega)D - \omega U$, and U, L, and D are respectively the element above the diagonal, the element below the diagonal and the diagonal of A. In fact, we have $A = U + L + D$. The iterative scheme converges quickly if the largest eigenvalues of $(M_\omega^{-1} N_\omega)$ in absolute value is small and less than 1. We therefore what the value of ω that minimizes the largest eigenvalues. The following function selects the optimal ω using a grid search. It is not efficient but it works:

```
getOmega <- function(A, from = 0.1, to = 1) {
    w <- seq(to, from, len = 100)
    ev <- vector()
    D <- diag(diag(A))
    U <- A * upper.tri(A)
    L <- A * lower.tri(A)
    for (i in 1:length(w)) {
        M <- D + w[i] * L
        N <- (1 - w[i]) * D - w[i] * U
        ev[i] <- max(abs(eigen(solve(M, N))$val))
    }
    w[which.min(ev)]
}
```

We can verify with the last to systems:

```
> A <- matrix(c(1,1,2.1,-2),2,2)
> b <- c(10,-2)
> w <- getOmega(A,0,3)
> res1 <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGS,omega=w)

Converged after  9 iterations

> A <- matrix(c(1,1,1.95,-2),2,2)
> w <- getOmega(A,0,3)
> resGS <- IterSolve(A,b,c(2.2,3.8),eps=1e-5,algo=getXiGS,omega=w)

Converged after  10 iterations
```

It is in fact very fast with the optimal ω.

Exercise 3.5. *Try to find the optimal ω for the Gauss-Jacobi method and write a function like the one above to compute it. Compare the convergence of Gauss-Seidel and Gauss-Jacobi using their optimal ω.*

Exercise 3.6. *Do the same for the fixed point algorithm.*

We conclude this chapter with an example of Nash equilibrium computation. The two reaction functions are:

$$p_1 = 1 + 0.75p_2$$

$$p_2 = 2 + 0.8p_1$$

In the following, we compare the convergence with different ω (find the optimal one), and Figure 3.9 shows the case $\omega = 1$.

```
> A <- matrix(c(1,-.8,-.75,1),2,2)
> b <- c(1,2)
> resGS <- IterSolve(A,b,c(2,1),eps=1e-5,algo=getXiGS)

Converged after  27 iterations

> resGJ <- IterSolve(A,b,c(2,1),eps=1e-5,algo=getXiGJ)

Converged after  50 iterations

> resGS2 <- IterSolve(A,b,c(2,1),eps=1e-5,algo=getXiGS,omega=.5)

Converged after  78 iterations

> resGJ2 <- IterSolve(A,b,c(2,1),eps=1e-5,algo=getXiGJ,omega=.5)

Converged after  96 iterations
```

In this example, reducing the value of ω does not help. Figure 3.10 shows us why. In fact, we can accelerate the convergence by choosing a value greater than 1.

```
> resGS3 <- IterSolve(A,b,c(2,1),eps=1e-5,algo=getXiGS,omega=1.3)

Converged after  13 iterations

> resGJ3 <- IterSolve(A,b,c(2,1),eps=1e-5,algo=getXiGJ,omega=1.3)
```

It works for the Gauss-Seidel but not for the Gauss-Jacobi, which shows that the optimal ω is not the same for the two algorithms. You can use the answer of Exercise 3.5 to show it.

Exercise 3.7. *Answer questions 3, 6, 7 and 8 in Judd*

```
> plotEqui(resGS,resGJ,A,b,8,Title="Nash Equilibrium",xlab="P2",ylab="P1")
```

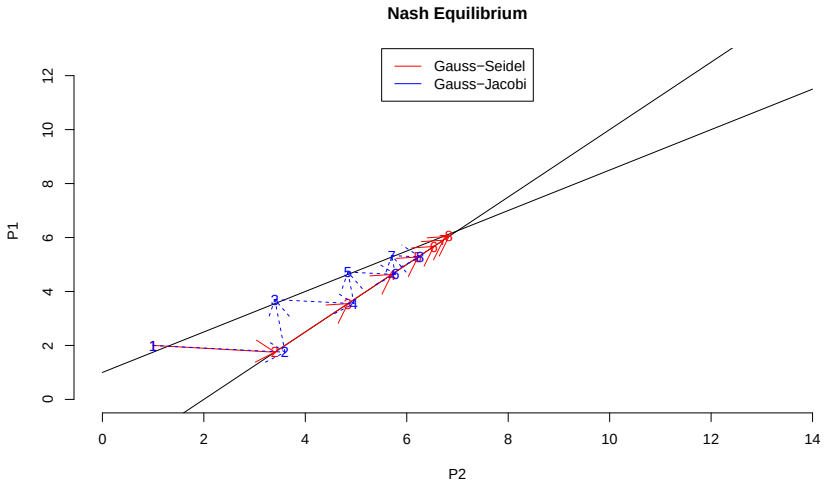


Figure 3.9: Gauss-Seidel and Gauss-Jacobi for the computation of a Nash equilibrium ($\omega = 1$)

```
> plotEqui(resGS2,resGJ2,A,b,8,Title="Nash Equilibrium",xlab="P2",ylab="P1")
```

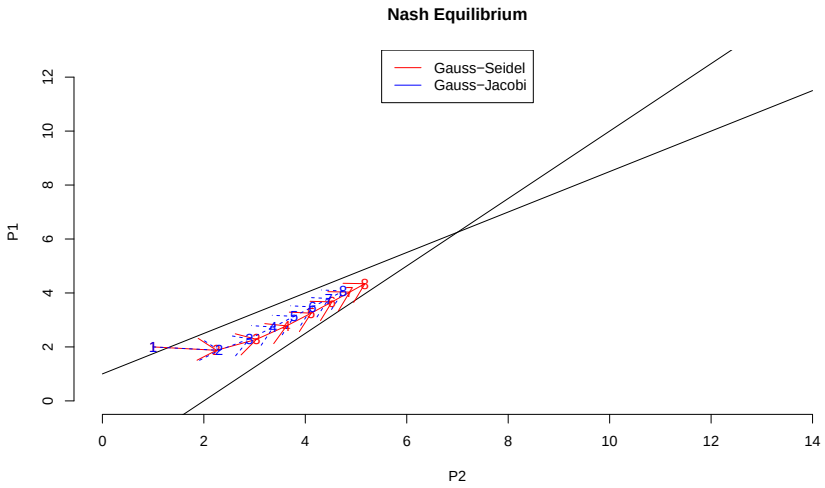


Figure 3.10: Gauss-Seidel and Gauss-Jacobi for the computation of a Nash equilibrium ($\omega = 0.5$)

Chapter 4

Optimization

Contents

4.1 One-dimensional problems

4.1.1 Derivative Free Methods

Suppose we want to find a local minimum of the following function, for which the shape is shown on Figure 4.1:

$$f(x) = \sin(x - 0.04x^2) - \frac{\sin(x)}{4}$$

The easier way to find the solution is by the Bracketing method. We first need to find three points, A, B and C, such that $f(A) > f(B)$ and $f(C) > f(B)$ as in Figure 4.1. The following function computes the solution using the Algorithm 4.1 of Judd (I also create a print method. Why not keeping our good habits):

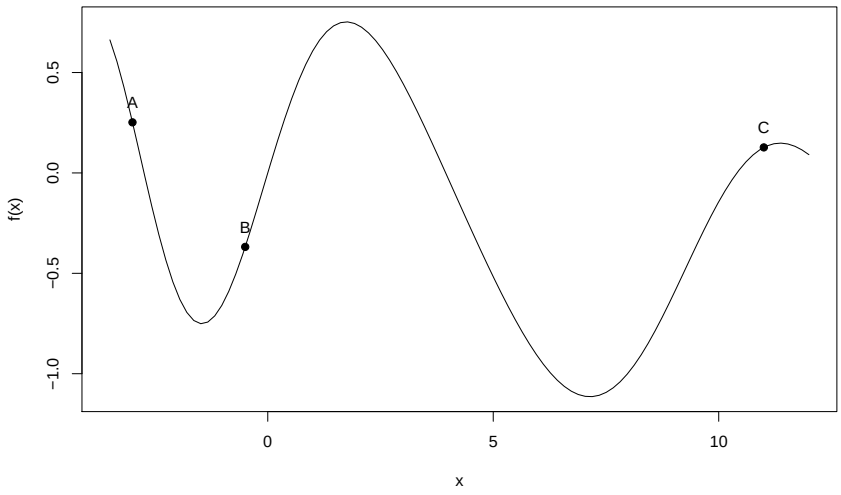


Figure 4.1: $f(x) = \sin(x - 0.04x^2) - \frac{\sin(x)}{4}$

```
Brack <- function(f, a, b, c, eps = 1e-08, maxit = 1000) {
    if (f(a) <= f(b) | f(c) <= f(b))
        stop("You must have f(a), f(c) > f(b)")
    if (!(b < c) | !(b > a))
        stop("You must have a<b<c")
    crit = 1000
    n <- 1
    x <- c(a, b, c)
    mess <- NULL
    conv <- T
    id <- 0
    fb <- f(b)
    while (TRUE) {
        d <- ifelse((b - a) < (c - b), (c + b)/2, (b + a)/2)
        fd <- f(d)
        if (d < b & fd > fb) {
            a <- d
        } else if (d < b & fd < fb) {
            c <- b
            b <- d
```

```
            fb <- f(b)
        } else if (d > b & fd < fb) {
            a <- b
            b <- d
            fb <- f(b)
        } else {
            c <- d
        }
        crit <- c - a
        x <- rbind(x, c(a, b, c))
        if (n >= maxit) {
            mess <- paste("maxit(", maxit, ") reached", sep = "")
            conv = F
            break
        }
        n <- n + 1
        if (crit < eps * abs(b))
            break
    }
    n <- nrow(x)
    ans <- list(obj = f(b), x = x, sol = b, name = "Bracketing Method",
        conv = conv, prec = (x[n, 3] - x[n, 1]), mess = mess)
    class(ans) <- "NonlinSol"
    return(ans)
}

print.NonlinSol <- function(obj) {
    n <- nrow(obj$x)
    cat("\nMethod: ", obj$name, "\n")
    if (obj$conv)
        cat("Message: Converged after ", (n - 1), " iterations",
            obj$mess, "\n\n") else cat("Message: ", obj$mess, "\n\n")
    if (length(obj$sol) == 1)
        cat("The solution is: ", obj$sol, ", and f(x) is ", obj$obj,
            "\n") else {
        cat("The solution is: \n")
        if (is.null(names(obj$sol)))
            names(obj$sol) <- paste("x", 1:length(obj$sol), sep = "")
        for (i in 1:length(obj$sol)) cat(names(obj$sol)[i], " = ",
            obj$sol[i], "\n")
        cat("\nf(x) is ", obj$obj, "\n")
```

```
    }
    cat("Precision: ", obj$prec, "\n")
}
```

Before we solve the problem, we have to ask ourselves: how should we pick the ε? We know that the solution is between a and c. Therefore, should we make it as small as possible? This is a very good application of floating-point arithmetic that we covered in Chapter 2. Suppose that the true solution is b (see [Press *et al.* 2007], Chapter 10). Then, a Taylor approximation implies (remember that the first derivative is zero at that point):

$$f(x) \approx f(b) + \frac{1}{2}f''(b)(x-b)^2 = f(b)\left(1 + \frac{f''(b)(x-b)^2}{2f(b)}\right)$$

The last term will be numerically equal to $f(b)$ whenever:

$$\frac{f''(b)(x-b)^2}{2|f(b)|} < \varepsilon_m,$$

where ε_m is the machine epsilon. Remember that by definition $(1+\varepsilon_m) = 1$ numerically. It implie that:

$$|x-b| < \sqrt{\varepsilon_m}\sqrt{\frac{2|f(b)|}{f''(b)}} = \sqrt{\varepsilon_m}|b|\sqrt{\frac{2|f(b)|}{b^2 f''(b)}} = \sqrt{\varepsilon_m}|b|O(1)$$

The moral is that there is no point of making the interval $[a, c]$ smaller than $\sqrt{\varepsilon_m}|b|$ because we would not see any difference in terms of function values. For example, if the middle point is 1, then setting the tolerance level to 10^{-8} is the best we can do. With the three points shown in Figure 4.1, the solution is:

```
> f <- function(x) sin(x-.04*x^2)-sin(x)/4
> Brack(f,-3,-0.5,11)

Method:  Bracketing Method
Message: Converged after  47  iterations

The solution is:  7.143987 , and f(x) is  -1.114449
Precision:  6.426126e-08
```

We can see how the algorithm works by looking at Figures 4.2 and 4.3. In the first one, we reach the global minimum and in the second we only find a local one. The result from the second set of starting values is:

```
> Brack(f,-3,-0.5,2)
```

```
Method:  Bracketing Method
Message: Converged after  47  iterations

The solution is:  -1.460872 , and f(x) is  -0.7512074
Precision:  9.313226e-09
```

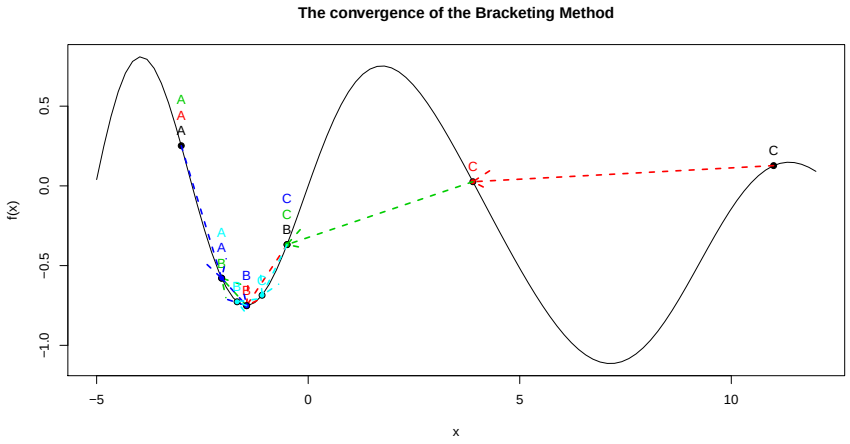
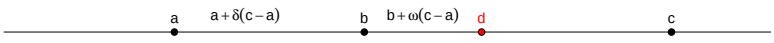


Figure 4.2: $f(x) = \sin(x - 0.04x^2) - \frac{\sin(x)}{4}$

The above method is not the most efficient one. The method put the fourth point in the middle of the largest interval between $[a, b]$ and $[b, c]$. We can improve the number of iterations by selecting another fraction. The Golden Section proceeds as follows: if $(b - a) > (c - b)$, then $d = b - \delta(c - a)$ and if $(b - a) < (c - b)$, then $d = a + \delta(c - a)$, where $\delta = (3 - \sqrt{5})/2$. Assume that $b = a + \delta(c - a)$, which forms the original three points, and the fourth point d is $b + \omega(c - a)$.



Since we either pick $\{a, b, d\}$ or $\{b, d, c\}$ the relative length is either:

$$\frac{d - a}{c - a} = \omega + \delta$$

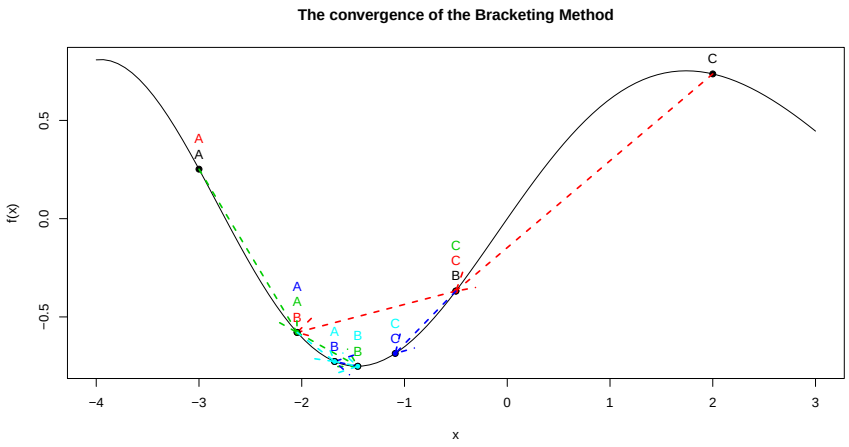


Figure 4.3: $f(x) = \sin(x - 0.04x^2) - \frac{\sin(x)}{4}$ (Different starting points)

or

$$\frac{c-b}{c-a} = 1 - \delta$$

We minimize the worse scenario by making it equal to the best one. In other words, we set $(\omega + \delta) = (1 - \delta)$ or $\omega = (1 - 2\delta)$. Also, we assume, like for d, that b was optimal so that $(b-a)/(c-a) = (d-b)/(c-b)$ which implies:

$$\delta = \frac{d-b}{c-b} = \frac{\omega(c-a)}{c-b} = \omega(1-\delta)$$

If we combine $\delta(1-\delta) = \omega$ and $\omega = (1-2\delta)$, we get a second order polynomial with the only positive solution being $(3-\sqrt{5})/2$. The following uses the optimal ratio:

```
> Brack2(f,-3,-0.5,2)

Method:  Bracketing Method
Message: Converged after  39  iterations

The solution is:  -1.460872 , and f(x) is  -0.7512074
Precision:  2.860287e-08
```

It is better, but not that much better. The algorithm has a linear convergence. There exists a super-linear method for one dimensional problems. It is the Brent's method. It only defers in the way the fourth point is selected.

4.1.2 Methods based on Derivatives

A method that only requires one staring point is the Newton's Method. It is based on the Taylor approximation of $f(x)$:

$$p(x) = f(a) + f'(a)(x-a) + \frac{f''(a)}{2}(x-a)^2$$

The solution of the minimization problem is:

$$x^* = a - \frac{f'(a)}{f''(a)}$$

We can therefore build our iterative scheme based on the solution:

$$x_{k+1} = x_k - \frac{f'(x_k)}{f''(x_k}$$

The problem here is that we need the first and second derivative. The function I am proposing is a general function that requires f to be an expression so that we can obtain the derivatives using D():

```
Newton <- function(f, x0, eps = 1e-08, delta = 1e-08, maxit = 1000) {
    go <- TRUE
    n <- 1
    mess <- NULL
    res <- c(x0, eval(f, list(x = x0)))
    Df <- D(f, "x")
    DDf <- D(Df, "x")
    conv <- T
    while (go) {
        x <- x0 - eval(Df, list(x = x0))/eval(DDf, list(x = x0))
        crit1 <- abs(x - x0)/(1 + abs(x0))
        crit2 <- abs(eval(Df, list(x = x0)))
        go <- !(crit1 < eps & crit2 < delta)
        res <- rbind(res, c(x, eval(f, list(x = x))))
        if (n >= maxit) {
            mess <- paste("maxit(", maxit, ") reached", sep = "")
            conv <- FALSE
            break
        }
        x0 <- x
        n <- n + 1
    }
```

```
    if (eval(DDf, list(x = x0)) <= 0)
        mess2 <- "not satisfied" else mess2 <- "satisfied"
    mess <- paste(mess, " (SOC ", mess2, ")", sep = "")
    n <- nrow(res)
    ans <- list(obj = res[n, 2], sol = x, x = res, name = "Newton's Method",
        conv = conv, prec = crit1, mess = mess)
    class(ans) <- "NonlinSol"
    return(ans)
}
```

We can try the function using the example we use above. We see that the method just finds stationary points. It could be a maximum or a minimum. We can see what happens if we start at 10 and 8.5:

```
> f <- expression(sin(x-.04*x^2)-sin(x)/4)
> Newton(f,10)

Method:  Newton's Method
Message: Converged after  6  iterations  (SOC not satisfied)

The solution is:  11.36565 , and f(x) is  0.1485208
Precision:  7.757233e-15

> Newton(f,8.5)

Method:  Newton's Method
Message: Converged after  5  iterations  (SOC satisfied)

The solution is:  7.143987 , and f(x) is  -1.114449
Precision:  3.667952e-10
```

By the number of iterations, it is much faster than the Bracketing Method. However, it is very sensitive to starting values when we have multiple extrema. Figure 4.4 shows the details of some iterations and different starting values (the functions for plotting the convergence of the the Bracketing and Newton's methods are available in the .R file of Chapter 4 on the website of the course).

If we look at the example page 98 of Judd, we want to maximize the utility function:

$$U = x^{1/2} + 2y^{1/2}$$

subject to the constraint $2x + 3y = 1$. We can solve this problem by substitution. By doing it, the problem is reduced to a one dimensional optimization problem:

$$U = \left(\frac{1-3y}{2}\right)^{1/2} + 2y^{1/2}$$

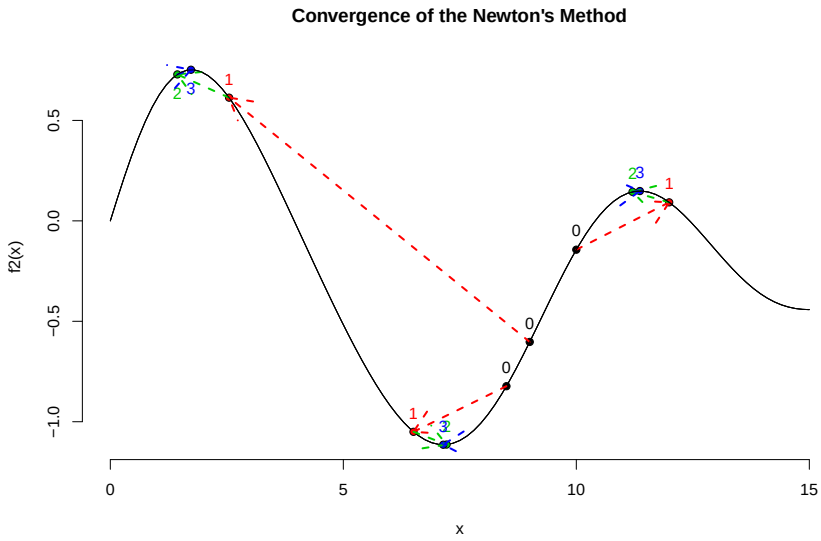


Figure 4.4: $f(x) = \sin(x - 0.04x^2) - \frac{\sin(x)}{4}$ (Newton's Method)

The solution must be between 0 and 1/3, so we can try the triplet (0,1/6,1/3) for the Bracketing method and a starting value if .1 for the Newton's method (we have to return the negative of the utility because we have developed minimization algorithms). Figures 4.5 and 4.6 show the details of the convergence.

```
> f <- function(x) -((1-3*x)/2)^.5-2*x^.5
> f2 <- expression(-((1-3*x)/2)^.5-2*x^.5)
> resB <- Brack(f,0,1/6,1/3)
> resN <- Newton(f2,.1)
> resB

Method:  Bracketing Method
Message: Converged after  47  iterations

The solution is:  0.2424242 , and f(x) is  -1.354006
Precision:  1.241763e-09

> resN

Method:  Newton's Method
Message: Converged after  6  iterations  (SOC satisfied)
```

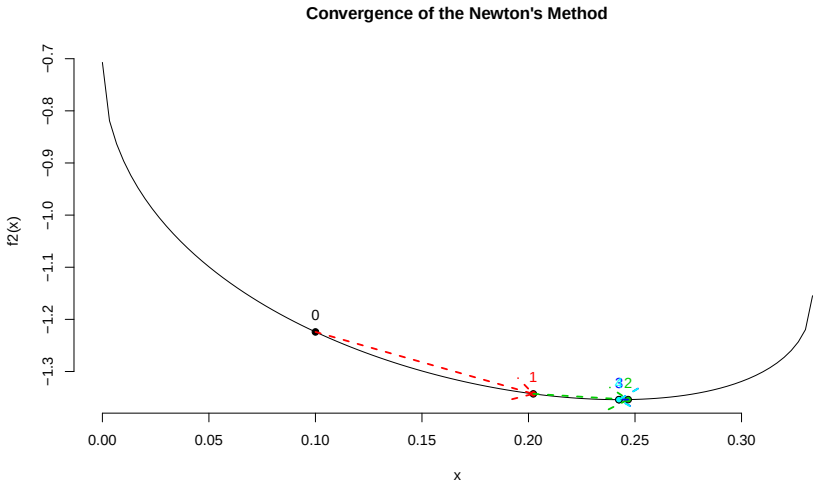


Figure 4.5: Minimization of $-U = -x^{1/2} - 2y^{1/2}$, with $x = (1 - 3y)/2$ (Newton's Method)

```
The solution is:  0.2424242 , and f(x) is  -1.354006
Precision:  1.268904e-14
```

The solution gives the optimal y. therefore have x =0.1364.

Suppose we want to solve the consumer problem:

$$\max_{x,y} -e^{-x} - e^{-y}$$

subject to

$$2x + 3y = 10000$$

which implies the following unconstrained problem

$$\max_{y} -e^{-5000+1.5y} - e^{-y}$$

```
> f3 <- expression(exp(-5000-1.5*x)+exp(-x))
> resN <- try(Newton(f3,100,maxit=600))
> resN

Method:  Newton's Method
Message:  maxit(600) reached (SOC satisfied)

The solution is:  700 , and f(x) is  9.859677e-305
Precision:  0.001428571
```

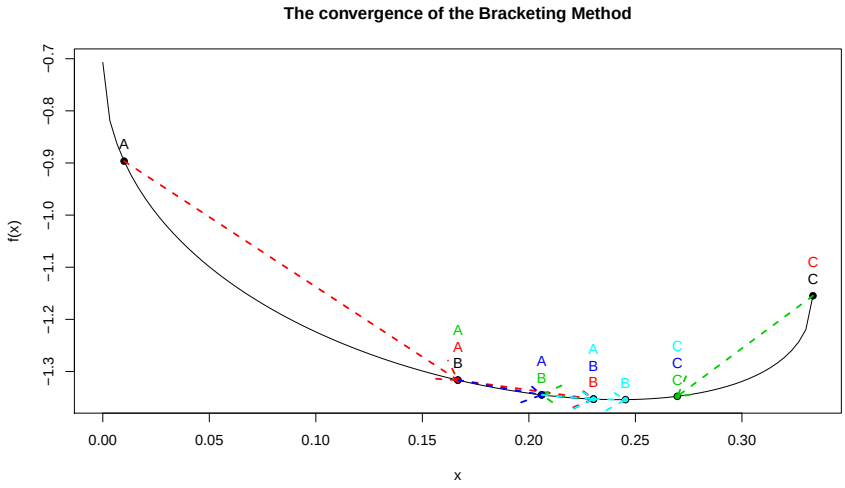


Figure 4.6: Minimization of $-U = -x^{1/2} - 2y^{1/2}$, with $x = (1-3y)/2$ (The Bracketing Method)

This is a case of scaling problem. The algorithm reached at some point the zero (underflow), which result in a failure (if we don't restrict the number of iterations). One solution to this problem is to rewrite the problem as:

$$y - x = \log(2/3)$$

$$2x + 3y = 10000$$

And solve it using matrix algebra:

```
> A = matrix(c(-1,2,1,3),2,2)
> x = solve(A,c(log(2/3),10000))
> x

[1] 2000.243 1999.838
```

4.2 Multidimensional Optimization

4.2.1 A monopoly problem

Consider the problem in which a monopoly maximizes the following profit function:

$$\Pi(Y,Z) = P_y(Y,Z)Y + P_z(Y,Z)Z - C_y(Y) - C_z(Z)$$

where the inverse demands $P_y(Y,Z)$ and $P_z(Y,Z)$ are derived from the utility function:

$$\begin{aligned} U =& (Y^\alpha + Z^\alpha)^{\eta/\alpha} + M \\ =& u(Y,Z) + M \end{aligned}$$

where M is the dollar expenditure on other goods. In other words, the consumer's problem is:

$$\max_{Y,Z} u(Y,Z) + (I - P_z Z - P_y Y),$$

where I is the consumer's income. It implies that $P_y(Y,Z) = u_y(Y,Z)$ and $P_z(Y,Z) = u_z(Y,Z)$. The monopoly problem is therefore:

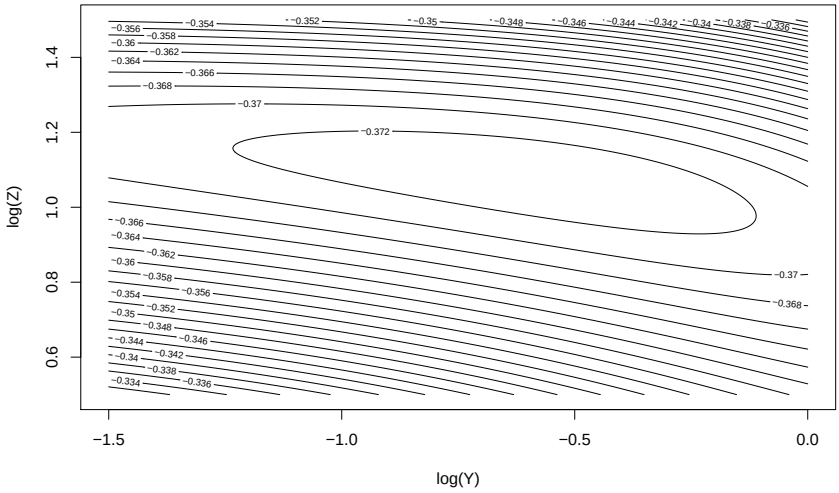
$$\max_{Y,Z} u_y(Y,Z)Y + u_z(Y,Z)Z - C_y(Y) - C_z(Z),$$

where, $C_y(Y) = 0.62Y$, $C_z(Z) = 0.60Z$, $\alpha = 0.98$, and $\eta = 0.85$. In the book, the author suggests to redefine the variables Y and Z to allow the admissible space to be the real line. Because α is less than one, Y and Z cannot be negative. Such restrictions may create problems. So we will solve for $y = \log Y$ and $z = \log Z$ instead. The function is

```
Profit <- function(y, z) {
    Y = exp(y)
    Z = exp(z)
    a = 0.98
    n = 0.85
    A = n * (Y^a + Z^a)^(n/a - 1)
    R = A * (Y^a + Z^a) - 0.62 * Y - 0.6 * Z
    return(-R)
}
```

There are two ways to see the shape of a three dimensional function in R. You can use the contour() or the wireframe() from the lattice package. For the latter, I am not transforming the variable because it makes the function look flat. It is easier that way to see the shape. The solution of the problem is $y = -0.562$ (or $Y = 0.57$) and $z = 1.077$ (or $Z = 2.936$).

```
> y <- seq(-1.5,0,length=200)
> z <- seq(0.5,1.5,length=200)
> x <- outer(y,z,Profit)
> contour(x=y,y=z,z=x,nlevels=20,xlab="log(Y)",ylab="log(Z)")
```

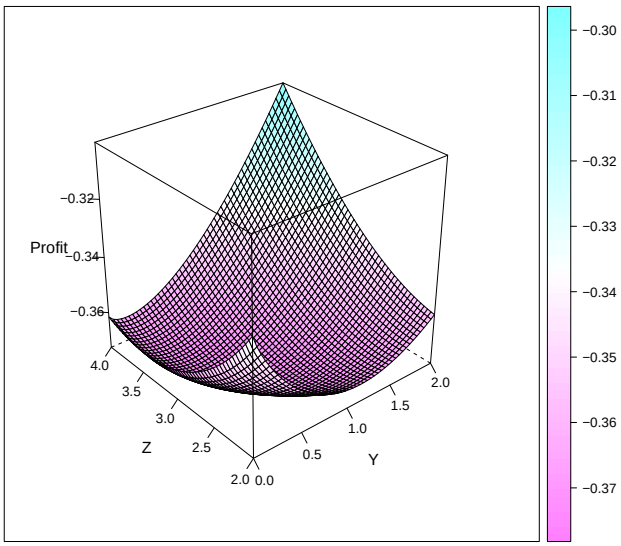



```
> pretty.print(Profit2)
```

```
Profit2 <- function(Y, Z) {
    a <- 0.98
    n <- 0.85
    A = n * (Y^a + Z^a)^(n/a - 1)
    R = A * (Y^a + Z^a) - 0.62 * Y - 0.6 * Z
    return(-R)
}
```

```
> library(lattice)
> z <- seq(2,4,length=50)
> y <- seq(0,2,length=50)
> res <- expand.grid(y,z)
> x <- Profit2(y<-res$Var1,z<-res$Var2)
```

```
> print(wireframe(x~y*z ,xlab="Y",ylab="Z",zlab="Profit",
+ scales = list(arrows = FALSE), drape = TRUE, colorkey = TRUE))
```



Exercise 4.1. *Build an algorithm that finds the minimum of a function using the Grid Search method. The function will be: Grid(f,from, to, n, eps), where f is a function of x, a $k \times 1 vector$, $from$ and to are the lower and upper bounds of x, n is the number of points per variable, and eps if the tolerance level. Test your function using the above example.*

4.2.2 Newton's Method

The first method is the Newton's Method. It is the multidimensional version of the one presented in Section 4.1. The procedure is:

$$x_{k+1} = x_k - H(x_k)^{-1} J(x_k),$$

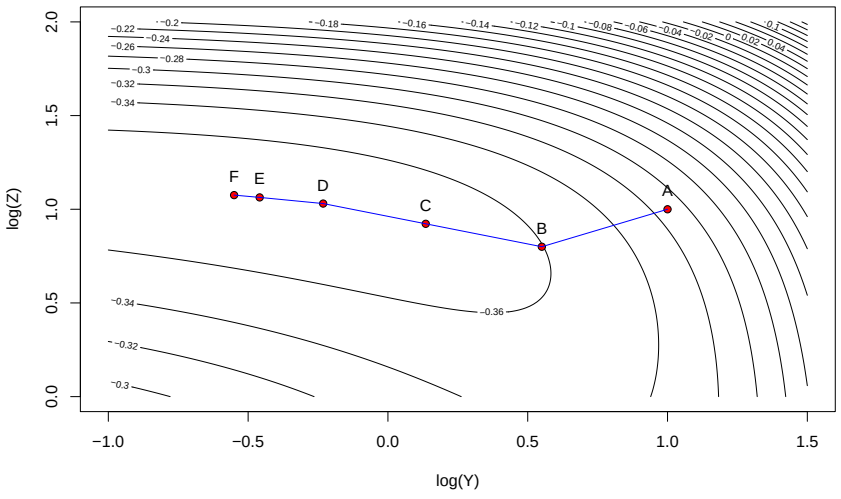
where $J()$ is the Jacobian and $H()$ the Hessian of the function we are minimizing. If $f()$ is an expression, it is easy to build the algorithm:

```
getDer <- function(f, x) {
    # x must contain the names of the variables
    n <- length(x)
    x <- as.list(x)
    J <- vector()
    H <- matrix(0, n, n)
    for (i in 1:n) {
        Df <- D(f, names(x[i]))
        J[i] <- eval(Df, x)
        for (j in 1:i) H[i, j] <- eval(D(Df, names(x[j])), x)
```

```
    }
    H[upper.tri(H)] <- H[lower.tri(H)]
    dimnames(H) <- list(names(x), names(x))
    names(J) <- names(x)
    return(list(H = H, J = J))
}

MNewton <- function(f, x0, eps = 1e-08, delta = 1e-08, maxit = 1000) {
    n <- 1
    conv = TRUE
    mess <- NULL
    fx <- eval(f, as.list(x0))
    res <- c(x0, fx)
    while (TRUE) {
        resD <- getDer(f, x0)
        H <- resD$H
        J <- resD$J
        x <- x0 - solve(H, J)
        fx <- eval(f, as.list(x))
        res <- rbind(res, c(x, fx))
        crit1 <- sqrt(crossprod(x - x0))/(1 + sqrt(crossprod(x0)))
        if (crit1 < eps) {
            crit2 <- sqrt(crossprod(J))/(1 + abs(fx))
            if (crit2 < delta)
                break
        }
        if (n >= maxit) {
            mess <- paste("maxit(", maxit, ") reached", sep = "")
            conv = FALSE
            break
        }
        x0 <- x
        n <- n + 1
    }

    n <- nrow(res)
    ans <- list(obj = res[n, ncol(res)], sol = x, x = res, name = "Newton's Method for M
        conv = conv, prec = crit1, mess = mess)
    class(ans) <- "NonlinSol"
    return(ans)
}
```

We can then try it with the monopoly problem, and plot the result on a contour plot:

```
> f <- expression(-0.85*(exp(y)^0.98+exp(z)^0.98)^(0.85/0.98-1)*(exp(y)^0.98 +
+         exp(z)^0.98)+0.62*exp(y)+0.6*exp(z))
> res <- MNewton(f,c(y=1,z=1))
> res

Method:  Newton's Method for Multidimensional Problems
Message: Converged after  9  iterations

The solution is:
y  =  -0.5625466
z  =  1.076945

f(x) is  -0.3731764
Precision:  3.098286e-15

> y <- seq(-1,1.5,length=200)
> z <- seq(0,2,length=200)
> x <- outer(y,z,Profit)
> contour(x=y,y=z,z=x,nlevels=20,xlab="log(Y)",ylab="log(Z)")
> text(res$x[1:6,1],res$x[1:6,2]+.1,c("A","B","C","D","E","F"))
> points(res$x[1:6,1],res$x[1:6,2],pch=21,bg=2)
> lines(res$x[1:6,1],res$x[1:6,2],col=4)
```



As for the unidimensional case, the method works well when we start not too far from the solution or if the function is well behaved. For the monopoly problem, we reach the solution using almost any starting values.

```
> MNewton(f,c(y=-3,z=7))

Method:  Newton's Method for Multidimensional Problems
Message: Converged after  14  iterations

The solution is:
y  =  -0.5625466
z  =  1.076945

f(x) is  -0.3731764
Precision:  1.217689e-14
```

```
> MNewton(f,c(y=7,z=12))

Method:  Newton's Method for Multidimensional Problems
Message: Converged after  22  iterations

The solution is:
y  =  -0.5625466
z  =  1.076945

f(x) is  -0.3731764
Precision:  4.912389e-09
```

Exercise 4.2. *Write a function that combines the Newton's and the Grid Search methods. It must use the grid search function you built for Exercise 4.1 to find a starting vector. The latter is then, use to initiate the Newton's Method. Try it with the monopoly problem.*

4.2.3 Direction Set Methods

Most optimization algorithms in R or any other numerical software are Direction Set Methods. The general step is

$$x_{k+1} = x_k + \lambda_k s_k,$$

where s_k is a vector representing the search direction and λ_k is a scalar. All methods differ in their respective choice of the search direction s_k. On the other hand, the method for computing λ_k is identical. If we want to minimize $f(x)$, λ_k is defined as:

$$\lambda_k = \arg\min_{\lambda} f(x_k + \lambda s_k)$$

Exercise 4.3. *Write a function that compute λ_k. The function must have the form: getLambda(f, x, s), where f is either an expression or a function (it is up to you). You can also allow the two possibilities. You can verify your function by using the Profit function. You should get (The function is hidden from the notes):*

```
> print(getLambda(f,c(y=1,z=1),c(1,0)))

[1] -1.378165
```

We can summarize the different methods as follows (we consider the problem of minimizing $f(x)$, with $x \in \mathbb{R}^n$:

- **Coordinate Direction:** $s_k = e_i$ for $i = 1, ..., n$ for each iteration (n directions by iteration), where e_i is the $n \times 1$ vector with the i^{th} element equals to 1 and all others being equal to zero. (Always find a minimum when the function is smooth but may be slow)

- **Steepest Descent:** $s_k = -J(x_k)$ (Always find a minimum when the function is smooth but may be slow)

- **Newton's Method with Line Search:** $s_k = -H(x_k)^{-1}J(x_k)$. As opposed to the Newton's Method, it will always go downhill.

- **Broyden-Fletcher-Goldfarb-Shanno (BFGS):** $s_k = -H(x_k)^{-1}J(x_k)$, but H_k is just an approximation of the hessian matrix. Starting with $H_0 = I$, the updates are:
$$H_{k+1} = H_k - \frac{H_k z_k z_k' H_k}{z_k' H_k z_k} + \frac{y_k y_k'}{y_k' z_k},$$
where $z_k = x_{k+1} - x_k$ and $y_k = J(x_{k+1}) - J(x_k)$. Whenever, $y_k' z_k \approx 0$, $H_{k+1} = H_k$.

- **Conjugate Gradient:** This method does not require the Hessian matrix; only the Jacobian. The steps are: $s_0 = -J(x_0)$ and
$$s_{k+1} = -J(x_{k+1}) + \frac{\|J(x_{k+1})\|^2}{\|J(x_k)\|^2} s_k$$
and reset s_k to $-J(x_k)$ every n iterations.

- **Gauss-Newton Method for Nonlinear Least Squares:** This method is specific to the following problem:
$$f(x) = \sum_{i=1}^{T} e_i^2(x),$$

where $e_i(x)$ is the i^{th} residual (here, x is the vector of coefficients). Let the $T \times n$ matrix $J(x)$ be the Jacobian of the vector of residuals $e(x)$. Than the Gauss-Newton step is:

$$s_k = -[J(x_k)'J(x_k)]^{-1}[J(x_k)'e(x_k)]$$

It is like the Newton's Method but the Hessian is approximated by $[J(x_k)'J(x_k)]$.

We first consider an application of the Gauss-Newton method. Lets consider the following Box-Cox transformation:

$$\frac{y_i^\lambda - 1}{\lambda} = \alpha + \beta z_i + e_i$$

The vector x is $\{\lambda, \alpha, \beta\}$. The i^{th} line of J is then:

$$J(x)[i,] = \frac{\partial e_i}{\partial x} = \begin{pmatrix} \frac{y_i^\lambda[\lambda \log(y_i) - 1] + 1}{\lambda^2} & -1 & -z_i \end{pmatrix}$$

The following function applies the method but without line search:

```
GaussNewton <- function(f, x0, dat, eps = 1e-08, delta = 1e-08,
    maxit = 1000) {
    # f produces the vector of residuals dat must be a list, x0
    # a named vector
    Jfct <- function(x, dat) {
        J <- eval(D(f, names(x)[1]), c(as.list(x), dat))
        for (i in 2:length(x)) J <- cbind(J, eval(D(f, names(x)[i]),
            c(as.list(x), dat)))
        return(J)
    }
    n <- 1
    conv = TRUE
    mess <- NULL
    fx <- eval(f, c(as.list(x0), dat))
    res <- c(x0, sum(fx^2))
    while (TRUE) {
        J <- Jfct(x0, dat)
        H <- crossprod(J)
        J <- crossprod(J, fx)
        x <- c(x0 - solve(H, J))
        names(x) <- names(x0)
        fx <- eval(f, c(as.list(x), dat))
        res <- rbind(res, c(x, sum(fx^2)))
```

```
        crit1 <- c(sqrt(crossprod(x - x0))/(1 + sqrt(crossprod(x0))))
        if (crit1 < eps) {
            crit2 <- sqrt(crossprod(J))/(1 + abs(fx))
            if (crit2 < delta)
                break
        }
        if (n >= maxit) {
            mess <- paste("maxit(", maxit, ") reached", sep = "")
            conv = FALSE
            break
        }
        x0 <- x
        n <- n + 1
    }
    n <- nrow(res)
    ans <- list(obj = res[n, 2], sol = x, x = res, name = "Gauss-Newton's Method for NLS Pr
        conv = conv, prec = crit1, mess = mess)
    class(ans) <- "NonlinSol"
    return(ans)
}
```

We can see that the method does not work well for the Box-Cox estimation. Even if we try different starting values, the algorithm diverges. The problem is that the approximated Hessian becomes singular.

```
> f <- expression((y^l-1)/l -a -z*b)
> library(Ecdat)
> data(Consumption)
> C <- Consumption[,"ce"]
> z <- ts(1:length(C),freq=4,start=c(1947,1))
> dat <- list(y=C,z=z)
> res2 <- try(GaussNewton(f,c(l=.25,a=56,b=.2),dat,maxit=50,eps=1e-4))
> cat(res2[1])

Error in solve.default(H, J) :
  system is computationally singular: reciprocal condition number = 1.1135e-16
```

In some cases, however, it works fine. Consider the following nonlinear model:

$$Y_i = \alpha_1 + \alpha_2\alpha_3 x_i + \alpha_2^2 z_i + \varepsilon_i$$

In the following, I test the method using simulated data with $\alpha_1 = 2$, $\alpha_2 = 3$, and $\alpha_3 = 5$. We can see that the method works fine.

```
> x <- rnorm(200)
> z <- rnorm(200)
> y <- 2+3*5*x+9*z+rnorm(200)
> f <- expression(y-a1-a2*a3*x-a2^2*z)
> dat <- list(y=y,x=x,z=z)
> x0 <- c(a1=0,a2=1,a3=1)
> res3 <- try(GaussNewton(f,x0,dat,maxit=100))
> print(res3)

Method:  Gauss-Newton's Method for NLS Problems
Message: Converged after  7  iterations

The solution is:
a1  =  1.989565
a2  =  3.021293
a3  =  5.019381

f(x) is  3.021293
Precision:  0
```

Exercise 4.4. *Reproduce the results from Table 4.12 (Section 4.11) of Judd. You have to compare the Newton and Gauss-Newton Methods for the following model:*

$$y = \alpha x_1 + \beta x_2 + \beta^2 x_3 + \varepsilon$$

The residual sum of squares is:

$$\begin{aligned} S(\alpha, \beta) =& 38.5 - 5.24\alpha - 7.56\alpha^2 - 6.10\beta + 9.96\alpha\beta \\ & - 3.44\beta^2 + 11.4\alpha\beta^2 + 11.6\beta^3 + 7.71\beta^4 \end{aligned}$$

I conclude the section with a function to compute the BFGS method. For that function, I require f to be a function and we have to provide a function that computes the Jacobian. This setup does not exclude the use of symbolic derivatives. Here is an example using the Box-Cox model:

```
fBC <- function(beta, dat) {
    e <- expression((y^l - 1)/l - a1 - a2 * x)
    sum(eval(e, c(as.list(beta), dat))^2)/2
}

DfBC <- function(beta, dat) {
    e <- expression((y^l - 1)/l - a1 - a2 * x)
```

```
    J <- eval(D(e, names(beta)[1]), c(as.list(beta), dat))
    for (i in 2:length(beta)) J <- cbind(J, eval(D(e, names(beta)[i]),
        c(as.list(beta), dat)))
    et <- eval(e, c(as.list(beta), dat))
    crossprod(J, et)
}
```

To allow both the case of theoretical and empirical models, The "..." can be passed to f and *grad* when we need to use data or set other parameter values.

```
BFGS <- function(f, x0, grad, eps = 1e-08, delta = 1e-08, maxit = 100,
    ...) {
    n <- 1
    conv = TRUE
    mess <- NULL
    fx <- f(x0, ...)
    res <- c(x0, fx)
    H <- diag(length(x0))
    while (TRUE) {
        J <- grad(x0, ...)
        s <- solve(H, -J)
        l <- getLambda(f, x0, s, -50, 50, ...)
        x <- x0 + l * s
        names(x) <- names(x0)
        fx <- f(x, ...)
        res <- rbind(res, c(x, fx))
        crit1 <- sqrt(crossprod(x - x0))/(1 + sqrt(crossprod(x0)))
        if (crit1 < eps) {
            crit2 <- sqrt(crossprod(J))/(1 + abs(fx))
            if (crit2 < delta)
                break
        }
        if (n >= maxit) {
            mess <- paste("maxit(", maxit, ") reached", sep = "")
            conv = FALSE
            break
        }
        zk <- (x - x0)
        yk <- J - grad(x, ...)
        T1 <- c(t(yk) %*% zk)
        T2 <- H %*% zk %*% t(zk) %*% H
```

```
        T3 <- c(t(zk) %*% H %*% zk)

        if (abs(T1) > 1e-07)
            H <- H - T2/T3 + (yk %*% t(yk))/T1
        n <- n + 1
        x0 <- x
    }

    n <- nrow(res)
    ans <- list(obj = res[n, 2], sol = x, x = res, name = "BFGS Method",
        conv = conv, prec = crit1, mess = mess)
    class(ans) <- "NonlinSol"
    return(ans)
}
```

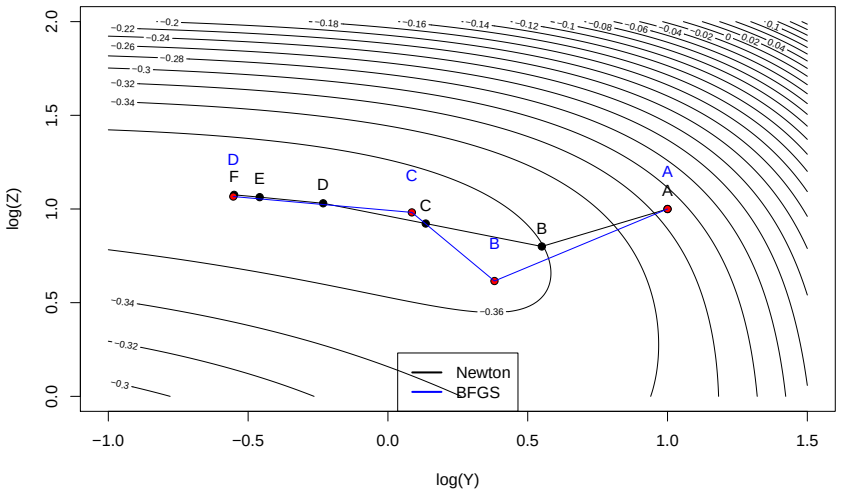
Lets try it on the monopoly problem:

```
f <- function(x) {
    fexp <- expression(-0.85 * (exp(y)^0.98 + exp(z)^0.98)^(0.85/0.98 -
        1) * (exp(y)^0.98 + exp(z)^0.98) + 0.62 * exp(y) + 0.6 *
        exp(z))
    eval(fexp, as.list(x))
}

Df <- function(x) {
    fexp <- expression(-0.85 * (exp(y)^0.98 + exp(z)^0.98)^(0.85/0.98 -
        1) * (exp(y)^0.98 + exp(z)^0.98) + 0.62 * exp(y) + 0.6 *
        exp(z))
    Df <- vector()
    for (i in 1:length(x)) Df[i] <- eval(D(fexp, names(x)[i]),
        as.list(x))
    Df
}
```

```
> res4 <- BFGS(f,x0=c(y=1,z=1),grad=Df)
> res4

Method:  BFGS Method
Message: Converged after  8  iterations

The solution is:
y  =  -0.5625466
```

```
z  =  1.076945

f(x) is  1.076945
Precision:  3.479056e-09
```

The convergence is faster than the Newton's method. We see why on the next figure



Exercise 4.5. *Answer the following questions*

1. *Write a function that solves optimization problems by the Coordinate Direction with Line Search.*

2. *Write a function that solves optimization problems by the Steepest Descent with Line Search.*

3. *Write a function that solves optimization problems by the Newton's Method with Line Search.*

4. *Write a function that solves optimization problems by the Conjugate Gradient with Line Search.*

5. *Using the above monopoly example, Compare the Coordinate Direction, the Steepest Descent, the Newton's Method with Line Search, the Conjugate Gradient, the BFGS, and the Newton's Method on a contour plot.*

6. *Compare your methods with optim() (compare the values of the coefficients and the function, and the number of iterations)*

Exercise 4.6. *Answer question 1 of Chapter 4 of Judd (but do not use the Polytope method).*

Exercise 4.7. *Answer question 2 of Chapter 4 of Judd.*

4.2.4 Finite Differences

To avoid having to derive the analytical derivatives, it is possible to compute the derivatives using finite differences. The derivatives are:

$$f'(x) = \lim_{h \to 0} \frac{f(x+h) - f(x)}{h}$$

We can approximate the derivatives by:

$$f'(x) \approx \frac{f(x+h) - f(x)}{h}$$

for some small h. To be precise, h should be of order $\sqrt{\varepsilon_f}|x_c|$, where ε_f is the rounding error from evaluating f(x) and x_c is $[f(x)/f''(x)]^{1/2}$ (see [Press *et al.* 2007] page 229 for more details). This is meant to minimize the error. However, the following rule works most of the time: $h = \max(\varepsilon_1|x|, \varepsilon_2)$, where ε_1 can be around the square root of the machine-epsilon (10^{-8}), and ε_2 is a not too small number. The latter is to prevent problems when x is close to zero. If we set $\varepsilon_2 = 10^{-4}$, h will take that value whenever $|x| < 10^4$. The following computes the numerical derivative of any function:

```
myDerive <- function(f, x, eps1 = 1e-08, eps2 = 1e-04) {
    h <- max(eps1 * abs(x), eps2)
    (f(x + h) - f(x))/h
}
```

Lets try it for the following functions at $x = 3$: $f1(x) = exp(x)$, $f2(x) = log(x)$, $f3(x) = (x^2 - x)$, $f4(x) = x^3 \sin(x)$: A better precision can be obtained by using the

	Estimated derivative	True Derivative	relative error
f1(x)	20.08654	20.08554	0.00005
f2(x)	0.33333	0.33333	0.00002
f3(x)	5.00010	5.00000	0.00002
f4(x)	-22.92229	-22.91956	-0.00012

following formula:

$$f'(x) \approx \frac{f(x+h) - f(x-h)}{2h},$$

which requires h to be of order $\varepsilon_f^{1/3}|x_c|$. Comparing the two methods is left as an exercise.

Exercise 4.8. *Write a function that computes the derivative of $f(x)$ using the above formula. Compare it with the first method using the same 4 functions.*

Exercise 4.9. *Write two functions to compute the Jacobian and the Hessian of $f(x)$, where $x \in \mathbb{R}^n$. Use the second method presented above.*

4.3 Constrained optimization

Suppose we want to solve:

$$\max_{x_1,x_2} x_1^{1/3} x_2^{2/3}$$

subject to:

$$3x_1 + 5x_2 = 1000$$

In this section, we only look at the Penalty Method. Instead of imposing the constraint we penalize the objective function if it violates it. We can write the model as follows:

$$\max_{x_1,x_2} x_1^{1/3} x_2^{2/3} - P(3x_1 + 5x_2 - 1000)^2$$

P is the cost of violating the constraint. We can than apply any method (the true solution is $x_1 = 111.11$, and $x_2 = 133.33$):

```
> f <- expression(-x1^(1/3)*x2^(2/3) + 10*(3*x1+5*x2-1000)^2)
> x0 <- c(x1=10,x2=10)
> MNewton(f,x0,eps=1e-8,delta=1e-8,maxit=1000)

Method:  Newton's Method for Multidimensional Problems
Message: Converged after  5  iterations

The solution is:
x1  =  111.1118
x2  =  133.3342

f(x) is  -125.4719
Precision:  1.062379e-10
```

Here, the precision is not valid.w={0,.5,.8,1.1,2,2,2,1.5,1,0} We see that the third decimal is contaminated. To increase the precision, we need to increase P.

```
> f <- expression(-x1^(1/3)*x2^(2/3) + 10^3*(3*x1+5*x2-1000)^2)
> MNewton(f,x0,eps=1e-8,delta=1e-8,maxit=1000)
```

```
Method:  Newton's Method for Multidimensional Problems
Message: Converged after  5  iterations

The solution is:
x1  =  111.1111
x2  =  133.3333

f(x) is  -125.4715
Precision:  1.062403e-10
```

The solution is much more accurate. It even works for corner solution such as:

$$\max_{x_1,x_2} x_1 + x_2$$

subject to

$$3x_1 + 5x_2 = 1000$$

$$x_1, x_2 \geq 0,$$

where the solution is $x_1 = 1000/3 = 333.33$, and $x_2 = 1$.

```
> f <- function(x)
+         {
+         -x[1]-x[2]+1000*(3*x[1]+5*x[2]-1000)^2+
+         1000*(min(0,x[2]))^2 + 1000*(min(0,x[1]))^2
+         }
> Df <- function(x)
+         {
+         D1 <- -1+6000*(3*x[1]+5*x[2]-1000)
+         D2 <- -1+10000*(3*x[1]+5*x[2]-1000)
+         D1 <- D1 + ifelse(x[1]>=0,0,2000*x[1])
+         D2 <- D2 + ifelse(x[2]>=0,0,2000*x[2])
+         return(c(D1,D2))
+         }
> print(try(BFGS(f,x0=c(x1=10,x2=10),grad=Df)))

Method:  BFGS Method
Message:  maxit(100) reached

The solution is:
x1  =  333.3339
x2  =  -0.0003336555
```

```
f(x) is  -0.0003336555
Precision:  2.999955e-09
```

Exercise 4.10. *Solve the problem:*

$$\max_{x_1,x_2} x_1^2 + x_2^2$$

subject to

$$6x_1 + 8x_2 = 4800,$$

using the Penalty Method and the BFGS algorithm. Choose P to obtain a 4-digit precision.

Exercise 4.11. *Consider the following problem:*

$$\max_{x_1,x_2} = (x_1^\alpha + x_2^\alpha)^{\eta/\alpha}$$

subject to

$$P_1(1-\tau)x_1 + P_2(1-\tau)x_2 = I,$$

where τ is the tax rate. Using the Penalty Method and the BFGS algorithm, write a function that plot the estimated demand function for x_1. The function must look like x1(p1,p2,t,alpha,eta,I).

4.4 Applications

4.4.1 Principal-Agent Problem

An agent offers his service to a principal. The possible outputs are $\{y_1, ..., y_n\}$ and the wage given to the agent by the principal is w_i iif $y = y_i$ because y is the only thing the principal observes. The level of effort, $L \in \{L_1, ..., L_m\}$, that the agent chooses, affects the distribution of output through the conditional distribution $g_i(L) = Prob(y = y_i|L = L)$. The best alternative contract for the agent pays R. Therefore, he will take the job if the expected utility is at least R. The principal's problem is:

$$\max_{L,w_i} E[U^P(y - w_i)]$$

subject to

$$E[U^A(w, L)] \geq E[U^A(w, L_i)] \quad i = 1, ..., m \text{ Incentive constraints}$$
$$E[U^A(w, L)] \geq R \text{ Reservation constraint}$$

We suppose there are 2 states and the principal is risk neutral. The values are: $L \in \{0, 1\}$, $\{y_1, y_2\} = \{0, 2\}$ with probability $\{0.2, 0.8\}$ if $L = 1$ and $\{0.6, 0.2\}$ if $L = 0$. The

utility function of the agent is $-e^{-2w} + 1 - d(L)$, where $d(0) = 0$ and $d(1) = 0.1$. The agent's utility from his best alternative is $R = -e^{-2} + 0.9$. The principal's problem is therefore:

$$\max_{L^*, w_1, w_2} E(y - w|L)$$

subject to

$$\begin{aligned} E[d(w) - d(L^*)|L = L^*] &\geq E[d(w) - d(0)|L = 0] \\ E[d(w) - d(L^*)|L = L^*] &\geq E[d(w) - d(1)|L = 1] \\ E[d(w) - d(L^*)|L = L^*] &\geq R \end{aligned}$$

Exercise 4.12. *Write a function that solves the above Principal-Agent's problem. It is not like in the textbook because Judd sets L^* to 1. Here L is discrete and w_i are continuous variables. Use the numerical algorithm that you want.*

4.4.2 Efficient Outcomes with Adverse Selection

We have two types of agent and a social planner that offers insurance. There are two states: a bad one (2), and a good one (1). Types H and L receive $e_1 > e_2$ with probability π^H and π^L respectively. with $\pi^L < \pi^H$. The proportion of type i is θ^i, for $i = L, H$. In each state j, agents of type i pay a premium of $e_j - y_j^i$ and consumes y_j^i. The profit of the social planner is therefore:

$$\Pi = \sum_{i=H,L} \theta^i [\pi^i (e_1 - y_1^i) + (1 - \pi^i)(e_2 - y_2^i)]$$

The expected utility of type i agents is therefore:

$$U^i(y^i) = \pi^i u^i(y_1^i) + (1 - \pi^i) u^i(y_2^i) \quad i = H, L$$

Suppose the Social Planner puts a weight λ on type H agents and $(1 - \lambda)$ on type L, his problem is:

$$\max_{y_j^i} \lambda U^H(y^H) + (1 - \lambda) U^L(y^L)$$

subject to

$$\begin{aligned} U^H(y^H) &\geq U^H(y^L) \\ U^L(y^L) &\geq U^L(y^H) \\ \Pi &\geq 0 \end{aligned}$$

So you want the type H to prefer the insurance that provides the contingent consumption $\{y_1^H, y_2^H\}$ and the type L to prefer $\{y_1^L, y_2^L\}$, and you want the Social Planner to have none negative profit.

Exercise 4.13. *Write a function to solve the above Adverse Selection problem for $\lambda = \{0, .25, .5, .75, 1\}$ and $\theta^H = \{0.1, 0.75\}$. You can suppose that $\pi^L = 0.5$, $\pi^H = 0.8$, $e_1 = 1$, $e_2 = 0$, and $u^i(y) = -e^{-y}$ for $i = L, H$. Interpret your results.*

4.4.3 Computing Nash Equilibrium.

We consider a general simultaneous game with n players. We suppose that each player i has a finite number J_i of possible strategies: $\{s_{1i}, ..., s_{J_i i}\}$. A mixed strategy for player i, σ_i, is a $J_i \times 1$ vector of probabilities associated with each strategy. Therefore, $\sigma_{ij} \geq 0$ and $\sum_{j=1}^{J_i} \sigma_{ij} = 1$. To understand the notation, let us consider the following battle of sexes game:

		Player 2	
		Opera	Hockey
Player 1	Opera	1 1	0 0
	Hockey	0 0	1 1

We have $J_1 = J_2 = 2$, and $s_i = \{\text{Opera,Hockey}\}$ for $i = 1, 2$. A mixed strategy for player i is $\sigma_i = \{p_i, (1 - p_i)\}$ where $p_i = Prob(s_i = \text{Opera})$. Let $M(s)$ be the payoff function. For a given vector of strategies, s, it returns an $n \times 1$ vector of payoffs. In the battle of sexes game, $M(s)$ is represented by the above matrix. We have, for example, $M(\text{Opera,Opera}) = \{1, 1\}'$, or $M(\text{Opera,Hockey}) = \{0, 0\}'$. We can generalize the payoff function to include mixed strategies:

$$M_i(\sigma) = \sum_s \sigma(s) M_i(s)$$

In our example, $\sigma_{i1} = p_i$ and $\sigma_{i2} = (1 - p_i)$. Therefore:

$$\begin{aligned} M_1(\sigma) =& p_1[p_2(1) + (1 - p_2)(0)] + (1 - p_1)(p_2(0) + (1 - p_2)(1)] \\ =& p_1 p_2 - (1 - p_1)(1 - p_2) \\ =& M_2(\sigma), \end{aligned}$$

We define $M_i(s_{ij}, \sigma_{-i})$ as the payoff of player i when he plays the pure strategy s_{ij} and the other players play the mixed strategy σ. Let us define the following function:

$$v(\sigma) = \sum_{i=1}^{n} \sum_{s_{ij}} [\max\{M_i(s_{ij}, \sigma_{-i}) - M_i(\sigma), 0\}]^2$$

McKelvey (1992) shows that Nash Equilibia are both the minima and the zeros of $v(\sigma)$. In our example, $M_1(s_{11}, \sigma_{-1}) = p_2$ and $M_1(s_{12}, \sigma_{-1}) = (1 - p_2)$, and $M_2(s_{21}, \sigma_{-2}) = p_1$ and $M_2(s_{22}, \sigma_{-2}) = (1 - p_1)$. Therefore,

$$\begin{aligned} v(\sigma) \equiv& v(p_1, p_2) \\ =& [\max\{0, p_2 - M_1(\sigma)\}]^2 + [\max\{0, (1 - p_2) - M_1(\sigma)\}]^2 \\ &+ [\max\{0, p_1 - M_2(\sigma)\}]^2 + [\max\{0, (1 - p_1) - M_2(\sigma)\}]^2 \end{aligned}$$

It means that playing any pure strategy cannot result in payoffs higher than the payoffs from playing the mixed strategy σ. The different equilibria are obtained by minimizing $v(\sigma)$ using different starting values, and by verifying that the solution that we obtain implies that $v(\sigma) = 0$.

Exercise 4.14. *Write a function that computes Nash equilibria for general 2-player games. The number of possible strategies for each player may differ. The matrix of payoffs can be a list of matrices (2 $J_1 \times J_2$ matrices) or a 3 dimensional array ($J_1 \times J_2 \times 2$). Use your function to answer question 4 of Chapter 4 of Judd.*

4.4.4 Portfolio Problem

Consider an economy with n assets. Asset 1 is risk free and its price is $p_1 = 1$. This is a two period model in which investors are endowed with $\{e_1, ..., e_n\}$ units of assets in period 1 and must choose how much to consume and how much to save for next period consumption. They can purchase $\{\omega_1, ..., \omega_n\}$ units of assets in period one at $\{1, p_2, ..., p_n\}$. The assets will be worth $\{Z_1, ..., Z_n\}$ in period 2. Period 1's budget constraint is therefore:

$$\sum_{i=1}^{n} p_i \omega_i + c = \sum_{i=1}^{n} p_i e_i$$

and the investors wants to maximize the expected utility of the two periods:

$$EU = u(c) + E\left\{ u\left(\sum_{i=1}^{n} \omega_i Z_i \right) \right\}$$

Exercise 4.15. *Answer the following questions:*

1. *Solve the Portfolio Problem with: $n = 3$, $u(c) = -e^{-ac}$, $a \in \{-0.5, -1, -5\}$, $Z_1 = 2$, $Z_2 \sim \{0.72, 0.92, 1.12, 1.32\}$ with probabilities $\{1/4, 1/4, 1/4, 1/4\}$, $Z_3 \sim \{0.86, 0.96, 1.06, 1.16\}$ with probabilities $\{1/4, 1/4, 1/4, 1/4\}$, $p = \{1, .5, .5\}$, and $e = \{2, 2, 2\}$. We also suppose that Z_2 and Z_3 are independent. Interpret your results (for the all a's).*

2. *Suppose now that $p = \{1, .3, .4\}$. Is there a solution to the problem? Why? Add the assumption that short sales are forbidden and try to solve the problem for all a's. Interpret the results.*

4.4.5 Dynamic Optimization

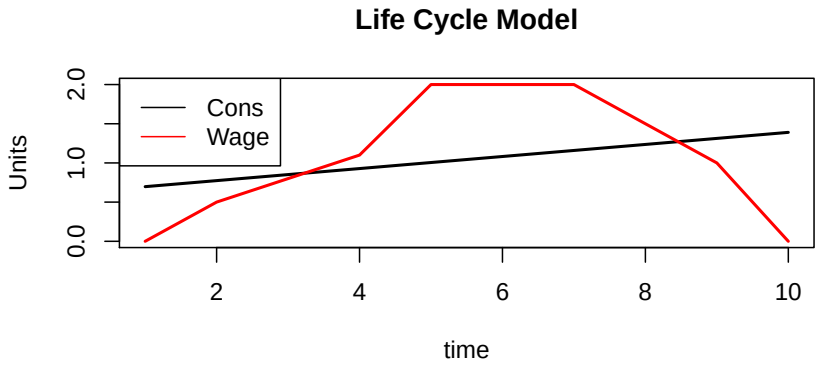
Consider an individual who lives n periods. At each period t, he allocates his wage w_t between consumption c_t and saving S_t. We suppose the interest rate r is constant. The

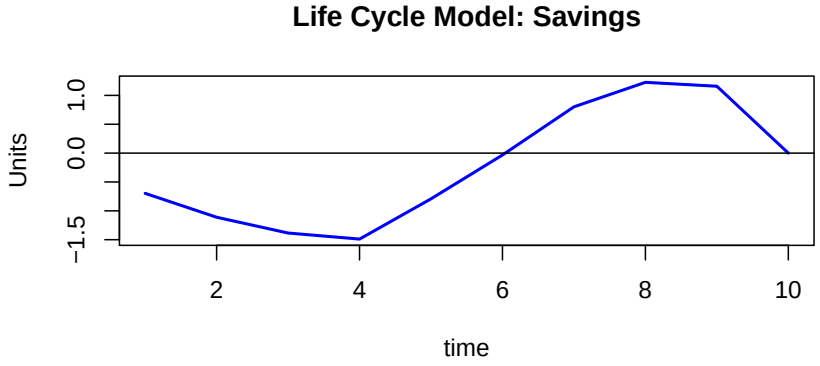
individual's problem is to maximize his future discounted utility:

$$\max_{S_t} \sum_{t=1}^{T} \beta^t u(S_{t-1}(1+r) + w_t - S_t),$$

subject to $S_0 = S_T = 0$. We therefore have to solve for S_t, $t = 1, ..., (T-1)$.

Consider the following case: $u(c) = -exp(-c)$, $\beta = 0.9$, $r = .0.2$, $T = 10$, and $w = \{0, .5, .8, 1.1, 2, 2, 2, 1.5, 1, 0\}$. The following graph shows the result:





Exercise 4.16. *Write a function that solves the above dynamic optimization problem with* $r \in \{-.05, 0.2, 0.5\}$. *Plot* S_t *and* C_t *for the different* r_t *and interpret your results.*

Chapter 5

Nonlinear Equations

Contents

5.1 One-dimensional problems

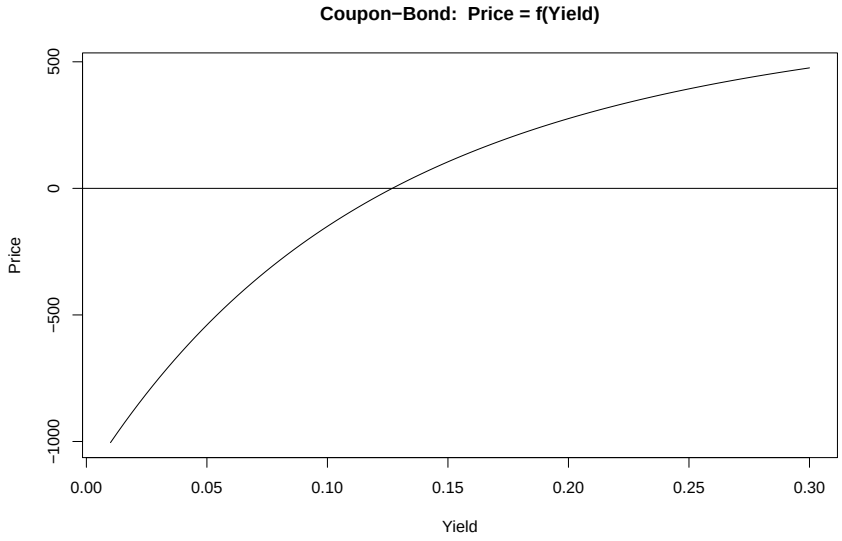
Consider the problem of computing the yield to maturity of a coupon-bond with semi-annual coupon of \$50, par value of \$1,000, maturity of 10 years, and a price of \$850. The formula that links the bond price and the yield is:

$$P = \frac{C}{y/2} + \left(PAR - \frac{C}{y/2}\right)(1 + y/2)^{-2T},$$

where C is the coupon, y is the yield to maturity compounded semiannually, T is the maturity, and PAR is the par value. In our problem, we want to solve:

$$f(y) = 850 - \frac{50}{y/2} - \left(1000 - \frac{50}{y/2}\right)(1 + y/2)^{-20} = 0$$

The following graph shows the shape of $f(y)$:



One possibility is to solve the problem using a grid-search. In the above example, we know that the solution must be between 0 and 1, which makes it easy to construct the grid. The following function is an example of how to do it. The stopping rule is: stop if a) $f(x_i) < 0$, $f(x_j) > 0$,and either b) $\max(x_i, x_j) - min(x_i, x_j) < \varepsilon(1 + |x_i| + |x_j|)$, or c) $|f((x_i + x_j)/2)| < \delta$.

```
YieldGrid <- function(from, to, n, eps = 1e-06, delta = 1e-06,
    maxit = 100, P = 850, PAR = 1000, C = 50, N = 2, T = 10) {
    f <- function(y) P - C/(y/N) - (PAR - C/(y/N)) * (1 + y/N)^(-N *
        T)
    y <- seq(from, to, len = n)
    fVal <- f(y)
    neg <- fVal < 0
    if (all(neg) | all(!neg))
        stop("There is no solution between from and to")
    t <- 1

    while (TRUE) {
        if (neg[1]) {
            to <- y[which(!neg)][1]
            from <- y[which(!neg) - 1][1]
        } else {
            to <- y[which(neg)][1]
            from <- y[which(neg) - 1][1]
        }
```

```
        check <- (to - from) < eps * (1 + abs(from) + abs(to)) |
            abs(f((from + to)/2)) < delta
        if (t >= maxit) {
            mess <- "No convergence: maxit reached"
            break
        }
        if (check) {
            mess <- paste("Converged after ", t, " iterations",
                sep = "")
            break
        }
        y <- seq(from, to, len = n)
        fVal <- f(y)
        neg <- fVal < 0
        t <- t + 1
    }
    ans <- list(sol = (from + to)/2, fct = f((from + to)/2),
        message = mess, iter = t, name = "Grid Search for Yield to Maturity",
        prec = to - from)
    class(ans) <- "Zeros"
    return(ans)
}

print.Zeros <- function(obj) {
    cat("\nMethod: ", obj$name, "\n")
    cat("Message: ", obj$mess, "\n\n")

    if (length(obj$sol) == 1)
        cat("The solution is: ", obj$sol, ", and f(x) is ", obj$fct,
            "\n") else {
        cat("The solution is: \n")
        if (is.null(names(obj$sol)))
            names(obj$sol) <- paste("x", 1:length(obj$sol), sep = "")
        for (i in 1:length(obj$sol)) cat(names(obj$sol)[i], " = ",
            obj$sol[i], "\n")
        cat("\nf(x) is ", obj$fct, "\n")
    }
    cat("Precision: ", obj$prec, "\n")
}
```

The function is for general case and it produces an object of class "Zeros". All algorithms

of this chapter will produce the same type of object, The solution is:

```
> YieldGrid(.01,1,50,eps=1e-9)

Method:  Grid Search for Yield to Maturity
Message:  Converged after 6 iterations

The solution is:  0.1268917 , and f(x) is  1.666213e-07
Precision:  7.152515e-11
```

The method converges after 6 iterations. It may look efficient at first but since there are 50 function evaluations per iteration, the solution is reached after 300 function evaluations. We can do much better than that.

5.1.1 The Bisection Method

There is no analytical solution to the above problem, bu we can easily find the solution using a bracketing method called the Bisection. All we need is two points $a < b$ that are such that the signs of $f(a)$ and $f(b)$ are different. We then consider a third point $c = (a + b)/2$, and replace a by c if the sign of $f(a)$ and $f(c)$ are the same, and inversely if the signs of $f(b)$ and $f(c)$ are the same. The Stopping rule is: stop if either $b - a < \varepsilon(1 + |a| + |b|)$, or $|f((a + b)/2)| < \delta$. The following function computes the zero of a function between a and b using that method:

```
Bisection <- function(f, a, b, eps = 1e-07, delta = 1e-07, maxit = 100) {
    fa <- f(a)
    fb <- f(b)
    t <- 1
    if (a >= b)
        stop("a must be strictly smaller than b")
    if (fa * fb >= 0)
        stop("f(a) and f(b) have different signs")
    res <- vector()
    while (TRUE) {
        fc <- f(c <- (a + b)/2)
        if (fa * fc > 0) {
            a <- c
            fa <- fc
        } else {
            b <- c
            fb <- fc
        }
```

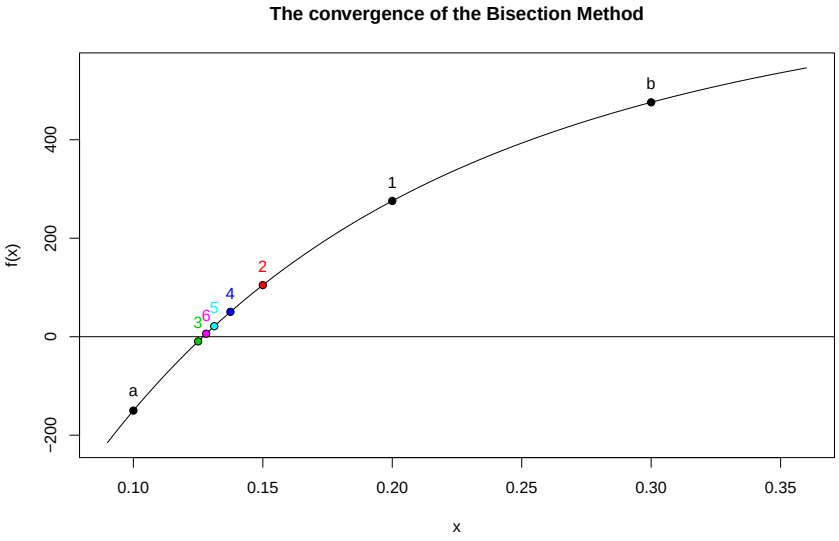
```
        res <- rbind(res, c(c, fc))
        if (t >= maxit) {
            mess <- "No convergence: maxit reached"
            break
        }
        check <- (b - a) < eps * (1 + abs(a) + abs(b)) | abs(fc) <
            delta
        if (check) {
            mess <- paste("Converged after ", t, " iterations",
                sep = "")
            break
        }
        t <- t + 1
    }
    ans <- list(sol = c, fct = fc, message = mess, iter = t,
        name = "Bisection", prec = (b - a), x = res)
    class(ans) <- "Zeros"
    return(ans)
}
```

We can then try it using the same problem:

```
> f <- function(y,P=850, PAR=1000, C=50, N=2, T=10)
+         P-C/(y/N)-(PAR-C/(y/N))*(1+y/N)^(-N*T)
> Bisection(f,.01,1)
```

```
Method:  Bisection
Message:  Converged after 23 iterations

The solution is:  0.1268917 , and f(x) is  -0.0004022902
Precision:  1.180172e-07
```

It is much better than the grid search if we consider that the algorithm evaluated the function only 23 times. The following graph shows the convergence of the method.



The solution of course depends on the choice of a and b. Is there are multiple solutions, it will find one solution in $[a, b]$. To see that, consider an exchange economy with 2 goods and 2 agents. The utility of agent i is (page 154 of Judd):

$$u_i(x_1, x_2) = \frac{a_1^i x_1^{\gamma_i+1}}{\gamma_i + 1} + \frac{a_2^i x_2^{\gamma_i+1}}{\gamma_i + 1} \quad , i = 1, 2,$$

where $a_j^i \geq 0$, and $\gamma_i < 0$. Let $\eta_i = -1/\gamma_i$, $e^i = \{e_1^i, e_2^i\}$ be the endowment of agent i, and $Y^i = p_1 e_1^i + p_2 e_2^i$ be the income of agent i. The equilibrium condition is $d_j^1(p) + d_j^2(p) = e_j^1 + e_j^2$ for goods $j = 1, 2$. By Walras's law, we only need to solve for one of the two goods. If we normalize the prices such that $p_1 + p_2 = 1$, the equilibrium condition is:

$$f(p_1) = d_1^1(p_1, 1 - p_1) + d_1^2(p_1, 1 - p_1) - e_1^1 - e_1^2 = 0$$

with

$$d_1^1(p_1, 1 - p_1) = \frac{(a_1^1)^{\eta_1}}{(a_1^1)^{\eta_1} p_1^{1-\eta_1} + (a_2^1)^{\eta_1}(1 - p_1)^{1-\eta_1}} Y^1 p_1^{-\eta_1}$$

$$d_1^2(p_1, 1 - p_1) = \frac{(a_1^2)^{\eta_2}}{(a_1^2)^{\eta_2} p_1^{1-\eta_2} + (a_2^2)^{\eta_2}(1 - p_1)^{1-\eta_2}} Y^2 p_1^{-\eta_2}$$

To solve the problem, I am constructing a new object of type utility, and we define two agents with the parameter values determined on page 154 of Judd.

```
CES <- function(par) {
    names(par) <- NULL
    good = TRUE
    if (length(par) != 5 | par[3] >= 0 | any(par[1:2] < 0) |
```

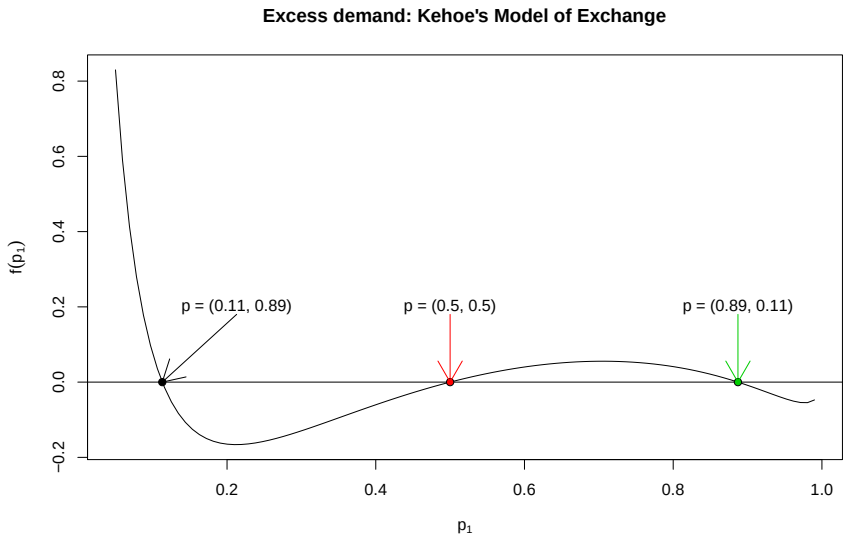
```
        any(par[4:5] < 0))
        good <- FALSE
    par <- c(a = par[1:2], gamma = par[3], eta = -1/par[3], e = par[4:5])
    f <- expression(a1 * x1^(gamma + 1)/(gamma + 1) + a2 * x2^(gamma +
        1)/(gamma + 1))
    X1 <- expression((a1^eta/(a1^eta * p1^(1 - eta) + a2^eta *
        p2^(1 - eta))) * (p1 * e1 + p2 * e2) * p1^(-eta))
    X2 <- expression((a2^eta/(a1^eta * p1^(1 - eta) + a2^eta *
        p2^(1 - eta))) * (p1 * e1 + p2 * e2) * p2^(-eta))
    Y <- expression(e1 * p1 + e2 * p2)
    Indif <- expression((((gamma + 1) * U - a1 * x1^(gamma +
        1))/a2)^(1/(gamma + 1)))
    fct <- paste("U = (", par[1], "*X1^", par[3] + 1, " + ",
        par[2], "*X2^", par[3] + 1, "/(", par[3] + 1, sep = "")
    ans <- list(Uexp = f, Sol = list(X1 = X1, X2 = X2), par = par,
        name = "CES", fct = fct, Indif = Indif, good = good,
        Y = Y)
    class(ans) <- "Utility"
    return(ans)
}
```

```
> cons1 <- consumer("John",c(1024,1,-5,12,1),utility="CES")
> cons2 <- consumer("Bill",c(1,1024,-5,1,12),utility="CES")
```

We can then easily compute the function that defines the equilibrium condition:

```
Kehoe <- function(p1) {
    d1 <- sapply(1:length(p1), function(i) solve(cons1, c(p1[i],
        1 - p1[i]), F)$x1)
    d2 <- sapply(1:length(p1), function(i) solve(cons2, c(p1[i],
        1 - p1[i]), F)$x1)
    d1 + d2 - cons1$par[4] - cons2$par[4]
}
```

The following graph shows the shape of the excess demand function. There are three possible equilibria.



If we try to solve it using the above Bisection method using different a and b, we obtain:

```
> Bisection(Kehoe,.01,.4)

Method:  Bisection
Message:  Converged after 22 iterations

The solution is:  0.1129238 , and f(x) is  2.06554e-07
Precision:  9.298325e-08

> Bisection(Kehoe,.4,.7)

Method:  Bisection
Message:  Converged after 19 iterations

The solution is:  0.5000002 , and f(x) is  9.765621e-08
Precision:  5.722046e-07

> Bisection(Kehoe,.7,.9)

Method:  Bisection
Message:  Converged after 19 iterations

The solution is:  0.8870762 , and f(x) is  -2.175291e-08
Precision:  3.814697e-07
```

Easy when we know the solutions. If the interval contains more than one solution, the result is uncertain:

```
> Bisection(Kehoe,.01,.9)

Method:  Bisection
Message:  Converged after 23 iterations

The solution is:  0.1129239 , and f(x) is  -1.799073e-07
Precision:  1.060963e-07

> Bisection(Kehoe,.01,.99)

Method:  Bisection
Message:  Converged after 1 iterations

The solution is:  0.5 , and f(x) is  3.552714e-15
Precision:  0.49

> Bisection(Kehoe,.1,.99)

Method:  Bisection
Message:  Converged after 21 iterations

The solution is:  0.887076 , and f(x) is  9.026282e-08
Precision:  4.243851e-07
```

5.1.2 Newton's Method

For the Newton's method, we first get the linear approximation of $f(x)$ around x_0, and find the zero of the linear function. We have $f(x) \approx f(x_0) + f'(x_0)(x - x_0) = 0$, which implies that $x = x_0 - f(x_0)/f'(f_0)$. The algorithm is therefore:

$$x_{k+1} = x_k - \frac{f(x_k)}{f'(x_k)}$$

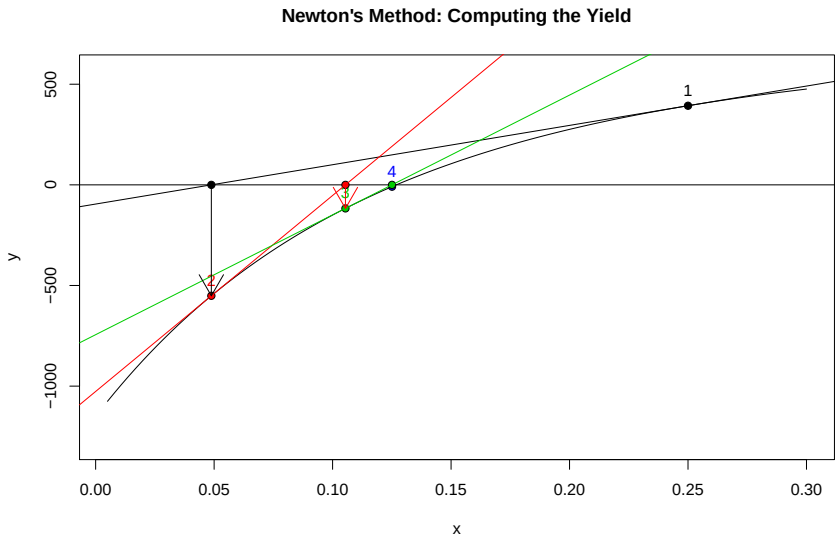
The stopping rule is similar to the one we used in the last chapter except that we want to check if $f(x_{k+1}) = 0$ is satisfied instead of $f'(x_{k+1}) = 0$. So we stop if $|x_k - x_{k+1}| < \varepsilon(1 + |x_{k+1}|)$ and conclude that we have a solution if $|f(x_{k+1}| < \delta$. I wrote a function to compute the solution using the Newton's Method. I don't show it to you because it is the next exercise. The function requires as arguments, $f(x)$ and $df(x)$. We can test it using the the above examples.

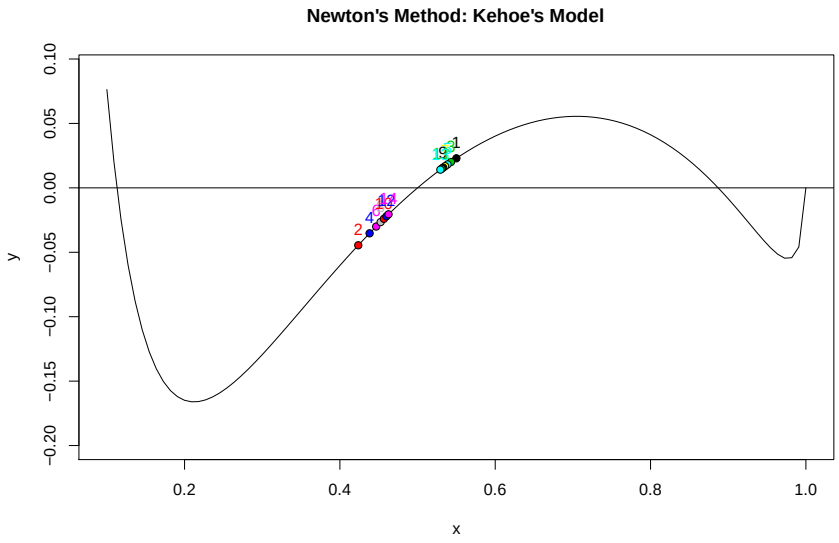
```
> Yield <- NewtonNL(f,df,.25)
> Equil <- NewtonNL(Kehoe,dKehoe,.55)
> Yield
```

```
Method:  Newton
Message:  Converged after 6 iterations

The solution is:  0.1268917 , and f(x) is  0
Precision:  6.642408e-10
```

```
> Equil
```

```
Method:  Newton
Message:  No convergence: maxit reached (Bad convergence, f(x) not zero)

The solution is:  0.5129672 , and f(x) is  0.006465041
Precision:  0.01818518
```

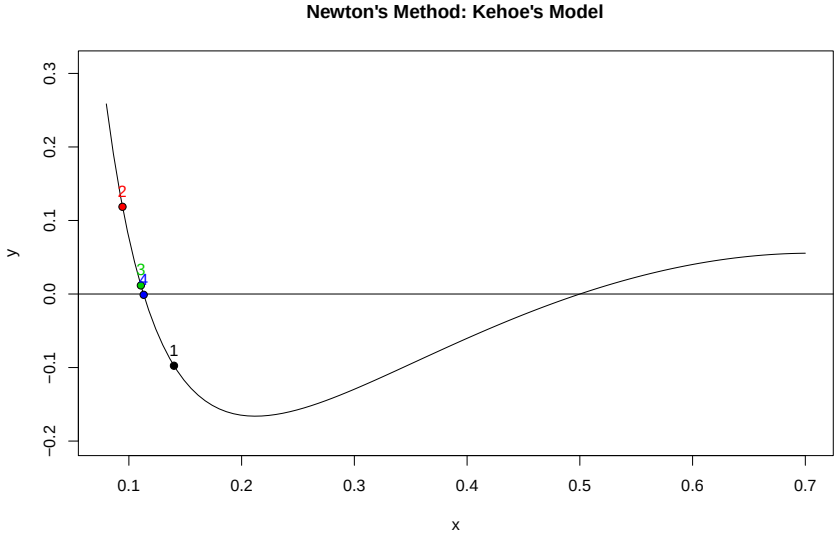




The method works fine for the Yield problem, but not for the Kehoe's model. We can see on the graph that it gets stuck in a cycle around the solution. This result depends on the properties of the function around the solution. If we try another starting value, we see that the first equilibrium can easily be found. But for many starting values, the Newton's method diverges (try it).

```
> print(Equil2 <- NewtonNL(Kehoe,dKehoe,.14))
```

```
Method:  Newton
Message:  Converged after 8 iterations

The solution is:  0.1129238 , and f(x) is  3.594499e-08
Precision:  5.734584e-08
```



Exercise 5.1. *Write a function that solve $f(x) = 0$ using the Newton's Method. Test it on the previous examples.*

Exercise 5.2. *Write a function that solve $f(x) = 0$ using the Newton's Method with acceleration or stabilization parameter ω. Test it on the previous examples.*

5.2 Multivariate Nonlinear Equations

Here, we consider methods to solve $f(x) = 0$, where f is a function from $\mathbb{R}^n$ to $\mathbb{R}^n$. We consider the following Duopoly problem: There are two goods, X and Z, and the utility of consumers is

$$U = u(Y, Z) + M = (1 + Y^\alpha + Z^\eta)^{\eta/\alpha} + M$$

The profit functions of firm Y and Z are:

$$\Pi^Y(Y, Z) = u_y(Y, Z)Y - C_Y Y,$$

and

$$\Pi^Z(Y, Z) = u_z(Y, Z)Z - C_z Z.$$

The first order condition is:

$$\frac{\partial \Pi^Y(Y, Z)}{\partial Y} = 0$$

and

$$\frac{\partial \Pi^Z(Y, Z)}{\partial Z} = 0$$

My function produces a vector $f(x)$ or the Jacobian $J(x)$.

```
Pi <- function(x, d = 0) {
    Y <- exp(x[1])
    Z <- exp(x[2])
    alpha <- 0.999
    eta <- 0.2
    Cy <- 0.07
    Cz <- 0.08
    U <- expression((1 + Y^alpha + Z^alpha)^(eta/alpha))
    dUy <- D(U, "Y")
    Piy <- paste(dUy[2], dUy[1], dUy[3], "*Y-Cy*Y", sep = "")
    Piy <- parse(text = Piy)
    dUz <- D(U, "Z")
    Piz <- paste(dUz[2], dUz[1], dUz[3], "*Z-Cz*Z", sep = "")
    Piz <- parse(text = Piz)
    dPiy <- D(Piy, "Y")
    dPiz <- D(Piz, "Z")
    if (d == 0)
        c(eval(dPiy), eval(dPiz)) else {
        J <- c(eval(D(dPiy, "Y")), eval(D(dPiz, "Y")), eval(D(dPiy,
            "Z")), eval(D(dPiz, "Z")))
        matrix(J, 2, 2)
    }
}
```

5.2.1 Newton's Method

The multivariate version of the Newton's method is:

$$x_{k+1} = x_k - J(x_k)^{-1} f(x_k)$$

```
NewtonMNL <- function(f, x0, eps = 1e-07, delta = 1e-07, maxit = 100) {
    t <- 1
    f0 <- f(x0)
    df0 <- f(x0, 1)
    while (TRUE) {
        x <- x0 - solve(df0, f0)
        f0 <- f(x)
        df0 <- f(x, 1)
        if (t >= maxit) {
            mess <- "No convergence: maxit reached"
            break
```

```
        }
        check <- sqrt(crossprod(x - x0)) < eps * (1 + sqrt(crossprod(x0)))
        if (check) {
            mess <- paste("Converged after ", t, " iterations",
                sep = "")
            break
        }
        t <- t + 1
        x0 <- x
    }
    if (sqrt(crossprod(f0)) > delta)
        mess <- paste(mess, " (Bad convergence, f(x) not zero)",
            sep = "")
    ans <- list(sol = x, fct = f0, message = mess, iter = t,
        name = "Multivariate Newton for Nonlinear System", prec = sqrt(crossprod(x -
            x0))/(1 + sqrt(crossprod(x0))))
    class(ans) <- "Zeros"
    return(ans)
}

> NewtonMNL(Pi,c(-1.9,-1.4))

Method:  Multivariate Newton for Nonlinear System
Message:  Converged after 22 iterations

The solution is:
x1  =  -0.1374651
x2  =  -0.5759185

f(x) is  4.646666e-10 2.077254e-09
Precision:  5.820559e-08
```

5.2.2 Gauss Methods

As for the linear case, you can solve the problem using methods such as Gauss-Jacobi or Gauss-Seidel. They replace the n-dimensional problem by n one-dimensional problems. There are two possible approaches. In the first, the one-dimensional problems are solve completely, and in the second, they are solved using a linear approximation. For the Gauss-Jacobi, we obtain x_i^{k+1} either by solving

$$f(x_{-i}^k, x_i^{k+1}) = 0$$

or using the the Taylor approximation:

$$x_i^{k+1} = x_i^k - \frac{f^i(x^k)}{f^i_{x_i}(x_k)}$$

For the Gauss-Seidel, we update the x_i^k as soon as there are available. I give you the result using the function I wrote. You have to write your own function as an exercise.

```
Method:  Gauss-Jacobi for Nonlinear System
Message:  Converged after 17 iterations

The solution is:
x1  =  -0.1374662
x2  =  -0.5759235

f(x) is  7.309127e-08 1.641704e-07
Precision:  5.029531e-09

Method:  Gauss-Seidel for Nonlinear System
Message:  Converged after 9 iterations

The solution is:
x1  =  -0.1374662
x2  =  -0.5759236

f(x) is  7.311276e-08 1.642665e-07
Precision:  2.692622e-09

Method:  Linear Gauss-Jacobi for Nonlinear System
Message:  Converged after 32 iterations

The solution is:
x1  =  -0.1374652
x2  =  -0.5759184

f(x) is  1.217085e-10 -4.077542e-10
Precision:  9.638562e-09

Method:  Linear Gauss-Seidel for Nonlinear System
Message:  Converged after 28 iterations

The solution is:
```

```
x1  =  -0.1374651
x2  =  -0.5759184

f(x) is  1.028884e-10 -2.664104e-10
Precision:  8.026069e-09
```

Exercise 5.3. *Write a function to solve the system of n equations $f(x) = 0$ using the Gauss-Jacobi and Gauss-Seidel methods. For solving the one-dimensional problems, use the R function uniroot()*

Exercise 5.4. *Write a function to solve the system of n equations $f(x) = 0$ using the linear approximation version of the Gauss-Jacobi and Gauss-Seidel methods.*

5.2.3 Broyden's Method

The Broyden's method is similar to the Newton's method with the exception that it approximate the Jacobian and update it at each iteration as the BFGS method does for the Hessian matrix. Let A_k be the approximation of $J(x_k)$, starting with $A_0 = I$, the update is:

$$A_{k+1} = A_k + \frac{(y_k - A_k s_k)s_k'}{s_k' s_k}$$

where $y_k = f(x_{k+1}) - f(x_k)$. The idea is to have a matrix A_{k+1} that satisfies $A_{k+1}s_k = f(x_k + s_k) - f(x_k)$, a properties that is satisfied by the Jacobian. In fact, for any direction q, $J(x)q$ approximates $f(x+q) - f(x)$. In the one dimensional case, we have $f'(x)h \approx f(x+h) - f(x)$. You can verified that the above updating scheme satisfies $A_{k+1}s_k = y_k$.

```
Method:  Broyden's Method
Message:  Converged after 36 iterations

The solution is:
x1  =  -0.1374651
x2  =  -0.5759184

f(x) is  -1.434133e-11 1.172107e-11
Precision:  6.79486e-08
```

As it is expected, the approximated Jacobian makes it a little slower than the Newton's Method. The advantage is for large systems because it avoids the computation of the Jacobian at each iteration for which the number of operations is of order n^2.

Exercise 5.5. *Write a function that solves $f(x) = 0$, for $f(x) : \mathbb{R}^n \to \mathbb{R}^n$, using the Broyden's Method. Test your method on the above duopoly example.*

5.2.4 The nleqslv package

The nleqslv package of [Hasselman 2012] provides functions for solving systems of nonlinear equations. The main function is nleqslv() which uses either the Newton or the Broyden's method. The function uses a method similar to the one we saw in the last chapter for improving the convergence speed. The updating scheme is $x_{k+1} = x_k + \lambda s_k$. The lambda is selected using a kind of line search. The criterion is base on the impact of the step on $f(x)'f(x)$. The options are:

- The first three are respectively x_0, f and J, where f and J are functions.
- method = either "Broyden" of "Newton"
- global = different method for selecting the λ. You can choose "none" if you want $\lambda = 1$
- xscalm = method for re-scaling the x's. You always make sure the x_i's have comparable scales.
- control = list(): Many parameter to adjust if you want. For example, xtol and ftol are what we call ε and δ in the above algorithms, maxit the number of iterations, trace=1 will print the details of each iterations, and a bunch of other tuning parameters.

To see how it works, we apply it to the duopoly problem.

```
> library(nleqslv)
> dPi <- function(x)
+         Pi(x,1)
> nleqslv(c(-1,-2),Pi,dPi)

$x
[1] -0.1374651 -0.5759186

$fvec
[1] -1.782566e-09  3.254971e-09

$termcd
[1] 1

$message
[1] "Function criterion near zero"

$scalex
```

```
[1] 1 1

$nfcnt
[1] 15

$njcnt
[1] 1
```

See the help() to understand all code. In particular we see that there is only one Jacobian evaluation (because it is the Broyden's Method) and 15 function evaluations.

5.2.5 Example

Consider the endowment economy in which there are m goods, and n agents with utilities:

$$u^i(x) = \sum_{j=1}^{m} \frac{a_{ij} x_j^{v_{ij}+1}}{1+v_{ij}}, \quad i = 1, ..., n,$$

endowed with e_{ij} units of good j, where $m = n = 10$, and the coefficients are obtained randomly as follows (for a, e and v, the i^{th} row is for the i^{th} agent and the j^{th} column the j^{th} good):

```
> set.seed(445)
> n <- 10
> m <- 10
> a <- matrix(runif(n*m,1,10),n,m)
> v <- matrix(runif(n*m,-3,-0.5),n,m)
> e <- matrix(runif(n*m,1,5),n,m)
```

By using Walras law and the normalization $\sum_{i=1}^{m} p_i = 1$, the problem is to solve the following equations:

$$\begin{aligned} E_1(p) &= 0 \\ E_2(p) &= 0 \\ &\vdots \\ E_{m-1}(p) &= 0 \\ \sum_{i=1}^{m} p_i &= 1, \end{aligned}$$

where $E_i(p)$ is the excess demand of good i.

Exercise 5.6. *Solve the equilibrium problem of the above endowment economy. Use the algorithm that you want but $E_i(p)$ must be obtained numerically using the optimizer of your choice.*

Chapter 6

Numerical Calculus

Contents

6.1 Numerical Integration

We introduce the section with two examples. In the first, we consider the following portfolio optimization problem:

$$\max_{\omega_i} E\left[U\left(\sum_{i=1}^{n}\omega_i Z_i\right)\right] \tag{6.1}$$

subject to

$$\sum_{i=1}^{n} p_i(\omega_i - e_i) = 0 \tag{6.2}$$

It may look like a simple maximization problem, but it is not. The difficulty comes from the fact that we have to maximize an expected value, which can be written as:

$$E\left[U\left(\sum_{i=1}^{n}\omega_i Z_i\right)\right] = \int\int\cdots\int U\left(\sum_{i=1}^{n}\omega_i Z_i\right) f(Z_1, Z_2, ..., Z_n) dZ_1 dZ_2 \cdots dZ_n$$

In the basic model, we assume that the preferences are mean-variance, an assumption that can be satisfied if either $U()$ is quadratic or the vector Z is characterized by an elliptical distribution. In that case. only the mean and the variance matter, and the investors choose a combination of the risk free asset and the market portfolio. It simplifies the problem, but does not eliminate the need to compute integrals. For

the applications bellow, we will assume that investors have a CRRA utility function $u(c) = c^{1+\gamma}/(1+\gamma)$. For Z, we will make different assumptions.

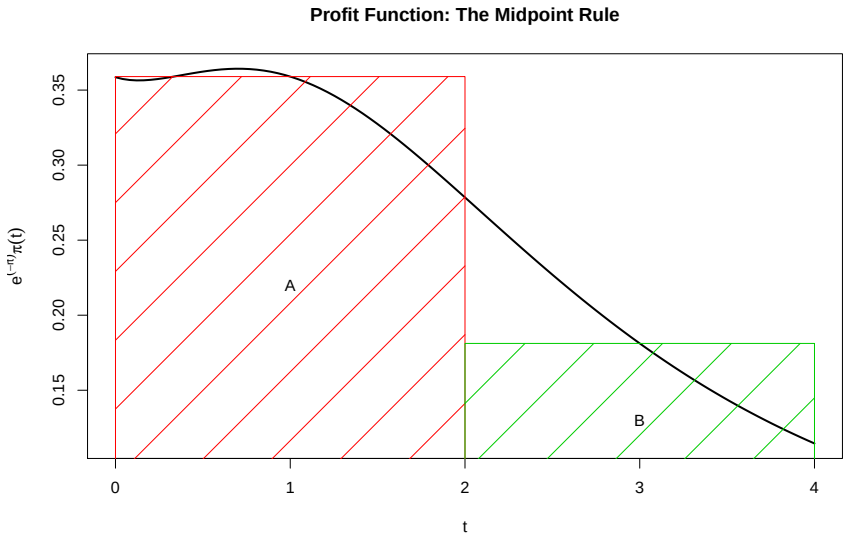
The second problem is quite simple. We only want to compute the future profit of a firm over the horizon $t = [0, T]$, with $q(t) = 3 - (1 + t + t^2)e^{-t}$, $P(q(t)) = q(t)^{-2}$, and $C(q(t)) = q(t)^{3/2}$. The profit is therefore is:

$$\int_0^T e^{-rt}[P(q(t))q(t) - C(q(t))]dt \tag{6.3}$$

We will just cover few methods to understand the idea behind numerical integration, and conclude by showing you the tools available in R.

6.1.1 Newton-Cotes

The following graph shows the shape of the profit function in equation (6.3) for the horizon [0,4] with the Midpoint rule.



The midpoint rule approximate the integral by adding the areas of the rectangles A and B. The error of the method is given by $(b-a)^3 f''(\xi)/96$, where ξ is between a and b. Therefore, the method is exact when $f(x)$ is a straight line because in that case $f''(\xi) = 0$. Here the integral as been divided in 2. In general, the method is:

$$\int_a^b f(x)dx \approx \sum_{i=1}^{n} hf(x_i)$$

and the error is given by the expression $h^2(b-a)f''(\xi)/24 = (b-a)^3 f(\xi)/(24n^2)$ for n equally spaced points, which implies that the error is of order n^{-2}. In the example

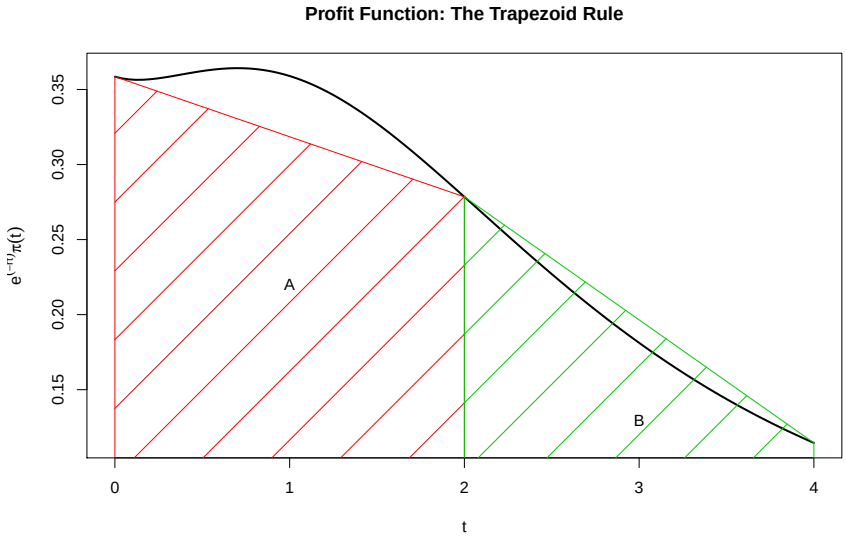
shown on the graph, $n = 2$, $x_1 = 1$, $x_2 = 3$, and $h = 2$. We can easily build a function for this method:

```
MidPoint <- function(f, a, b, n, ...) {
    h <- (b - a)/n
    x <- seq(a + h/2, b - h/2, len = n)
    sum(h * f(x, ...))
}
```

```
> print(Int1 <- MidPoint(Prof,0,4,20))
```

```
[1] 1.058281
```

The error is 2.8e-05. The Trapezoid rule is represented in the next graph.



And the approximation is valid up to $h^2(b-a)f''(\xi)/12$. Therefore, there is no clear difference between the two method. The method is

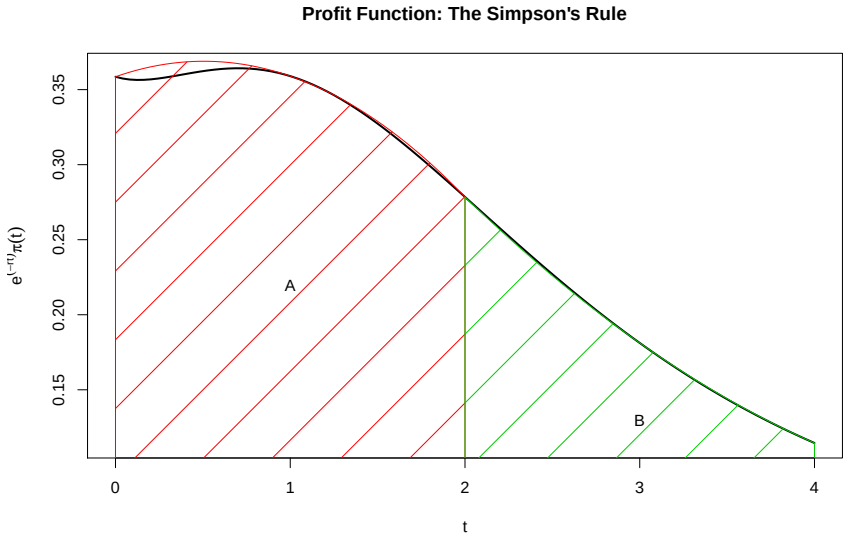
$$\int_a^b f(x)dx \approx \frac{h}{2}[f(a) + 2f(x_1) + \cdots + 2f(x_{n-1}) + f(b)]$$

```
Trapezoid <- function(f, a, b, n, ...) {
    x <- seq(a, b, len = n)
    h <- x[2] - x[1]
    sum(h * c(f(x[-c(1, n)], ...), f(x[c(1, n)], ...)/2))
}
```

```
> print(Int2 <- Trapezoid(Prof,0,4,20))
```

```
[1] 1.058194
```

The error is 6e-05, which a little higher than the one from the Midpoint rule. The Simpson's Rule, approximate the function between points by a second order polynomial as shown on the following graph, and compute the analytical integral of this approximation.



The error is of order n^{-4} (or $O(h^4)$) if the fourth derivative of $f(x)$ is bounded. In fact, the expression for the error is $h^4(b-a)f^{(4)}(\xi)/180$ which is the kind of expression used by functions such as integrate() in R to estimate the error. It can be computed as follows.

```
Simpson <- function(f, a, b, n, ...) {
    n <- floor(n/2) * 2 + 1
    x <- seq(a, b, len = n)
    z <- rep(c(4, 2), (n - 3)/2)
    z <- c(1, z, 4, 1)
    h <- x[2] - x[1]
    sum(z * f(x, ...) * h/3)
}
```

```
> print(Int3 <- Simpson(Prof,0,4,20))
```

```
[1] 1.058266
```

The error is 1.3e-05.

Suppose we want to compute $E(X)$, where the density of X is $f(x)$. Then, we need to get:

$$\int_{-\infty}^{\infty} xf(x)dx$$

For the integral to be bounded, we need the integrand $xf(x)$ to go to zero when $|x|$ goes to infinity. Therefore, we can approximate the integral by $\int_a^b xf(x)dx$, for some good choice of a and b. Here, we allow the upper and lower bounds to be different. Let $f(x)$ be the density of a $N(5,1)$, here is few results using different a and b:

```
> f <- function(x)
+         x*dnorm(x,mean=5)
> Simpson(f,-4,4,40)

[1] 0.5512882

> Simpson(f,2,8,40)

[1] 4.986499

> Simpson(f,0,10,40)

[1] 4.999997
```

It is clear here that $(-4,4)$ is not the right choice because the integrand is not centered at 0. In some special cases, we can recompute the same integral using a change of variables to make the bounds finite. For example, we can use the following change of variable for the above integral: $x(z) = \log[z/(1-z)]$, which implies:

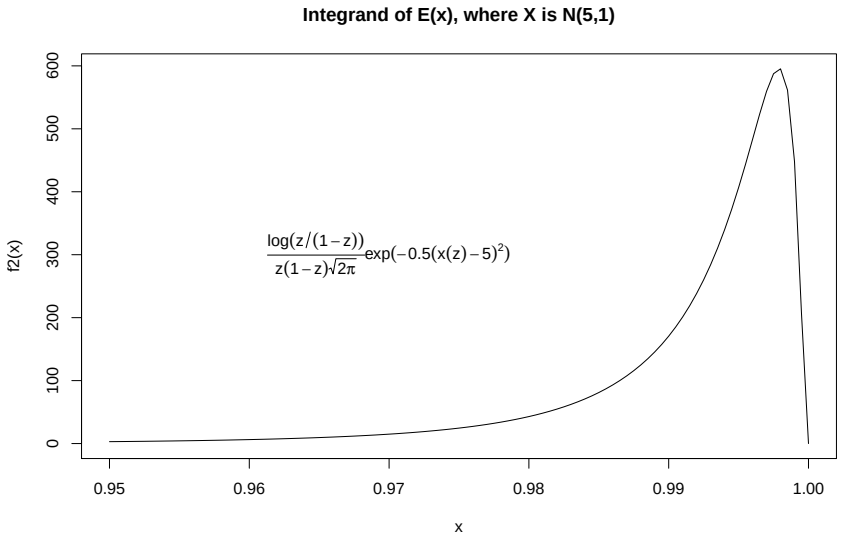
$$\int_{-\infty}^{\infty} xf(x)dx = \int_0^1 \frac{1}{z(1-z)} x(z)f(x(z))dz$$

We can verify that the derivatives of the new integrand are all bounded if $f(x)$ is the density of a normal distribution (a necessary requirement). The following, function would do the job:

```
f2 <- function(z) {
    x <- log(z/(1 - z))
    i <- ifelse(z == 1 | z == 0, 0, x * dnorm(x, mean = 5)/(z *
        (1 - z)))
    ifelse(abs(i) < 1e-13, 0, i)
}

> Simpson(f2,0,1,40)
```

```
[1] 0.896398
```

The result is not very good. The problem here is that the function is close to zero almost everywhere except between 0.9 and 1, as we can see on the following graph:



We need more points when the slope of the function changes quickly. We also want to avoid adding values that are dominated by rounding errors:

```
> Simpson(f2,0.8,1,1000)
```

```
[1] 4.999595
```

6.1.2 Gauss Methods

The Gauss approach is to approximate the function using orthogonal basis, and to choose optimal weights and nodes simultaneously. In fact, the nodes and weights are such that

$$\int_a^b f(x)w(x)dx = \sum_{i=1}^{n} \omega_i f(x_i)$$

holds exactly for all polynomial of degree $2n-1$, $f(x)$. The integrating function $w(x)$ defines the inner product $< f, g >$ so that the basis used to approximate $f(x)$ are orthogonal and standardized with respect to this inner product (see Chapter 6 of Judd for more details). The different sets of basis are given in Table 6.3, page 204, of Judd. There is an optimal quadrature for each $w(x)$, but we can also do a change of variable when $w(x)$ is missing. For example, the Gauss-Chebyshev, $w(x) = (1-x^2)^{-1/2}$, and it

is defined only between -1 and 1, but we can modify a simple integral as follows:

$$\int_a^b f(x)dx = \frac{b-a}{2}\int_{-1}^{1} f\left(\frac{(x+1)(b-a)}{2}+a\right)\frac{(1-x^2)^{1/2}}{(1-x^2)^{1/2}} = \int_{-1}^{1} g(x)(1-x^2)^{-1/2}dx$$

which can be approximated as:

$$\begin{aligned}\int_{-1}^{1} g(x)(1-x^2)^{-1/2}dx \approx & \frac{\pi}{n}\sum_{i=1}^{n} g(x_i) \\ = & \frac{\pi}{n}\sum_{i=1}^{n}\left(\frac{b-a}{2} f\left(\frac{(x_i+1)(b-a)}{2}+a\right)(1-x_i^2)^{1/2}\right)\end{aligned}$$

with

$$x_i = \cos\left(\frac{2i-1}{2n}\pi\right)$$

We see that the weights ω_i for that method are all equal to π/n. The following, implement the Gauss-Chebyshev method

```
GaussChebyshev <- function(f, a, b, n, ...) {
    x <- cos((2 * (1:n) - 1) * pi/(2 * n))
    y <- f((x + 1) * (b - a)/2 + a, ...) * (1 - x^2)^(0.5) *
        pi * (b - a)/(2 * n)
    sum(y)
}
```

```
> GaussChebyshev(f2,0,1,40)

[1] 4.848546
```

The function does not do as bad as the Simpson method which performs badly even with n=200:

```
> Simpson(f2,0,1,200)

[1] 4.344921

> GaussChebyshev(f2,0,1,200)

[1] 4.999986
```

The package "statmod" by [Smyth *et al.* 2011] has a tool to compute the nodes and weights for many quadratures. For example, we could rewrite the GaussChebyshev() function as follows:

```
GaussChebyshev <- function(f, a, b, n, ...) {
    x <- gauss.quad(n, kind = "chebyshev1")$nodes
    y <- f((x + 1) * (b - a)/2 + a, ...) * (1 - x^2)^(0.5) *
        pi * (b - a)/(2 * n)
    sum(y)
}
```

```
> library(statmod)
> GaussChebyshev(f2,0,1,200)

[1] 4.999986
```

For Gauss-Legendre, $w(x) = 1$, and the range is $[-1, 1]$. It is therefore easy to compute $\int_a^b f(x)dx$. We only need a change of variable for the range $[a, b]$. Here is the method:

```
GaussLegendre <- function(f, a, b, n, ...) {
    res <- gauss.quad(n, kind = "legendre")
    x <- res$nodes
    w <- res$weights
    y <- w * f((x + 1) * (b - a)/2 + a, ...) * (b - a)/2
    sum(y)
}
```

```
> GaussLegendre(f2,0,1,200)

[1] 4.999998
```

The Gauss-Hermite quadrature is particularly useful to compute $E(f(x))$ when $x \sim N(\mu, \sigma^2)$. Indeed, its integrating function is $w(x) = e^{-x^2}$, and the range is $[-\infty, \infty]$. The approximation is:

$$\int_{-\infty}^{\infty} f(y)e^{-y^2}dx \approx \sum_{i=1}^{n} \omega_i f(y_i)$$

If we want to compute $E[f(y)]$, where $y \sim N(\mu, \sigma^2)$, we need to define the new variable $x = (y - \mu)/(\sigma\sqrt{2})$ which implies:

$$E[f(y)] = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(\sigma x\sqrt{2} + \mu)e^{-x^2}dx$$

When we use the gauss.quad() function to generate the weights and nodes, $[a, b]$ is a function of the number of points n. By increasing n we automatically increase a and $|b|$, as we can see:

```
> gauss.quad(4,kind="hermite")$nodes
```

```
[1] -1.6506801 -0.5246476  0.5246476  1.6506801
```

```
> gauss.quad(10,kind="hermite")$nodes
```

```
 [1] -3.4361591 -2.5327317 -1.7566836 -1.0366108 -0.3429013  0.3429013
 [7]  1.0366108  1.7566836  2.5327317  3.4361591
```

```
> gauss.quad(20,kind="hermite")$nodes
```

```
 [1] -5.3874809 -4.6036824 -3.9447640 -3.3478546 -2.7888061 -2.2549740
 [7] -1.7385377 -1.2340762 -0.7374737 -0.2453407  0.2453407  0.7374737
[13]  1.2340762  1.7385377  2.2549740  2.7888061  3.3478546  3.9447640
[19]  4.6036824  5.3874809
```

Therefore, the function only depends on n.

```
GaussHermite <- function(f, n, ...) {
    res <- gauss.quad(n, kind = "hermite")
    x <- res$nodes
    w <- res$weights
    y <- w * f(x, ...)
    sum(y)
}
```

Suppose we want to compute the expected utility $E(u(c))$, where $c = 1 + e^z$, $z \equiv \log(Z) \sim N(\mu, \sigma^2)$ with, $\mu = 0.15$ and $\sigma = 0.25$, and $u(c) = c^{1+\gamma}/(1+\gamma)$, with $\gamma = -2$, then:

```
U <- function(x, mu, sigma, gamma) {
    y <- sqrt(2) * sigma * x + mu
    c <- 1 + exp(y)
    c^(1 + gamma)/(1 + gamma)/sqrt(pi)
}
```

```
> GaussHermite(U,200,mu=.15,sigma=.25,gamma=-2)
```

```
[1] -0.4631344
```

We can then see the impact of increasing σ or μ

```
> GaussHermite(U,200,mu=.15,sigma=.5,gamma=-2)
```

```
[1] -0.4646496
```

```
> GaussHermite(U,200,mu=.5,sigma=.25,gamma=-2)

[1] -0.3792901
```

The last quadrature is the Gauss-Laguerre. It is useful for computing future discounted profit or utility because $w(x) = e^{-x}$. You can apply the quadrature in the next exercise.

Exercise 6.1. *Use the Gauss-Laguerre quadrature to compute:*

$$\eta \left(\frac{\eta - 1}{\eta} \right)^{\eta - 1} \int_0^{\infty} e^{-rt} m(t)^{1-\eta} dt,$$

where $m(t) = 2 - e^{-\lambda t}$*, and* $\eta = 0.8$*. Try to reproduce Table 7.7, page 265 of Judd (you will need to do a change of variable here).*

Exercise 6.2. *Write a function that computes integrals with adaptive quadrature. The function starts with a small* n *and increases it until the value only changes by a certain tolerance level. Try to make it flexible and test it on the above examples.*

6.1.3 Numerical integration with R

The function integrate() can be use in general. However, we need to be careful. To estimate $E(Y)$, where $Y \sim N(5, 1)$, we can do it as follows:

```
> f <- function(x)
+         dnorm(x,mean=5)*x
> integrate(f,lower=-Inf,upper=Inf)

5 with absolute error < 6e-05
```

It is not recommended to use big numbers instead of infinity as we can see:

```
> integrate(f,lower=-1000,upper=1000)

0 with absolute error < 0
```

The algorithm fails in that case. I recommend you to read carefully the help file for integrate() before using it. The following shows how to compute the expected utility that we computed in the previous section.

```
> U2 <- function(x, mu, sigma, gamma)
+         {
+         c <- 1+exp(x)
+         u <- c^(1+gamma)/(1+gamma)
```

```
+         u*dnorm(x,mean=mu,sd=sigma)
+         }
> f <- function(x)
+         U2(x,.15,.25,-2)
> integrate(f,-Inf,Inf)

-0.4631344 with absolute error < 0.00011
```

Exercise 6.3. *In a statistical method called the Generalized Empirical Likelihood for a continuum, we need to compute an $n \times n$ matrix C with*

$$c_{ij} = \int_{-\infty}^{\infty} e^{-(x_i - x_j)^2 t^2} \phi(t) dt,$$

where $\phi(t)$ is the density of the standardized normal distribution, and x_i is observation i. Find a fast way to construct that matrix, and test your method with the 2000×1 vector x generated from a $N(10, 2)$.

6.1.4 Numerical derivatives with R

Here is how to do numerical derivative in R. The following is taken from help(numericDeriv) file.

```
> myenv <- new.env()
> assign("mean", 0., envir = myenv)
> assign("sd", 1., envir = myenv)
> assign("x", c(-2,0,2), envir = myenv)
> grad <- numericDeriv(quote(pnorm(x, mean, sd)), c("mean", "sd"), myenv)
> attr(grad,"gradient")

            [,1]       [,2]
[1,] -0.05399097  0.1079819
[2,] -0.39894228  0.0000000
[3,] -0.05399097 -0.1079819
```

Exercise 6.4. *Write a function df(f,x) and ddf(f,x) that return the Jacobian and Hessian of $f(x) : \mathbb{R}^n \to \mathbb{R}$, using numericDeriv().*

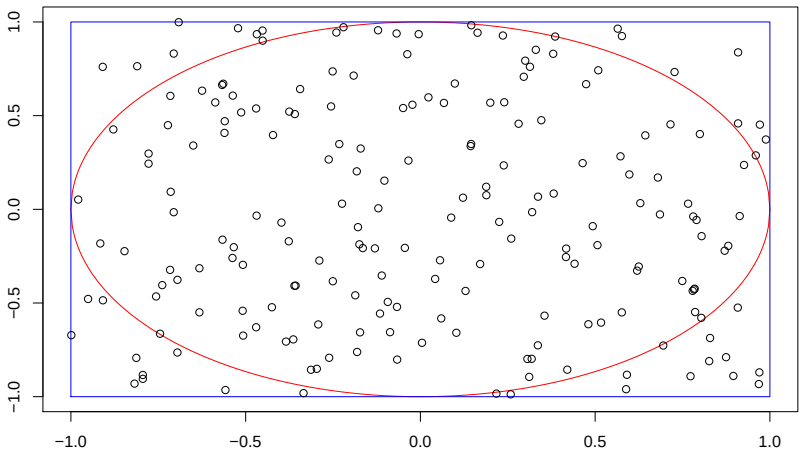
Chapter 7

Monte Carlo Simulation

Contents

7.1 Introduction

We want to look at methods to compute integrals or to solve optimization problems based on simulations. Here is a simple example. Suppose you want to compute the value of π. We all know that it is the area of a unit circle. But it is also the probability of being in a unit circle inside a 2×2 square if we randomly draw numbers uniformly over the square times the area of the square, which is 4. The following figure shows the idea.



By counting the proportion of points in the circle, we estimate π:

```
> n <- 2000000
> x <- runif(n,-1,1)
> y <- runif(n,-1,1)
> mean(abs(y^2+x^2)<=1)*4


[1] 3.141298
```

It is accurate up to 3 decimals. As you see, we need a lot of points to get that level of accuracy. In some problems, however, Monte Carlo simulations are the only feasible way to get an estimate of the solution we are looking for.

In order to perform Monte Carlo simulations, we need a random number generator. Such generators do not exist in practice. We use pseudo-random generators, which are deterministic formulas that generate numbers that approximate the properties of random numbers. That's the reason some purists will call these methods pseudo Monte Carlo to point out that we are not using real random numbers. A uniform pseudo random number can be generated as:

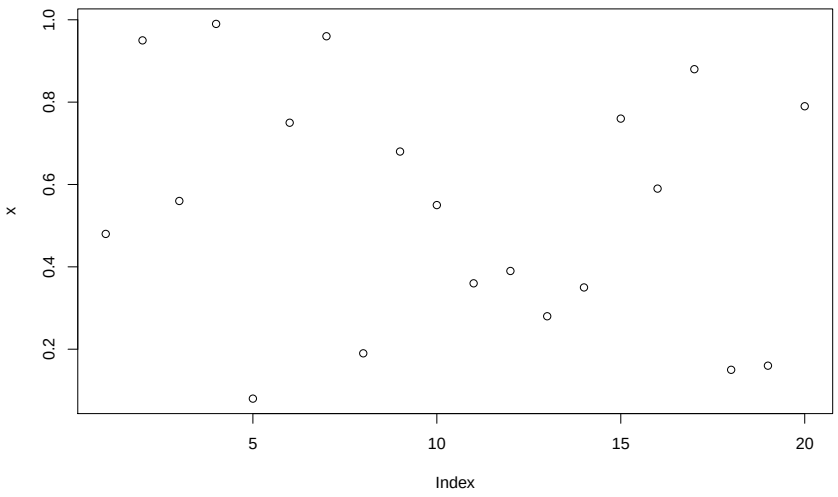
$$X_{k+1} = aX_k + b \ (mod \ m),$$

where $N \ (mod \ m)$ is the remainder of N/m, and X_0 is called the seed and must be an odd number. Therefore, for any given seed, we have the same sequence of pseudo random number. For example, consider the following homemade pseudo random generator:

```
myUnif <- function(n, a, c, m, seed) {
    seed <- (seed%/%2) * 2 + 1
    x <- seed
    for (i in 2:(n + 1)) x[i] <- (x[i - 1] * a + c)%%m
    return(x[-1]/m)
}
```

We can see on the following figure that the function produces numbers between 0 and 99 (because $0 \leq N \ (mod \ m) \leq (m-1)$) that look random.

```
> x <- myUnif(20,263,71,100,79)
> plot(x)
```



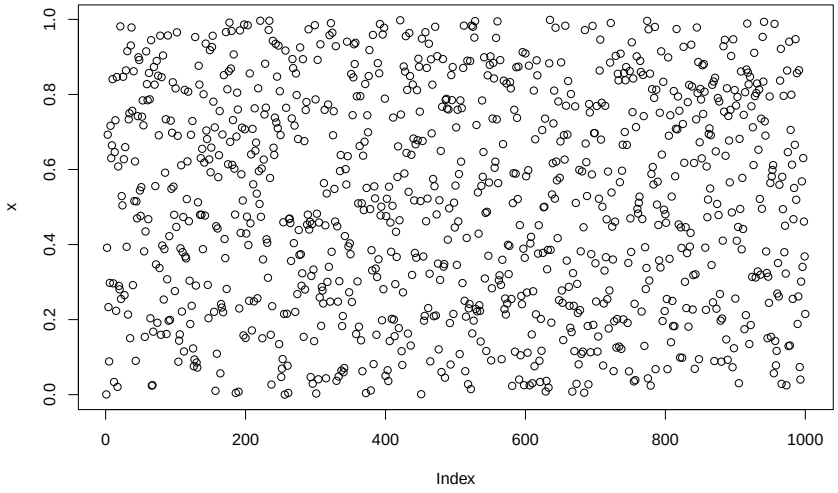
However, the sequence has a period of 20:

```
> x <- myUnif(40,263,71,100,79)
> matrix(x,ncol=2)[1:5,]
```

```
     [,1] [,2]
[1,] 0.48 0.48
[2,] 0.95 0.95
[3,] 0.56 0.56
[4,] 0.99 0.99
[5,] 0.08 0.08
```

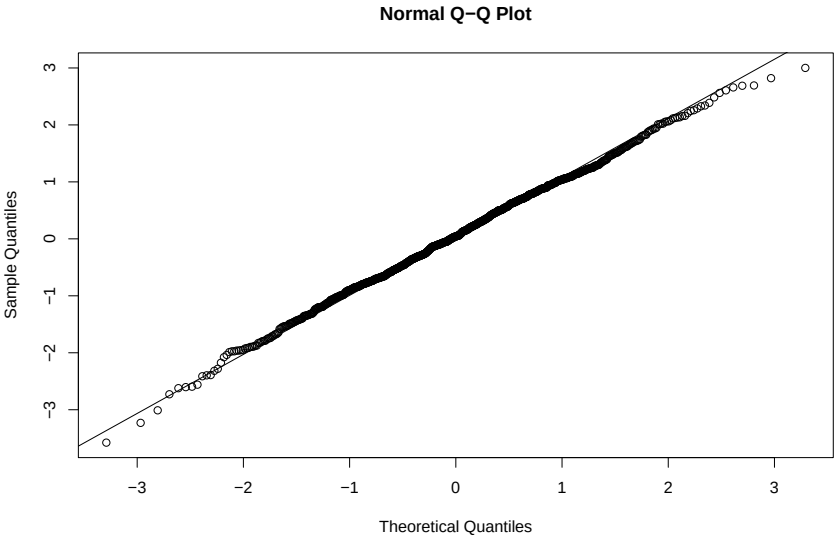
To get a longer sequence we have to change the seed every 20 numbers. Here is a much realistic choice of the parameters (the period is 536870912):

```
> x <- myUnif(1000,16807,0,2147483647,79)
> plot(x)
```



We call them pseudo random numbers because they are perfectly predictable once we know the seed. Other pseudo random numbers can be generated using the following. Let $F()$ be a distribution function. If $x \sim U(0,1)$, then $y = F^{-1}(x)$ has a distribution function $F(y)$. We can then construction a $N(0,1)$ pseudo random number as follows:

```
> x <- myUnif(1000,16807,0,2147483647,79)
> y <- qnorm(x)
> qqnorm(y)
> qqline(y)
```



7.2 Econometrics

We first look at some examples of Monte Carlo simulations in econometrics. In fact, many think that those numerical experiments are reserved to econometrics. We will see that it is not the case in the next sections.

One application is to analyze the properties of estimators. For example, the OLS estimator of the regression $Y = X\beta + u$, can be written as:

$$\hat{\beta} = \beta + (X'X)^{-1}X'u$$

We want to show that $\hat{\beta}$ is biased whenever $E(u|x) \neq 0$. In other words we want to measure $E(\hat{\beta})$ and see if it is equal to β. But $E(\hat{\beta})$ is:

$$E(\hat{\beta}) - \beta = \int \cdots \int (X'X)^{-1}X'uf(x_1, x_2, ..., x_k, u)dx_1 \cdots dx_k du$$

We could assume a distribution $f(x_1, x_2, ..., x_k, u)$ and compute the integral, but it would be hard for large systems. What we do instead, we generate samples, estimate $\hat{\beta}$ for each sample, and compute the sample mean of the $\hat{\beta}$'s. By the law of large numbers, this method should give us a consistent estimate of $E(\hat{\beta})$. For example, suppose that $u \sim N(0,1)$, $X_1 \sim U(0,1)$, $X_2 = .4u + 2Z + U(0,1)$, $Z \sim U(0,1)$, and $Y = 1 + 2X_1 + 3X_2 + u$. We don't know the joint distribution of X_1, X_2, and u. It is therefore hard to compute the integral. The Monte Carlo approach, however, is not too hard. We can compare the bias of OLS and GMM with 500 iterations and a sample size of 50. Notice that we would get a better estimate by increasing the number of iterations.

```
> library(gmm)
> library(multicore)
> set.seed(123)
> n <- 50
> N <- 500
> u <- matrix(rnorm(n*N),n,N)
> x1 <- matrix(runif(n*N),n,N)
> Z <- matrix(runif(n*N),n,N)
> x2 <- .4*u + 2*Z + matrix(runif(n*N),n,N)
> y <- 1+2*x1+3*x2+u
> beta <- mclapply(1:N,function(i) lm(y[,i]~x1[,i]+x2[,i])$coef)
> beta_GMM <- mclapply(1:N,function(i) gmm(y[,i]~x1[,i]+x2[,i],~x1[,i]+Z[,i])$coef)
> beta <- simplify2array(beta)
> beta_GMM <- simplify2array(beta_GMM)
> bias <- rowMeans(beta)-c(1,2,3)
> names(bias) <- c("b0","b1","b2")
```

```
> bias <- rbind(bias,rowMeans(beta_GMM)-c(1,2,3))
> rownames(bias) <- c("OLS","GMM")
```

	b0	b1	b2
OLS	-1.0689	0.0293	0.6965
GMM	-0.0099	0.0226	-0.0043

Table 7.1: Bias of OLS versus GMM

Computing biases and variances of estimators for small samples can only be done using Monte Carlo methods, because all we know about estimators in practice is how they behave when the sample size goes to infinity; thanks to the several central limit theorems and laws of large numbers. For example, GMM estimators are asymptotically unbiased, but in small samples, the bias increases with the number of moment conditions. We can easily show that results using simulations. Some economists derived some proofs which only applies to large samples, but to do so, they had to go through very messy algebraic manipulations. In the next sections, we use simulations as an alternative to methods we covered in previous chapters.

7.3 Integration

Consider the following integral:

$$I = \int_a^b f(x)dx$$

Suppose $X \sim U(a,b)$, what is the definition of the expected value of $f(x)$? It is simply

$$E(f(x)) = \frac{1}{b-a}\int_a^b f(x)dx$$

In other words:

$$\int_a^b f(x)dx = (b-a)E(f(x)) \quad \text{with} \quad X \sim U(a,b)$$

We can than estimate the integral using the sample mean of $f(x)$ and n $U(a,b)$ pseudo random numbers. Here is a small function:

```
MCInt <- function(f, a, b, n) {
    x <- runif(n, a, b)
    fv <- f(x)
```

```
    I <- mean(fv * (b - a))
    sigma <- sd(fv) * (b - a)/sqrt(n)
    return(list(I = I, sigma = sigma))
}
```

It returns the estimated integral and the estimated standard deviation of the estimate. Since it is an estimation, we need the standard error to measure the accuracy. Lets try it with the profit function (6.3) that we used in the last chapter. We want to compare it with the value obtained with integrate():

```
> integrate(Prof,0,4)

1.058253 with absolute error < 1.4e-10

> MCInt(Prof,0,4,1000)

$I
[1] 1.056388

$sigma
[1] 0.01073861
```

The variance of the estimated integral can be reduced by a proper choice of distributions and points. The main idea is to concentrate the points to areas in which the function $f(x)$ is high. Since the goal of the chapter is only to introduce you to Monte Carlo methods, we will skip that part.

This may seem useless, but suppose we want to compute $EU(c)$, where $c = \sum_{i=1}^{n} w_i r_i$ and $f(z_1, z_2, ...z_n)$ be the joint density of z. Then we need to compute an n^{th} order integral. Monte Carlo methods can be much faster in those cases. One area that uses simulations intensively to compute integrals is Bayesian econometrics, but it is beyond the scope of that course.

7.4 To be completed latter

In a future version of the notes, I will talk about methods such as Simulated Annealing which are simulations methods for minimizing functions of n variables. They are slow methods that approximate the minimum, but can solve problems that conventional method cannot. I'll reserve it for Numerical Method II

Exercise 7.1. *Consider the utility function* $U(c) = -e^{-c}$, *where* $c = (1 - w)R + wZ$, *with* $R = 1.01$, *and* $Z \sim N(1.06, 0.04)$. *Solve:*

$$\max_{w} -E(e^{-c})$$

using a Monte Carlo simulation to compute the expected values. Compare the precision of your solution for the number of points $N = 50, 200, 1000, 5000$.

Chapter 8

Differential Equations

Contents

8.1 Introduction

In this chapter, we are interested in problems that can be written as:

$$\frac{dy}{dx} = f(x, y), \tag{8.1}$$

where $x \in [a, b]$, $y \in \mathbb{R}^n$, and $f : \mathbb{R}^{n+1} \to \mathbb{R}^n$. This is called a system of first order "Ordinary Differential Equation" (ODE). This is a very general representation of differential equations because higher order equations can always be redefined as a first order equation be an appropriate change of variable. For example, the second order differential equation $y''(x) = f(y'(x), y, x)$ can be written as a system of two first order differential equations: $z'(x) = f(z, y, x)$, and $y'(x) = z$. The goal is to obtain the solution $y(x)$ that satisfies equation 8.1.

For example, consider the following simple Solow growth model:

$$\begin{aligned} \dot{k} \equiv \frac{dk}{dt} =& sf(k) - \delta k \\ f(k) =& k^{\alpha} \end{aligned} \tag{8.2}$$

This is a special case of equation 8.1 with $x = t \in [0, \infty]$, $y = k$, and $f(t, k) = sk(t)^{\alpha} - \delta k(t)$. Before going through numerical methods to solve ODE's, lets see how we can solve it analytically. I am not going into all possible cases. I just want to give you some notions. First, there is no analytical solution to the problem 8.2. We can write:

$$k(t) = k(0) + \int_0^t [sk(t)^{\alpha} - \delta k(t)]dt,$$

but we cannot solve it because we don't know the function $k(t)$. Second, we need more information in order to find $k(t)$. The ODE only informs us about the behavior of the derivative $\dot{k}$. Finding $k(t)$ only based on the problem 8.2 is like finding $x_t = f(t)$ based only on $(x_{t+1} - x_t) = a$. However, if we know that $x_0 = c$, we can obtain $x_t = x_0 + at$. Solutions to nonlinear differential equations only exist in closed form for a few cases.

Lets consider a simpler case:

$$y'(x) = ay(x) + b,$$

where $a < 0$. The solution of differential equation, as it is also the case for difference equations, has two parts: a complementary solution S_c and a particular solution S_p. To first is obtained by solving the homogeneous version of the ODE, $y'(x) = ay(x)$, and the second is the solution for a particular value of x, which is often the steady state value, $-b/a$. We can write the homogeneous part of the ODE as:

$$\frac{dy}{y} = adx$$

If we integrate both side, we obtain:

$$\begin{aligned} \int \frac{dy}{y} =& \int adx \\ \log(y) =& ax + C \\ S_c =& Ce^{ax} \end{aligned}$$

It implies that the general solution is $y(t) = Ce^{at} - b/a$. The final solution is obtained by setting $y(x)$, for $x \in [a, b]$, to some value y_0, which gives the value of the integrating constant $C = y_0 + b/a$. The solution is therefore:

$$y(t) = \left(y_0 + \frac{b}{a}\right) e^{at} - \frac{b}{a}$$

For nonlinear equations, there are special cases for which solutions can be found. For example, if the ODE can be written as $f(y)dy = g(x)dx$, in which case we say that the variables are separable, we can solve it by integrating both sides. However, separable variables is not a sufficient condition for the closed form solution to exist. For example, the Solow model can be written as:

$$\int \frac{1}{sk^{\alpha} - \delta k} dk = t + C,$$

but even if the integral exists, we cannot isolate $k(t)$. The problem with solving differential equations is like the problem of integrating. The best method is determined on a case by case basis. Fortunately, we have easier numerical methods to solve any ODE.

8.2 Finite Difference Methods for initial value problems

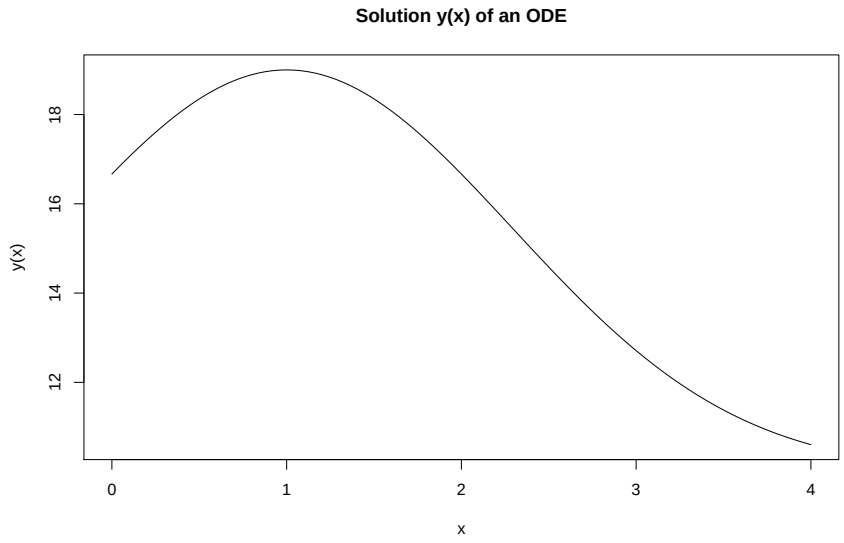
Lets consider the following ODE:

$$\frac{dy}{dx} = -0.6(y - 10)(x - 1) \tag{8.3}$$

with $y(0) = 9e^{-0.3} + 10$. It is a weird starting value that produce a nice solution:

$$y(x) = 9e^{-0.3(x-1)^2} + 10$$

The following graph shows the solution of the ODE:



8.2.1 Euler's Method

Lets consider the general case:

$$y'(x) = f(x, y),$$

for $x \in [a, b]$, and $y(a) = y_0$. Lets consider $n + 1$ points x_i, $i = 0, ..., n$, such that $x_i = a + ih$, where h is the step size. The Euler's method is based in the result:

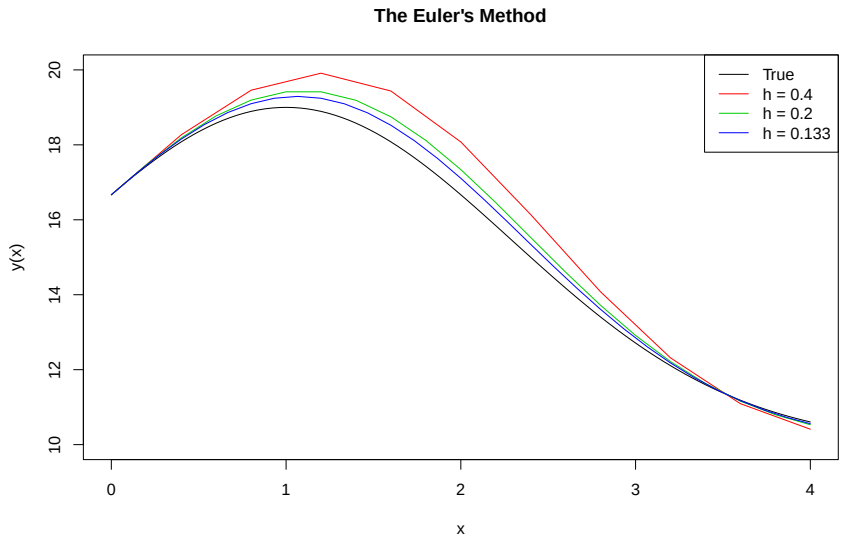
$$y(x_{k+1}) - y(x_k) = \int_{x_k}^{x_{k+1}} f(x, y(x))dx$$

By the rectangle rule, the right hand side can be approximated by $hf(x_k, y(x_k))$, which gives us the Euler's algorithm:

$$y_{k+1} = y_k + hf(x_k, y_k)$$

with the stating point $(x, y) = (a, y_0)$. The following figure show the result for the problem 8.3 for different h.

```
f <- function(x, y) -0.6 * (y - 10) * (x - 1)

myODE <- function(f, n, a, b, y0) {
    h <- (b - a)/n
    x <- a + h * (0:n)
    y <- y0
    for (i in 2:(n + 1)) y[i] <- y[i - 1] + h * f(x[i - 1], y[i - 1])
    return(list(x = x, y = y, h = h))
}
```



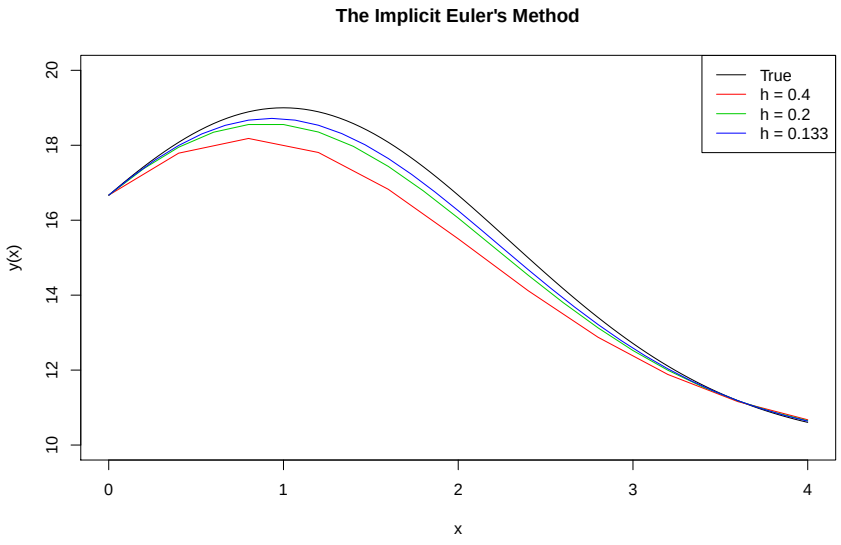
8.2.2 Implicit Euler's Method

We saw that the Euler's method overshoots the solution at the beginning. One way to improve the solution is to evaluate the function at the end point in the rectangle rule above. That results in the following implicit rule:

$$y_{k+1} = y_k + hf(x_{k+1}, y_{k+1})$$

It is an implicit rule because the value y_{k+1} is not expressed explicitly. We need to solve it using a method for nonlinear equation. In the following, I use the uniroot() function:

```
myODE2 <- function(f, n, a, b, y0, from = 0, to = 50) {
    h <- (b - a)/n
    f2 <- function(y, y1, x, h) y - y1 - h * f(x, y)
    x <- a + h * (0:n)
    y <- y0
    for (i in 2:(n + 1)) y[i] <- uniroot(f2, c(from, to), y1 = y[i - 1], x = x[i],
        h = h)$root
    return(list(x = x, y = y, h = h))
}
```



The method now undershoots the solution because it used the slope at the end points. Both methods converge linearly to the solution. In other words, the error is of order h. We can to better by using better integration rules.

8.2.3 Trapezoid Rule

Lets first rewrite the result from the fundamental theorem of calculus:

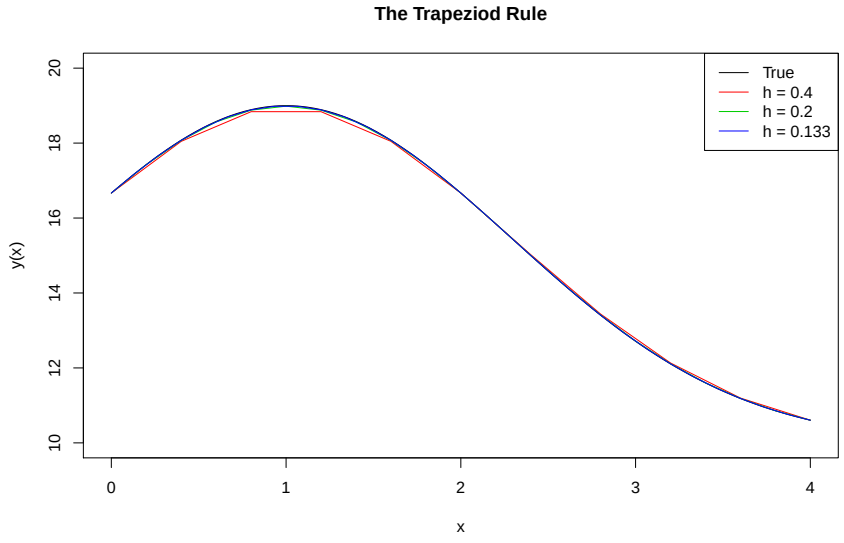
$$y(x_{k+1}) - y(x_k) = \int_{x_k}^{x_{k+1}} f(x, y(x))dx.$$

The right hand side can be computed by the Trapezoid method, which gives:

$$y_{k+1} = y_k + \frac{h}{2}\Big(f(x_k, y_k) + f(x_{k+1}, y_{k+1})\Big)$$

It is also an implicit method that requires us to solve a nonlinear equation, but the error is of order h^2 which is better than any Euler's Methods.

```
myODE3 <- function(f, n, a, b, y0, from = 0, to = 50) {
    h <- (b - a)/n
    f2 <- function(y, y1, x1, x, h) y - y1 - h * (f(x, y) + f(x1, y1))/2
    x <- a + h * (0:n)
    y <- y0
    for (i in 2:(n + 1)) y[i] <- uniroot(f2, c(from, to), y1 = y[i - 1], x1 = x[i -
        1], x = x[i], h = h)$root
    return(list(x = x, y = y, h = h))
}
```



The method work nicely even for small h ($h = .4$ corresponds to 10 points). This method, however, may not be convenient in some cases in which the nonlinear equation is hard to solve. The next method is explicit and can do even better than the Trapezoid rule.

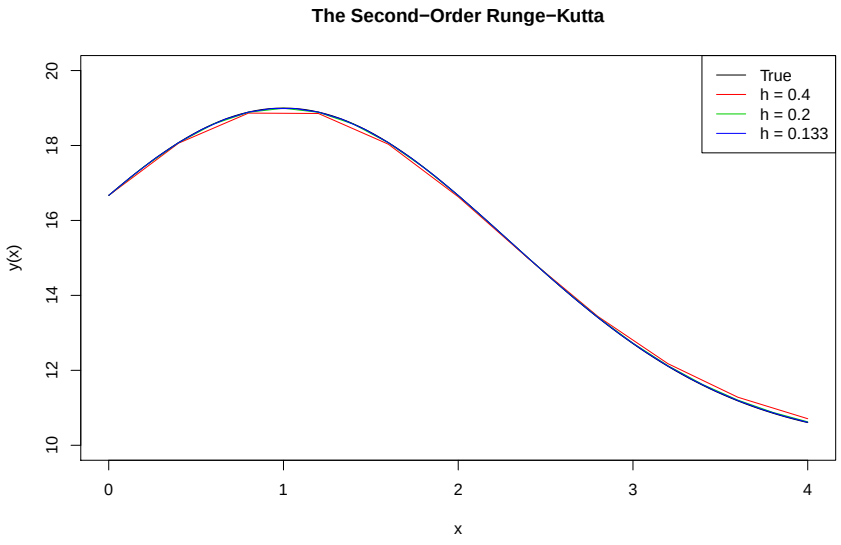
8.2.4 Runge-Kutta Method

There is more than one version of this method. The idea is similar to the Trapezoid rule because it computes $f(x, y)$ at more than one points in order to get a better approximation. The second-order Runge-Kutta (RK2) is like the Trapezoid, but the Euler's Y_{k+1} is used instead. Its error is also $O(h^2)$. Since it only depends on known values, we don't need to solve a nonlinear equation:

$$y_{k+1} = y_k + \frac{h}{2}\Big(f(x_k, y_k) + f(x_{k+1}, Y^E_{k+1})\Big),$$

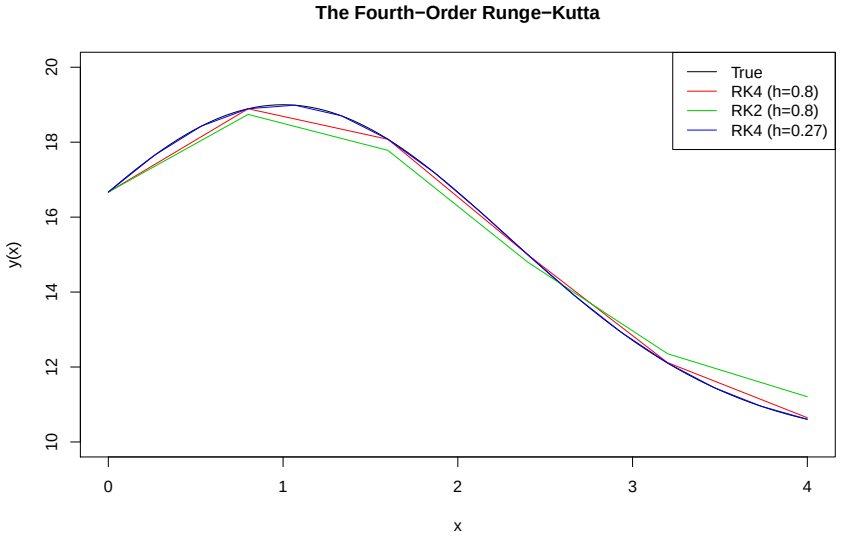
where $Y^E_{k+1} = y_k + hf(x_k, y_k)$

```
RK2 <- function(f, n, a, b, y0) {
    h <- (b - a)/n
    x <- a + h * (0:n)
    y <- y0
    for (i in 2:(n + 1)) {
        YE = y[i - 1] + h * f(x[i - 1], y[i - 1])
        y[i] <- y[i - 1] + h * (f(x[i - 1], y[i - 1]) + f(x[i], YE))/2
    }
    return(list(x = x, y = y, h = h))
}
```

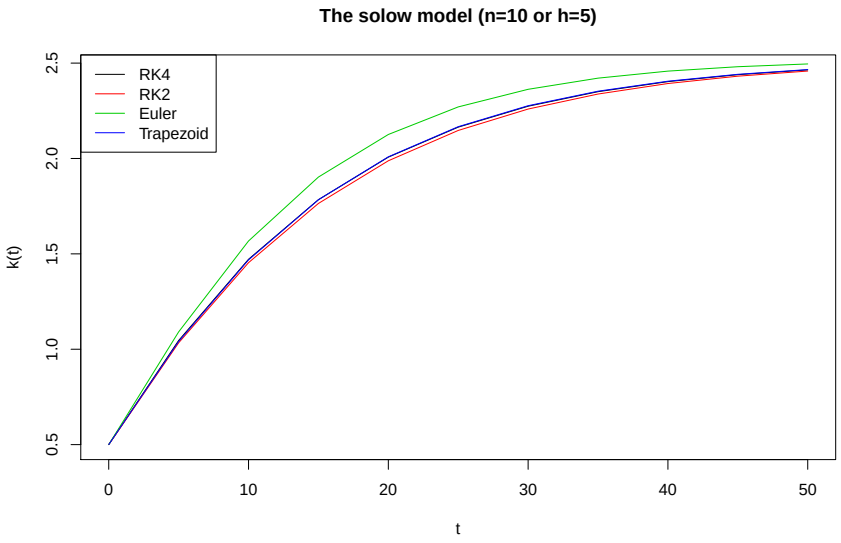


The fourth-order Runge-Kutta (RK4) evaluate $f(x, y)$ at 4 points and its error is $O(h^4)$

```
RK4 <- function(f, n, a, b, y0) {
    h <- (b - a)/n
    x <- a + h * (0:n)
    y <- y0
    for (i in 2:(n + 1)) {
        F1 <- f(x[i - 1], y[i - 1])
        F2 <- f(x[i - 1] + h/2, y[i - 1] + h * F1/2)
        F3 <- f(x[i - 1] + h/2, y[i - 1] + h * F2/2)
        F4 <- f(x[i], y[i - 1] + h * F3)
        y[i] <- y[i - 1] + h * (F1 + 2 * F2 + 2 * F3 + F4)/6
    }
    return(list(x = x, y = y, h = h))
}
```



Lets now compare few methods to the Solow model. We assume the following values: $s = 0.2$, $\delta = 0.1$, $\alpha = 0.25$, and $k(0) = 0.5$.



8.2.5 Example: Signaling Equilibrium

This example comes from Judd, page 347. It is a simplified version of a model developed by [Spence 1974]. It is an initial value problem with closed form solution. We can use it to compare the performance of the different methods.

In the model, individuals of type $n \in [n_m, n_M]$ (a measure of his ability) choose the level of education y. The cost of education is $C(y, n)$ with $C_y > 0$ and $C_n < 0$. Employers only observe y (the signal), which implies that wage, $w(y)$, only depends on it. Individuals maximize their net income $w(y) - C(y, n)$, which implies that $w'(y) = C_y(y, n)$. Output produced by each individual, $S(y, n)$, depends on his type and level of education, with $S_y > 0$, and $S_n > 0$. We assume a competitive equilibrium, which implies that $w(y) = S(y, n)$.

Because each type will choose different level of education, we have $y = y(n)$. To follow the book and the article, we will substitute the inverse of the optimal level of education $n = n(y)$ in the equilibrium condition in order to obtain the differential equation. The equilibrium conditions become:

$$w'(y) = C_y(y, n(y))$$

$$w(y) = S(y, n(y))$$

If we differentiate the second equation and substitutes the first in it, we obtain the Equation 10.4.1 of Judd:

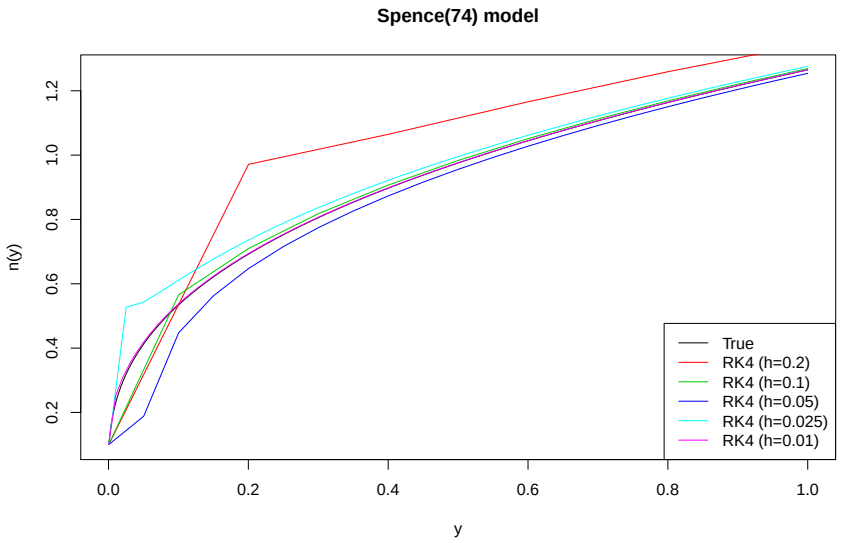
$$n'(y) = \frac{C_y(y, n(y)) - S_y(y, n(y))}{S_n(y, n(y))} \tag{8.4}$$

For the initial value, we assume that the individual with the lowest ability n_m chooses the level of education y_m that is socially optimal. It satisfies $S_y(y_m, n_m) = C_y(y_m, n_m)$. For the numerical example, we assume that $S(y, n) = ny^\alpha$, $C(y, n) = y/n$, $n_m = 0.1$, $\alpha = 0.25$, and $y_m = 0.00034$. The closed form solution is given by Equation 10.4.5 of Judd. The following solves the different equation 8.4.

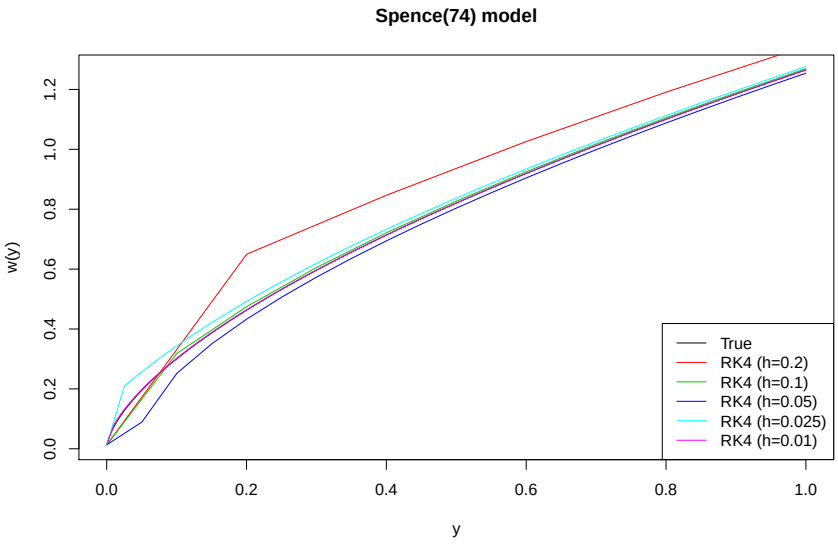
```
Spence <- function(y, alpha = 0.25, nm = 0.1) {
    ym <- (nm^2 * alpha)^(1/(1 - alpha))
    D <- (nm/ym^(-alpha))^2 * (1 + alpha)/2 - ym^(1 + alpha)
    y^(-alpha) * sqrt(2 * (y^(1 + alpha) + D)/(1 + alpha))
}
```

```
dN <- function(y, n, alpha = 0.25) (1/n - alpha * n * y^(alpha - 1))/y^alpha
```

```
> nm <- 0.1
> alpha <- 0.25
> b <- 1
> N <- c(5,10,20,40,100)
> ym <- (nm^2*alpha)^(1/(1-alpha))
> curve(Spence,ym,b,xlab="y",ylab="n(y)",main=
+ "Spence(74) model",n=2000)
> for(i in 1:length(N))
+         {
+         s <- RK4(dN,N[i],ym,b,nm)
+         lines(s$x,s$y,col=(i+1)) }
> l <- paste("RK4 (h=",round((b-ym)/N,3),")",sep="")
> legend("bottomright",c("True",l),col=1:(length(N)+1),lty=1)
```



We see that the choice of h matters most when the second derivative of the solution is the highest. We can also get the solution for $w(y)$, using the equilibrium condition.



8.3 Boundary values and the Shooting Method

Consider the life-cycle model in which consumers maximize the discounted future utility:

$$\max_c \int_0^T e^{-rt} u(c(t)) dt$$

subject to:

$$\dot{A} = f(A(t)) + w(t) - c(t),$$

and $A(0) = A(T) = 0$. The Hamiltonian is:

$$H = u(c) + \lambda(f(A) + w - c).$$

The solution implies the first order condition

$$u'(c) = \lambda$$

the constraint:

$$\dot{A} = f(A(t)) + w(t) - c(t),$$

and the costate equation:

$$\dot{\lambda} = \rho\lambda - \lambda f'(A)$$

If we substitute λ by $u'(c)$, and $\dot{\lambda}$ by $u''(c)\dot{c}$ in the last equation, we obtain the following system of differential equations:

$$\begin{aligned} \dot{A} =& f(A) + w - c \\ \dot{c} =& \frac{u'(c)}{u''(c)}(\rho - f'(A)) \end{aligned} \tag{8.5}$$

with initial value $A(0) = 0$, and boundary condition $A(T) = 0$.

This kind of problems is quite different from initial value problems because we need to restrict the last value without knowing the solution. The Shooting method is a trial-and-error approach. In the above problem, $A(T)$, given $A(0) = 0$, depends of the initial values $c(0)$. The method consists in guessing $c(0)$, and modifying it until $A(T)$ is sufficiently close to 0.

First, we need to adapt the RK4() function for system of equations. In the following, f is a function (x, y) which returns an $n \times 1$ vector, $x \in [a, b]$, and $y \in \mathbb{R}^n$.

```
RK4 <- function(f, n, a, b, y0, ...) {
    h <- (b - a)/n
    x <- a + h * (0:n)
    y <- matrix(y0, nrow = 1)
    for (i in 2:(n + 1)) {
        F1 <- f(x[i - 1], y[i - 1, ], ...)
        F2 <- f(x[i - 1] + h/2, y[i - 1, ] + h * F1/2, ...)
        F3 <- f(x[i - 1] + h/2, y[i - 1, ] + h * F2/2, ...)
        F4 <- f(x[i], y[i - 1, ] + h * F3, ...)
        yi <- y[i - 1, ] + h * (F1 + 2 * F2 + 2 * F3 + F4)/6
        y <- rbind(y, yi)
```

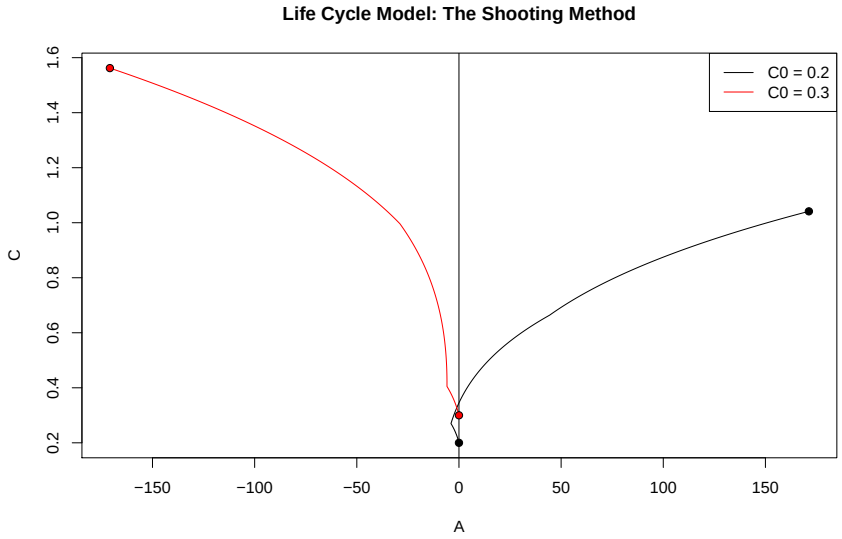
```
    }
    return(list(x = x, y = y, h = h))
}
```

For the numerical exercise, we assume that $u(c) = c^{1+\gamma}/(1+\gamma)$, $w(t) = 1$ if $M \leq t \leq R$ and 0 otherwise, $\rho = 0.04$, $f(A) = rA$ with $r = 0.10$, $\gamma = -0.5$, $T = 55$, $M = 10$, and $R = 40$. The following function returns the right hand side of the system 8.5, with $y = \{c, A\}'$:

```
LifeCycle <- function(x, y, rho = 0.04, r = 0.1, gamma = -2, M = 10, R = 40) {
    w <- (x <= R) * (x >= M)
    y1 <- r * y[2] + w - y[1]
    y2 <- (rho - r) * y[1]/gamma
    c(y2, y1)
}
```

Lets first start with $c(0) = 0.3$, and $c(0) = 0.2$:

```
> h <- .01
> c0 <- c(.2,.3)
> n <- floor(55/h)
> s <- RK4(LifeCycle,n,0,55,c(c0[1],0))
> s2 <- RK4(LifeCycle,n,0,55,c(c0[2],0))
```

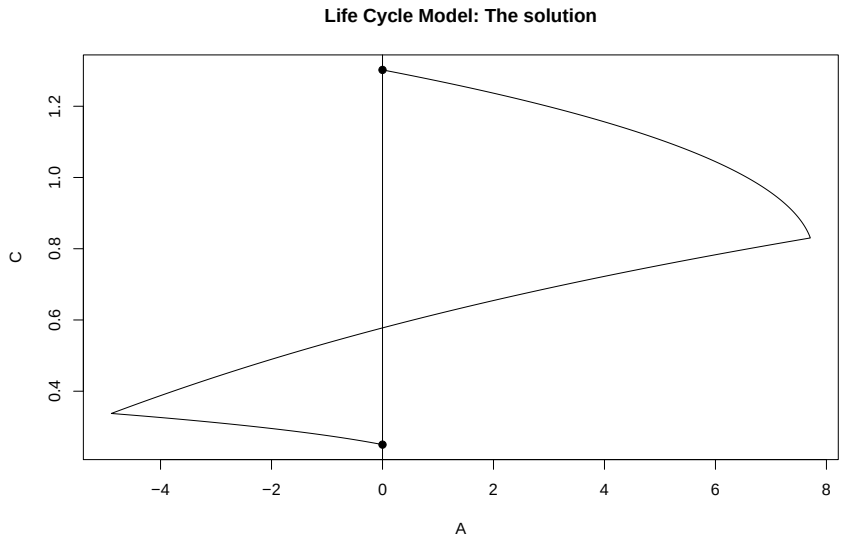


The end point of the solution path should be 0. For $c(0) = 0.2$, $A(55) > 0$, and for $c(0) = 0.3$, $A < 0$. The find the right $c(0)$ we can use a bisection method. The following is a function that can be used in the Bisection() function of Chapter 5:

```
> f <- function(c0)
+         {
+         n <- floor(55/0.01)
+         s <- RK4(LifeCycle,n,0,55,c(c0,0))
+         return(s$y[n+1,2])
+         }
> res <- Bisection(f,.2,.3)
> res


Method:  Bisection
Message:  Converged after 20 iterations

The solution is:  0.2500609 , and f(x) is  3.074027e-05
Precision:  9.536743e-08
```

We can then use that value to plot the solution.

```
> s <- RK4(LifeCycle,n,0,55,c(res$sol,0))
> plot(s$y[,2],s$y[,1],type="l",xlab="A",ylab="C",
+ main="Life Cycle Model: The solution")
> abline(v=0)
> points(c(0,0),c(res$sol,s$y[n+1,1]),pch=c(21,21),bg=c(1,1))
```



8.3.1 Infinite Horizon Models

Consider the following model:

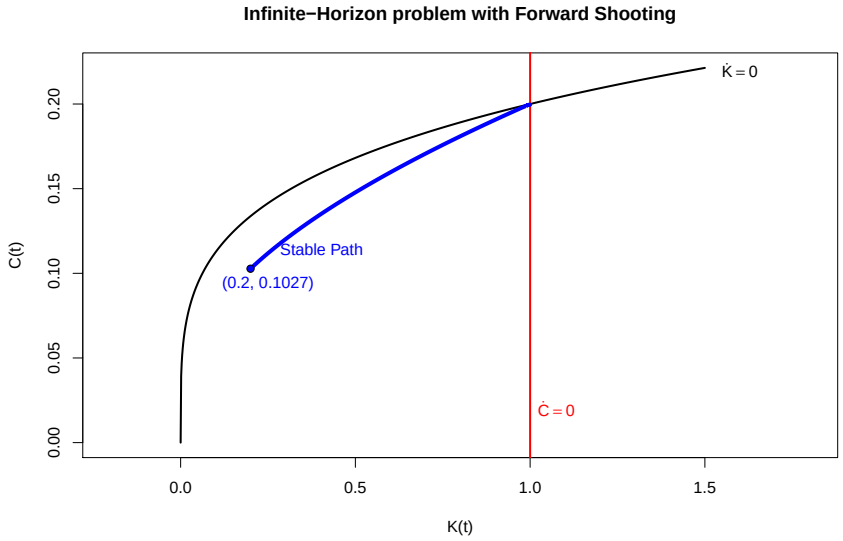
$$\max_c \int_0^\infty e^{-\rho t} u(c) dt$$

subject to $\dot{k} = f(k) - c$, and $k(0) = k_0$. We don't have explicit boundary conditions, but we have to assume that $\lim_{t\to\infty} |k(t)| < \infty$ (which also implies the convergence of $|c(t)|$). We know for the above model that the only possible path is the one that will make $k(t)$ and $c(t)$ converge to their respective steady state values, k^* and c^*. The first method is to forward shooting and it consists in choosing the path that leads as close as possible to the steady state. The following algorithm is the one proposed on page 357 of Judd, and it is for the case in which $k_0 < k^*$. We also use the specification given on page 359.

```
growth <- function(x, y) {
    y1 <- -(0.05 - 0.05 * y[2]^(-0.75)) * y[1]/2
    y2 <- 0.2 * y[2]^0.25 - y[1]
    c(y1, y2)
}

RK4G <- function(f, h, y0, maxit = 1000) {
    #The difference: it stops when either df/dy<0
    x <- 0
    y <- matrix(y0, nrow = 1)
    i <- 1
    while (TRUE) {
        F1 <- f(x[i], y[i, ])
        F2 <- f(x[i] + h/2, y[i, ] + h * F1/2)
        F3 <- f(x[i] + h/2, y[i, ] + h * F2/2)
        F4 <- f(x[i] + h, y[i, ] + h * F3)
        y1 <- y[i, ] + h * (F1 + 2 * F2 + 2 * F3 + F4)/6
        x <- c(x, x[i] + h)
        y <- rbind(y, y1)
        if (any(f(x[i + 1], y1) < 0))
            break
        if (i > maxit) {
            warning("maxit reached")
            break
        }
        i <- i + 1
```

```
    }
    return(list(T = i, y = y, x = x))
}


fShooting <- function(f, k0, h = 0.01, eps = 1e-07, maxit = 20) {
    cL <- 0
    cH <- 0.2 * k0^0.25
    cSteady <- 0.2
    i <- 1
    while (TRUE) {
        c0 <- (cL + cH)/2
        res <- RK4G(f, h, c(c0, k0), maxit = 2000)
        T <- res$T + 1
        if (abs(res$y[T, 1] - cSteady) < eps)
            break
        if (i > maxit) {
            warning("Maxit reached")
            break
        }
        ydot <- f(res$x[T], res$y[T, ])
        if (ydot[1] < 0)
            cL <- c0 else cH <- c0
        i <- i + 1
    }
    return(res)
}
```

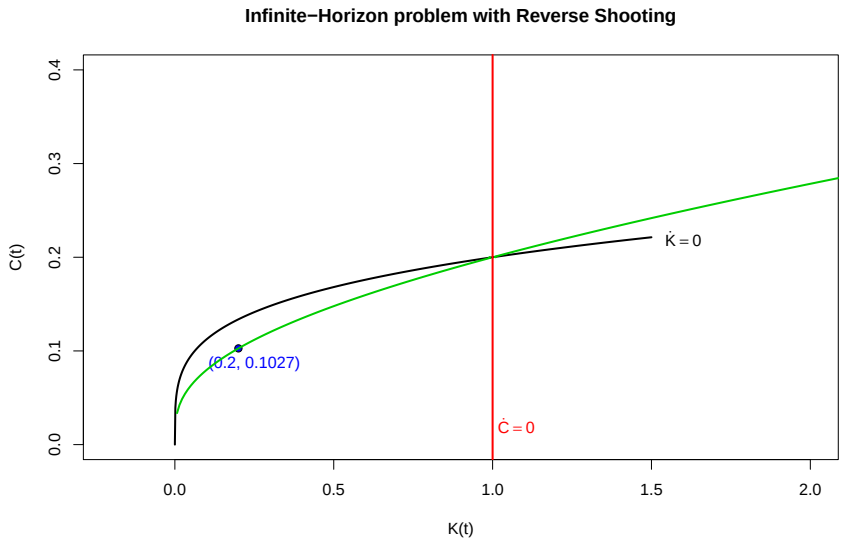
```
> res <- fShooting(growth,.2,eps=1e-3,maxit=1000,h=.1)
> k <- res$y[,2]
> c <- res$y[,1]
> curve(.2*x^.25,0,1.50,xlab="K(t)",ylab="C(t)",n=1000,xlim=c(-.2,1.8),
+         main="Infinite-Horizon problem with Forward Shooting",lwd=2)
> abline(v=1,lwd=2,col=2)
> text(1.075,.02,expression(dot(C)==0),col=2)
> text(1.6,.22,expression(dot(K)==0),col=1)
> lines(k,c,col=4,lwd=4)
> text(k[20],c[20],"Stable Path",col=4,pos=4)
> points(k[1],c[1],pch=21,bg=4)
> text(k[1]+.05,c[1],paste("(",round(k[1],3),", ",round(c[1],4),")",sep=""),pos=1,col=4)
```



This method is time consuming and hard to perform because a slight deviation from the stable path leads to the unstable one. Another way is to do the reverse shooting on $-f(x, y)$. The idea is to transform the stable path into the unstable one. From the phase diagram, a small deviation from the steady state leads to the unstable path. We can therefore use that property to generate the solution.

```
revGrowth <- function(x, y) {
    y1 <- -(0.05 - 0.05 * y[2]^(-0.75)) * y[1]/2
    y2 <- 0.2 * y[2]^0.25 - y[1]
    -c(y1, y2)
}
```

```
> res1 <- RK4(revGrowth,1000,0,300,c(.2,1.01))
> res2 <- RK4(revGrowth,1000,0,300,c(.2,.99))
> curve(.2*x^.25,0,1.50,xlab="K(t)",ylab="C(t)",n=1000,xlim=c(-.2,2),ylim=c(0,.4),
+         main="Infinite-Horizon problem with Reverse Shooting",lwd=2)
> abline(v=1,lwd=2,col=2)
> text(1.075,.02,expression(dot(C)==0),col=2)
> text(1.6,.22,expression(dot(K)==0),col=1)
> # differential equations (ODE), partial differential equations
>
> points(k[1],c[1],pch=21,bg=4)
> text(k[1]+.05,c[1],paste("(",round(k[1],3),", ",round(c[1],4),")",sep=""),pos=1,col=4)
> lines(res1$y[,2],res1$y[,1],col=3,lwd=2)
> lines(res2$y[,2],res2$y[,1],col=3,lwd=2)
```



We could then use those points to obtain $c(0)$ for different $k(0)$. The interpolation method is a nice way to do it:

```
> # x is K(0) and y is C(0)
> unlist(spline(res2$y[,2],res2$y[,1],xout=.2))

        x         y
0.2000000 0.1027205

> unlist(spline(res2$y[,2],res2$y[,1],xout=.5))

        x         y
0.5000000 0.1477963

> unlist(spline(res1$y[,2],res1$y[,1],xout=1.5))

        x         y
1.5000000 0.2417928
```

Another way to apply the reverse shooting method is to solve directly for the stable path $c(t) = C(k(t))$. If we differentiate the identity, we get $C'(k) = \dot{c}/\dot{k}$, starting at the steady states $C(K^*) = c^*$, which implies:

$$C'(k) = \frac{u'(C)}{u''(C)} \frac{\rho - f'(k)}{f(k) - C} \tag{8.6}$$

with $C'(k^*)$ given by Equation 10.7.7 of Judd.

Exercise 8.1. *Replicate Table 10.2 of Judd, using the reverse shooting method applied to the differential equation 8.6*

Exercise 8.2. *Answer Exercises 2, 5, and 6 of Judd (Chapter 10)*

We conclude the section with an example of reverse shooting for multidimensional problems. We consider the growth model with 3 sectors presented in exercise 7, with $u(c) = \log(c)$, $\rho = 0.05$, $\alpha_1 = 0.25$, $\alpha_2 = 0.35$, $\alpha_3 = 0.4$, $\gamma_1 = 10$, $\gamma_2 = 50$, $\gamma_3 = 100$, and $k_i(0) = 0.5$ for $i = 1, 2, 3$. First, we need to compute the steady state. I don't want to compute it manually, so I will use a method from Chapter 5. First, the solution implies the following differential equations.

$$\dot{\lambda}_i = \rho\lambda_i - \frac{\rho k_i^{\alpha_i - 1}}{C},$$

$$\dot{k}_i = I_i,$$

for $i = 1, 2, 3$ with

$$\lambda_i = \frac{1 + 2\gamma_i I_i}{C}$$

and

$$C = \rho\left(\frac{k_1^{\alpha_1}}{\alpha_1} + \frac{k_2^{\alpha_2}}{\alpha_2} + \frac{k_3^{\alpha_3}}{\alpha_3}\right) - \left(I_1 + I_2 + I_3 + \gamma_1 I_1^2 + \gamma_2 I_2^2 + \gamma_3 I_3^2\right)$$

The steady state values are $k_i^* = 1$, $I_i^* = 0$, and $\lambda_i^* = 1/C$. There is two approaches to solve the problem. First, we can follow the procedure on page 361 of Judd, and solve for $I_i(t)$ using the maximum principle (the first order conditions), and substitute the solution into the differential equations. However, there is no closed form solution $I_i(t)$. We can solve it using a nonlinear solver but it may be unstable because there are multiple solutions. The following follows that method:

```
MGrowth <- function(x, y) {
    alpha <- c(0.25, 0.35, 0.4)
    rho = 0.05
    gamma = c(10, 50, 100)
    I0 <- c(0, 0, 0)
    I <- function(I, K, Lambda) {
        C <- sum(rho * K^alpha/alpha) - sum(I) - sum(gamma * I^2)
        C * Lambda - 1 - 2 * gamma * I
    }
    Iv <- Broyden(I, I0, K = y[1:3], Lambda = y[4:6])$sol
    C <- sum(rho * y[1:3]^alpha/alpha) - sum(Iv) - sum(gamma * Iv^2)
    dy2 <- rho * y[4:6] - rho * y[1:3]^(alpha - 1)/C
    return(-c(Iv, dy2))
}
```

```
> SteadyC <- sum(rho/alpha)
> SteadyK <- c(1,1,1)
> SteadyL <- rep(1/SteadyC,3)
> y <- c(SteadyK*1.001,SteadyL)
> res1 <- RK4(MGrowth, n, 0, T, y)
```

I am not showing the result because it is not satisfying. In the second method, I substitute the λ_i and $\dot{\lambda}_i$ by I_i and $\dot{I}_i$. We replace λ_i by

$$\lambda_i = \frac{1 + 2\gamma_i I_i}{C}$$

and $\dot{\lambda}_i$ by

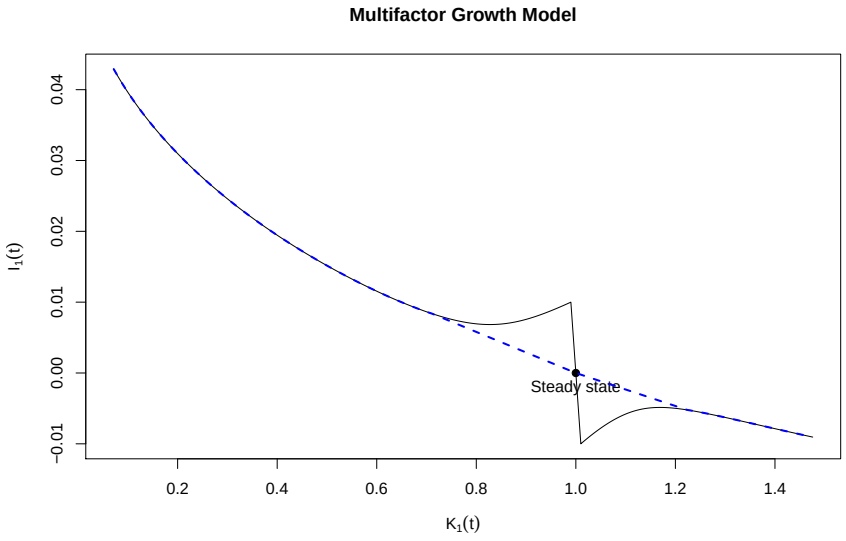
$$\dot{\lambda}_i = -\frac{1 + 2\gamma_i I_i}{C^2}\dot{C} + \frac{2\gamma_i \dot{I}_i}{C}$$

Because *dotC* depends on all $\dot{k}_i$ and $\dot{I}_i$, we need to solve a linear system of equations to obtain the 6 differential equations.

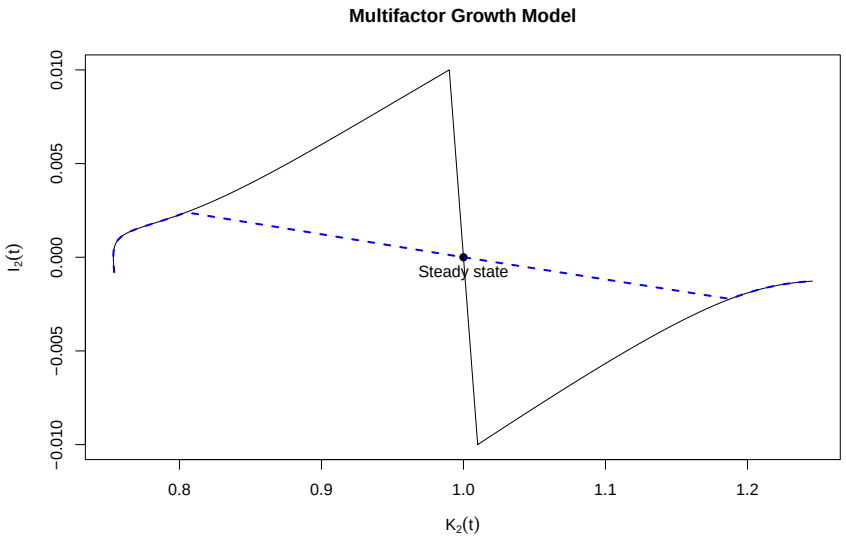
```
MGrowth2 <- function(x, y) {
    alpha <- c(0.25, 0.35, 0.4)
    rho = 0.05
    gamma = c(10, 50, 100)
    K <- y[1:3]
    I <- y[4:6]
    C <- sum(rho * y[1:3]^alpha/alpha) - sum(I) - sum(gamma * I^2)
    Ai <- -1/C^2 * (1 + 2 * gamma * I)
    Bi <- 2 * gamma/C
    Ei <- rho * (1 + 2 * gamma * I)/C - rho * K^(alpha - 1)/C
    A <- c(rho * K^(alpha - 1), -(1 + 2 * gamma * I))
    W <- Ai %o% A
    diag(W[1:3, 4:6]) <- diag(W[1:3, 4:6]) + Bi
    W <- rbind(W, cbind(diag(3), 0, 0, 0))
    -solve(W, c(Ei, I))
}
```

```
> T <- 73
> n <- 400
> SteadyK <- c(1,1,1)
> y <- c(SteadyK*1.01,rep(-0.01,3))
> res <- RK4(MGrowth2, n, 0, T, y)
> y <- c(SteadyK*.99,rep(0.01,3))
> res1 <- RK4(MGrowth2, n, 0, T, y)
```

```
> Y <- rbind(c(SteadyK,0,0,0),res$y)
> Y <- rbind(res1$y[(n+1):1,],Y)
> plot(Y[,1],Y[,4],type="l",main="Multifactor Growth Model",
+         xlab=expression(K[1](t)),ylab=expression(I[1](t)))
> points(SteadyK[1],0,pch=21,bg=1)
> text(SteadyK[1],0,"Steady state",bg=1,pos=1)
> Y <- rbind(c(SteadyK,0,0,0),res$y[-(1:(n/2)),])
> Y <- rbind(res1$y[(n+1):(n/2+1),],Y)
> lines(Y[,1],Y[,4],col=4,lty=2,lwd=2)
```




```
> Y <- rbind(c(SteadyK,0,0,0),res$y)
> Y <- rbind(res1$y[(n+1):1,],Y)
> plot(Y[,2],Y[,5],type="l",main="Multifactor Growth Model",
+         xlab=expression(K[2](t)),ylab=expression(I[2](t)))
> points(SteadyK[1],0,pch=21,bg=1)
> text(SteadyK[1],0,"Steady state",bg=1,pos=1)
> Y <- rbind(c(SteadyK,0,0,0),res$y[-(1:(n/2)),])
> Y <- rbind(res1$y[(n+1):(n/2+1),],Y)
> lines(Y[,2],Y[,5],col=4,lty=2,lwd=2)
```



8.4 Projection Methods (incomplete)

For now, I just give the idea behind the projection method. We don't have time this semester to go into more details. Suppose we want to solve $y'(t) = f(t, y)$ with $y(0) = y_0$. The idea is to approximate the $y(t)$ by another function $\phi(t)$ with the property $\phi(0) = y_0$, for an initial value problem, and $\phi(T) = y_T$, for a boundary value problem. Consider the example given on page 370 of Judd, $y'(t) = y(x)$, with $t \in [0, 3]$, and $y(0) = 1$. The solution is e^t. Consider the following approximation:

$$\phi(t; a) = 1 + \sum_{i=1}^{n} a_i t^i$$

then, the differential equation implies:

$$\sum_{i=1}^{n} i a_i t^{i-1} \approx 1 + \sum_{i=1}^{n} a_i t^i$$

or

$$R(x; a) = -1 + \sum_{i=1}^{n} a_i (i t^{i-1} - t^i) \approx 0,$$

where $R(x; a)$ is called the residual function. We want to choose a in such a way that $R(x; a)$ is as close to 0 as possible for all x. The simpler approach is to use the least square method, and minimize $\int_0^3 R(x; a)dx$. Suppose $n = 3, 4$, then:

```
R_LS <- function(a, from, to) {
    Rfct <- function(x) {
        n <- length(a)
        R <- -1
        for (i in 1:n) R <- R + a[i] * (i * x^(i - 1) - x^i)
        return(R^2)
    }
    integrate(Rfct, from, to)$value
}
```

We can get the coefficients a_i's by minimizing R_LS() (notice that the solution can be obtained by solving a linear system of equations).

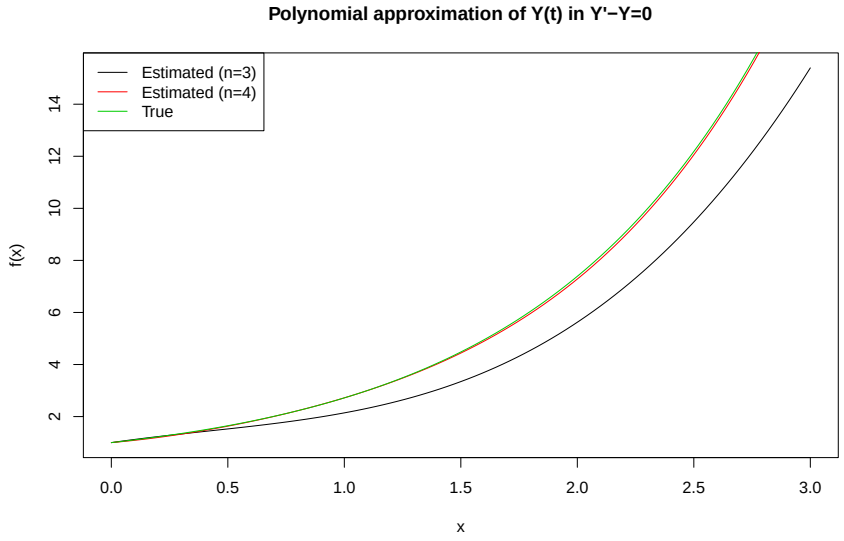
```
> res <- optim(c(0,0,0),R_LS,from=0,to=3,method="BFGS")
> res$par
```

```
[1]  1.2903209 -0.8064510  0.6586022
```

```
> f <- function(x)
+          apply(as.matrix(x),1,function(x) 1+sum(res$par*x^(1:length(res$par))))
> Q <- curve(f,0,3,main="Polynomial approximation of Y(t) in Y'-Y=0")
> res <- optim(c(0,0,0,0),R_LS,from=0,to=3,method="BFGS")
> res$par
```

```
[1]  0.7701986  1.1310133 -0.3906775  0.2090132
```

```
> lines(Q$x,f(Q$x),col=2)
> lines(Q$x,exp(Q$x),col=3)
> legend("topleft",c("Estimated (n=3)", "Estimated (n=4)", "True"),col=1:3,lty=1)
```



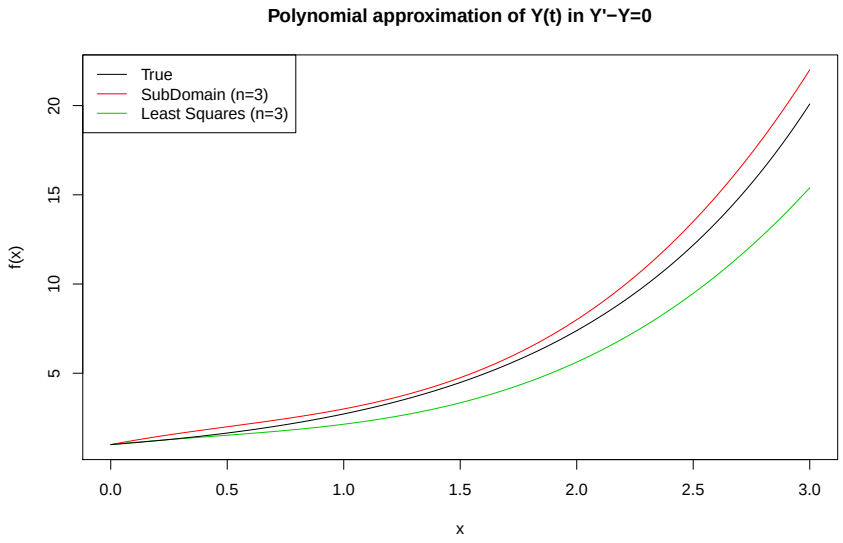
The Subdomain method finds the n a_i's that satisfy $\int_{D_i} R(x;a) = 0$ for the n intervals D_i.

```
R_SD <- function(a, from, to, D) {
    Rfct <- function(x) {
        n <- length(a)
        R <- -1
        for (i in 1:n) R <- R + a[i] * (i * x^(i - 1) - x^i)
        return(R)
    }
    from <- seq(from, to, length = (D + 1))
    r <- sapply(1:D, function(i) integrate(Rfct, from[i], from[i + 1])$value)
}
```

```
> res <- Broyden(R_SD,c(0,0,0),from=0,to=3,D=3)
> res$sol # see table 11.1 of Judd
```

```
[1]  2.5 -1.5  1.0
```

```
[1]  2.5 -1.5  1.0
```

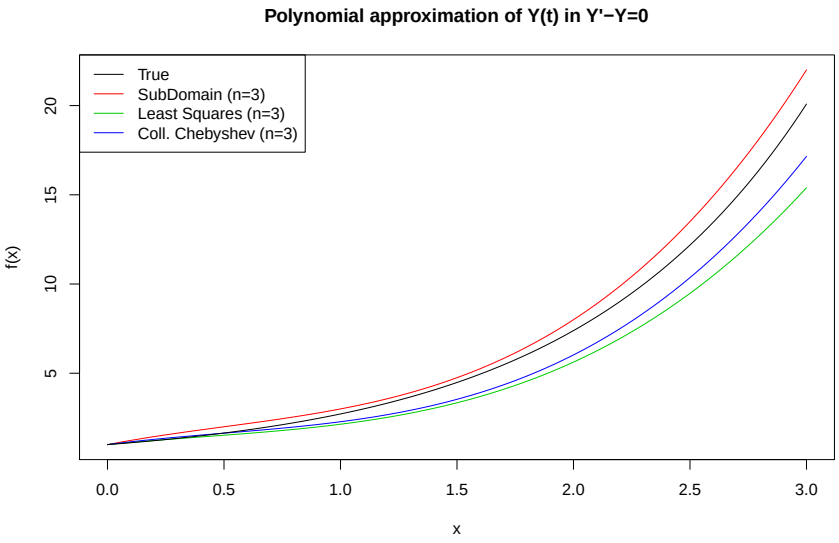


The method of collocation sets $R(x_i, a) = 0$ for n points x_i. The Uniform Collocation set the points uniformly between [0,3], and the Chebyshev Collocation is based on the Chebyshev nodes.

```
CollCheby <- function() {
    x <- 3/2 * c(cos(5 * pi/6) + 1, 1, cos(pi/6) + 1)
    A <- vector()
    for (i in 1:3) {
        w <- (1:3) * x[i]^(0:2) - x[i]^(1:3)
        A <- rbind(A, w)
    }
    return(solve(A, rep(1, 3)))
}
```

```
> a <- CollCheby()
> a
```

```
[1]  1.6923077 -1.2307692  0.8205128
```



Exercise 8.3. *Reproduce Table 11.2 of Judd*

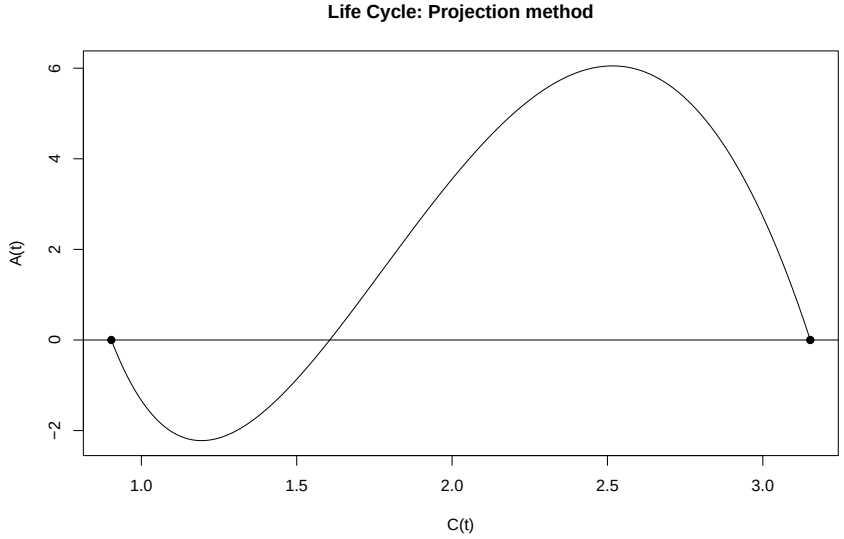
I conclude the section with the life cycle model. The following functions solve the problem using the Chebyshev polynomial and the Collocation method for obtaining the coefficients (The function are written for $t \in [a, b]$ with $A(a) = A(b) = 0$ as boundary condition. Also, we assume that $w(t) = 0.5 + t/10 - 4(t/50)^2$, and $u(c) = c^{\gamma+1}/\gamma + 1$ (see page 389 of Judd):

```
Cheby <- function(t, i, a, b) cos(i * acos(2 * t/(b - a) - 1))

DCheby <- function(t, i, a, b) sin(i * acos(2 * t/(b - a) - 1)) * (i *
    (2/(b - a)/sqrt(1 - (2 * t/(b - a) - 1)^2)))

A <- function(t, aVec, a, b) {
    # a[1] = a_0 and a[n] = a_(n-1)
    # valid for c as well
    n <- length(aVec)
    A <- rep(0, length(t))
    for (i in 1:n) A <- A + aVec[i] * Cheby(t, (i - 1), a, b)
    A
}

Adot <- function(t, aVec, a, b) {
    # a[1] = a_0 and a[n] = a_(n-1)
    # valid for c as well
    n <- length(aVec)
```

```
    A <- rep(0, length(t))
    for (i in 1:n) A <- A + aVec[i] * DCheby(t, (i - 1), a, b)
    A
}
```

```
getSol <- function(n, a, b) {
    w <- function(t) 0.5 + t/10 - 4 * (t/50)^2

    t <- gauss.quad(n - 1, kind = "chebyshev1")$node * (b - a)/2 + (b - a)/2
    f <- function(theta) {
        aVec <- theta[1:n]
        cVec <- theta[(n + 1):(2 * n)]
        R1 <- Adot(t, cVec, a, b) - 0.025 * A(t, cVec, a, b)
        R2 <- Adot(t, aVec, a, b) - 0.1 * A(t, aVec, a, b) - w(t) + A(t, cVec, a,
            b)
        R3 <- A(a, aVec, a, b)
        R4 <- A(b, aVec, a, b)
        c(R1, R2, R3, R4)
    }
    res <- Broyden(f, rep(0, 2 * n), maxit = 300, eps = 1e-09)
    t <- seq(a, b, length = 200)
    At <- A(t, res$sol[1:n], a, b)
    Ct <- A(t, res$sol[(n + 1):(2 * n)], a, b)
    list(Coef = res, At = At, Ct = Ct, t = t)
}
```

```
> library(statmod)
> res <- getSol(10,0,50)
> plot(res$Ct,res$At,type="l",main="Life Cycle: Projection method",
+                 ylab="A(t)",xlab="C(t)")
> points(res$Ct[c(1,length(res$t))],res$At[c(1,length(res$t))],
+                 pch=21,bg=1)
> abline(h=0)
```



See how fast is it compare to the shooting method.

Exercise 8.4. *Solve the growth model on page 392 of Judd. You must obtain $C(k)$ directly by approximating $C(k)$ using Chebyshev polynomials and the Collocation Method.*

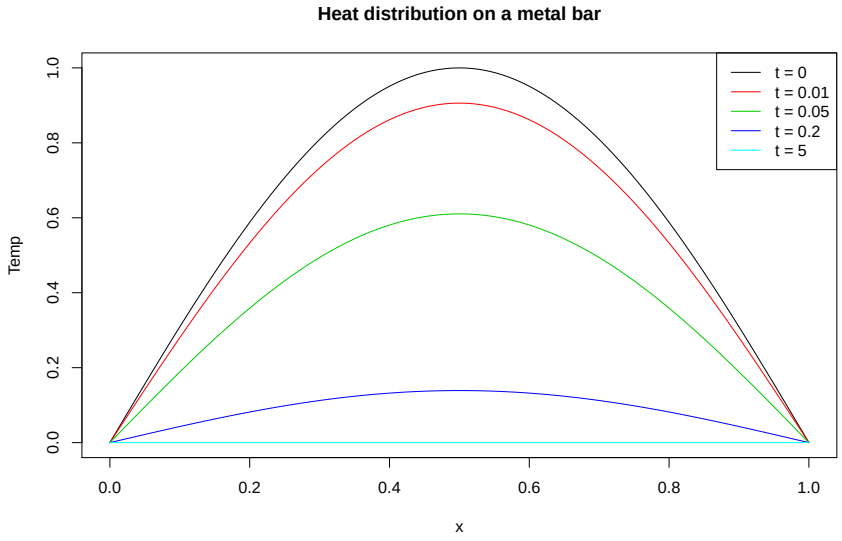
8.5 Partial Differential Equation: The Heat Equation

Let $\theta(x,t)$ be a function that returns the temperature of a metal bar at time $t \in [0,\infty]$, and location x. If we suppose that the length of the bar is 1, then $x \in [0,1]$, where 0 and 1 are the two extremities. The partial differential equation that represents how temperature is distributed along the bar is:

$$\theta_t - \theta_{xx} = 0$$

In the standard heat equation, we assume that something cool down the temperature at both extremities. We therefore have the boundary condition $\theta(0,t) = \theta(1,t) = 0$. It says that the change of temperature is proportional to the speed at which temperature moves from one point to another on the bar. Why would an economist cares about the heat equation? In some applications, the differential equation can be written as the heat equation. It is the case of the problem required to derive the Black and Scholes formula.

If we assume that $\theta(x,0) = \sin(\pi x)$, the solution is $\theta(x,t) = e^{-\pi^2 t}\sin(\pi x)$.



For a given t, we can use the following approximation:

$$\theta(x,t) \approx \hat{\theta}(x,t) = \sin(\pi x) + \sum_{i=1}^{n} a_i(t)(x - x^i)$$

The approximation satisfies the condition $\theta(x,0) = \sin(\pi x)$ if $a_i(0) = 0$. By construction, the condition $\theta(0,t) = \theta(1,t) = 0$ is satisfied. The unknown coefficients are functions of t. If we apply the heat equation to the approximation, and use projection conditions, we obtain a differential equation for $a_i(t)$ with the initial conditions $a_i(0) = 0$. We can use any method to solve initial value problems or use another projection method. Let, for example, $t \in [0,1]$. Since we need $a_i(0) = 0$, we can approximate the functions by:

$$a_i(t) = \sum_{j=1}^{m} a_{ij} t^j,$$

which gives:

$$\hat{\theta}(x,t) = \sin(\pi x) + \sum_{i=1}^{n} \sum_{j=2}^{m} a_{ij}(x - x^i)t^j$$

The projection methods consists in computing the residual function $R(x,t,a)$ and use conditions such as Chebyshev-Collocation or Galerkin to obtain the a_{ij}. We can show that for all cases, the problem can be written as a system of $(n-1)m$ linear equations $Ba = c$. The problem is to find the right method and the right basis functions so that the linear system if well-conditioned. We will instead solve it using finite difference (see [Golub & Ortega 1992]).

Let $\theta_i^k = \theta(x_i, t_k)$, with $i = 0, ..., n+1$, and $k = 0, ..., m$, then we can write the Heat equation using finite difference as (I use the implicit Euler method because of its stability, as shown bellow):

$$\frac{\theta_i^{k+1} - \theta_i^k}{h_t} = \frac{\theta_{i+1}^{k+1} - 2\theta_i^{k+1} + \theta_{i-1}^{k+1}}{h_x^2},$$

where $h_x = \Delta x$, and $h_t = \Delta t$. The boundary conditions imply that $\theta_0^k = \theta_{n+1}^k = 0 \; \forall \; k$, and $\theta_i^0 = \sin(\pi x_i)$. If we define μ as h_t/h_x^2, we can write the algorithm as:

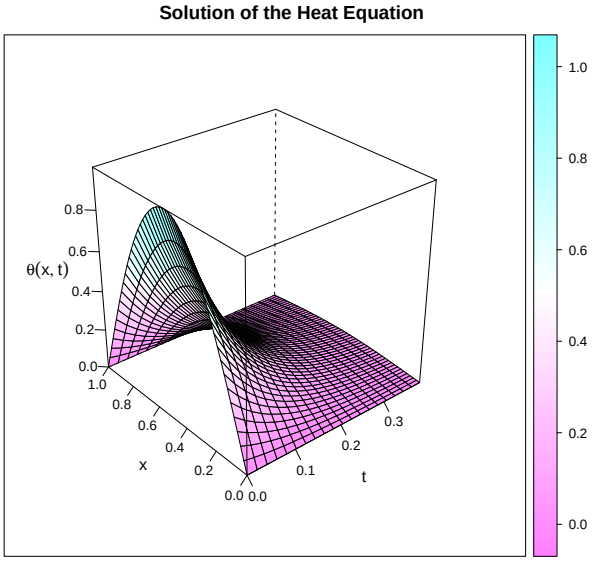
$$\begin{pmatrix} 1+2\mu & -\mu & 0 & 0 & \cdots & 0 \\ -\mu & 1+2\mu & -\mu & 0 & \cdots & 0 \\ 0 & \ddots & \ddots & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & \ddots & \ddots & 0 \\ 0 & \cdots & 0 & -\mu & 1+2\mu & -\mu \\ 0 & \cdots & 0 & 0 & -\mu & 1+2\mu \end{pmatrix} \theta^{k+1} = \theta^k,$$

where $\theta^k = \{\theta_1^k, ..., \theta_n^k\}'$. The transition matrix A is tridiagonal, which makes the system easy to solve, and is diagonally dominant. Also, its eigenvalues are all strictly greater than 1 which implies that the eigenvalues of A^{-1} are strictly less than one. The iterative procedure is therefore convergent. To see that, we can write A as $I + \mu B$, where B is also tridiagonal, with $B_{ii} = 2$ and $B_{i,i+1} = B_{i,i-1} = -1$. We can show that the i^{th} eigenvalue of B is $2[1 + \cos(i\pi/(n+1))]$. The i^{th} eigenvalue of A is therefore $1 + 2\mu[1 + \cos(i\pi/(n+1))] > 1$. The explicit Euler method does not possess this property. The following function computes the solution using this method:

```
Heat1 <- function(n, m, x = NULL, t = NULL) {
    # Implicit Euler
    if (is.null(t))
        t <- seq(0, 1, len = m) else m <- length(t)
    if (is.null(x))
        x <- seq(0, 1, len = n + 2) else n <- length(x) - 2
    a <- (t[2] - t[1])/(x[2] - x[1])^2
    A <- matrix(0, n, n)
    diag(A) <- 1 + 2 * a
    diag(A[-1, -n]) <- -a
    diag(A[-n, -1]) <- -a
    theta <- matrix(sin(pi * x[-c(1, n + 2)]), ncol = 1)
    for (i in 2:m) theta <- cbind(theta, solve(A, theta[, (i - 1)]))
    return(list(Theta = rbind(0, theta, 0), t = t, x = x))
}
```

We can then solve the problem quickly for all $t_k \in [0,1]$ and $x_i \in [0,1]$:

```
> library(lattice)
> res <- Heat1(50,50)
> p <- expand.grid(res$x,res$t[1:20])
> t <- p$Var2
> x <- p$Var1
> theta <- res$Theta
> wireframe(c(theta[,1:20])~t*x,zlab=expression(theta(x,t)),main="Solution of the Heat E
+          scales = list(arrows = FALSE),
+      drape = TRUE, colorkey = TRUE)
```



Before comparing the method with the true solution, we will look at an improve version of the above method. We can use the trapezoid rule:

$$\frac{\theta_i^{k+1} - \theta_i^k}{h_t} = \frac{\theta_{i+1}^k - 2\theta_i^k + \theta_{i-1}^k + \theta_{i+1}^{k+1} - 2\theta_i^{k+1} + \theta_{i-1}^{k+1}}{2h_x^2},$$

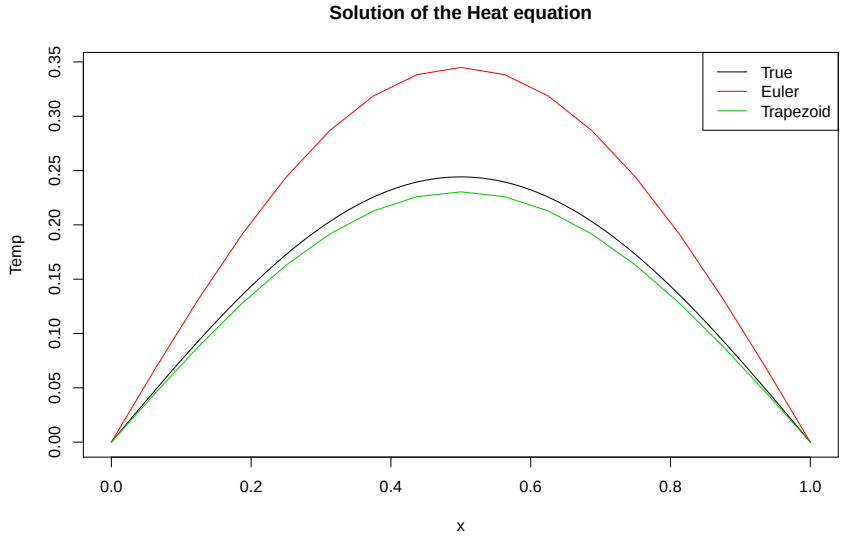
which implies the following system:

$$\begin{pmatrix} 1+\mu & -\mu/2 & 0 & 0 & \cdots & 0 \\ -\mu/2 & 1+\mu & -\mu/2 & 0 & \cdots & 0 \\ 0 & \ddots & \ddots & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & \ddots & \ddots & 0 \\ 0 & \cdots & 0 & -\mu/2 & 1+\mu & -\mu/2 \\ 0 & \cdots & 0 & 0 & -\mu/2 & 1+\mu \end{pmatrix} \theta^{k+1} = \begin{pmatrix} 1-\mu & \mu/2 & 0 & 0 & \cdots & 0 \\ \mu/2 & 1-\mu & \mu/2 & 0 & \cdots & 0 \\ 0 & \ddots & \ddots & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & \ddots & \ddots & 0 \\ 0 & \cdots & 0 & \mu/2 & 1-\mu & \mu/2 \\ 0 & \cdots & 0 & 0 & \mu/2 & 1-\mu \end{pmatrix} \theta^k$$

The iterative scheme can be written as $\theta^{k+1} = A^{-1}B\theta^k = D\theta^k$. We can also show the the eigenvalues of D are strictly less than 1. The following figure compare the methods:

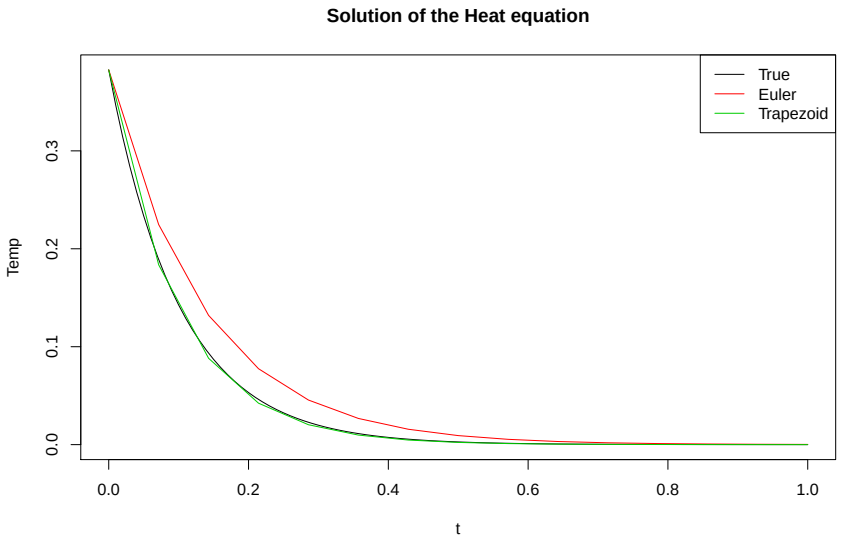
We can compare $\theta(x,t)$ for a given t:

```
> res1 <- Heat1(15,15)
> res2 <- Heat2(15,15)
> t <- res1$t[3]
> f <- function(x)
+         exp(-pi^2*t)*sin(pi*x)
> ylim=c(0,max(c(res1$Thet[,3],res2$Thet[,3])))
> Q <- curve(f,0,1,main="Solution of the Heat equation",xlab="x",ylab="Temp",ylim=ylim)
> lines(res1$x,res1$Theta[,3],col=2)
> lines(res2$x,res2$Theta[,3],col=3)
> legend("topright",c("True","Euler","Trapezoid"),col=1:3,lty=1)
```



or for a given x:

```
> f2 <- function(t)
+         exp(-pi^2*t)*sin(pi*x)
> x <- res1$x[3]
> Q <- curve(f2,0,1,main="Solution of the Heat equation",xlab="t",ylab="Temp")
> lines(res1$t,res1$Theta[3,],col=2)
> lines(res2$t,res2$Theta[3,],col=3)
> legend("topright",c("True","Euler","Trapezoid"),col=1:3,lty=1)
```



Exercise 8.5. *Write a function that solve the Heat equation by using the Trapezoid rule. In a table, compare the error for different m and n.*

8.5.1 Black and Scholes and the Heat Equation

I only cover the theory briefly. For more details, see [Hull 2011]. We consider an European Call option. The exercise price is K, the price of the underlying asset if S, and the expiration date is T. The value of such options at time t is $V(S,t)$. We want to derive its relation with time and the price of the underlying stock. In the Black and Scholes' formula, we assume that the stock price follows a geometric Brownian motion:

$$dS = S\mu dt + S\sigma dW$$

and that we can construct a portfolio in which we go short one option and long dV/dS of the underlying asset. The value of this portfolio is $\Pi = -V + S(dV/dS)$ and the return is $[-\Delta V + (dV/dS)\Delta S]/\Pi$. We can show that the portfolio is risk free, which implies that its return must be equal to the risk-free rate r. By Ito's Lemma, we have:

$$dV = \left(\mu S\frac{\partial V}{\partial S} + \frac{\partial V}{\partial t} + \frac{\sigma^2 S^2}{2}\frac{\partial^2 V}{\partial S^2}\right)dt + \sigma S\frac{\partial V}{\partial S}dW$$

By substituting dV and dS in $\Delta\Pi$, we see that dW vanishes which implies the absence of risk. Using $r\Pi dt = d\Pi$ with the above expression for Π and $\Delta\Pi$, we get the partial differential equation of Black and Scholes.

$$\frac{\partial V}{\partial t} + \frac{\sigma^2 S^2}{2}\frac{\partial^2 V}{\partial S^2} + rS\frac{\partial V}{\partial S} - rV = 0$$

with the condition: $V(S,T) = (S-K)^+$, $V(0,t) = 0$ and $V(S,t)$ converges to S as S goes to infinity. We can rewrite the partial differential equation as $\theta_t = \theta_{xx}$ by the appropriate change of variables. Let $x = log(S/K)$, $\nu = V/K$, and $\tau = (T-t)\sigma^2/2$. Then, we can write:

$$\frac{\partial \nu}{\partial \tau} = \frac{\partial^2 \nu}{\partial x^2} + (k_1 - 1)\frac{\partial \nu}{\partial x} - k_1 \nu$$

with $\nu(x,0) = (e^x - 1)^+$, $\nu(-\infty, \tau) = 0$ and $\nu(x,\tau) \approx S/K$ for large x. Let $\theta(x,\tau) = e^{-(\alpha x + \beta \tau)}\nu$, with $\alpha = (1-k_1)/2$, and $\beta = -(k_1+1)^2/4$, then the above equation can be written as:

$$\frac{\partial \theta}{\partial t} = \frac{\partial^2 \theta}{\partial x^2}$$

Exercise 8.6. *Consider an European Call option with exercise price K, expiration date T. The price of the underlying stock follows the process $dS = S\mu dt + S\sigma dW$. Using the method to solve the Heat Equation, write a function that computes the value of the option $V(t,S)$. Test it with different values of K, T, σ, and μ. Compare your solution to the true formula. (suppose $r = 0.01$)*

8.6 R packages for differential equations

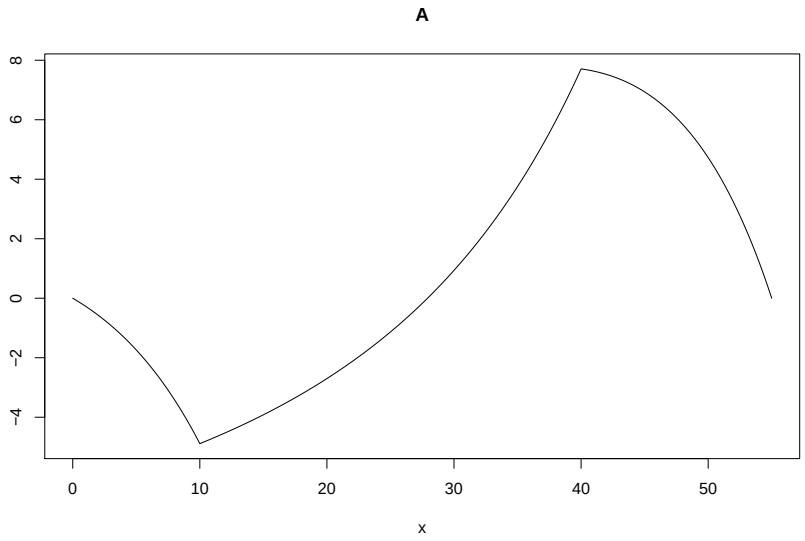
Here is a list of existing packages:

```
> bvpSolve   #Solvers for boundary value problems of ODEs
> ddesolve   #Solver for Delay Differential Equations
> deSolve    #General solvers for initial value problems of ordinary
>            #  differential equations (ODE), partial differential equations
>            #  (PDE), differential algebraic equations (DAE), and delay
>            #  differential equations (DDE)
> deTestSet  #   Testset for differential equations
> odesolve   #   Solvers for Ordinary Differential Equations
> PBSddesolve #     Solver for Delay Differential Equations
> rootSolve   #  Root finding, equilibrium and steady-state analysis of ODEs
> sde         #  Simulation and Inference for Stochastic Differential Equations
> Sim.DiffProc # Simulation of diffusion processes
> simecol     #  Simulation of ecological and other dynamic systems
```

I am not going to explain how these packages work. The manuals are detailed enough. Here is one example for boundary value problems:

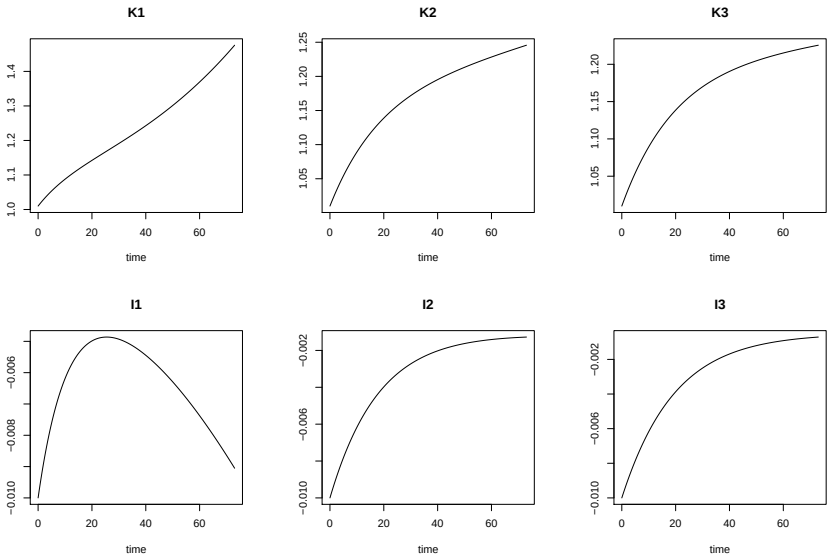
```
> library(bvpSolve)
> LifeCycle <- function(x,y,parms)
+         {
```

```
+         rho<-0.04
+         r <- 0.10
+         gamma <- -2
+         M <- 10
+         R <- 40
+         w <- (x<=R)*(x>=M)
+         y1 <- r*y[2]+w-y[1]
+         y2 <- (rho-r)*y[1]/gamma
+         list(c(y2,y1))
+         }
> init <- c(C=NA,A=0)
> end  <- c(C=NA,A=0)
> sol  <- bvpshoot(yini = init, x = seq(0, 55, by = 0.01),
+                 func = LifeCycle, yend = end,guess=.2)
> plot(sol,which="A")
```



And for initial value problem:

```
> library(deSolve)
> MGrowth3 <- function(x,y,parms)
+         {
+         res <- MGrowth2(x,y)
+         list(res)}
> y <- c(K=SteadyK*1.01,I=rep(-0.01,3))
> sol <- rk4(y,MGrowth3,times=seq(0,73,length=400),parms=NULL)
> plot(sol)
```


K1
K2
K3
I1
I2
I3
time
1.0
1.1
1.2
1.3
1.4
1.05
1.10
1.15
1.20
1.25
−0.010
−0.008
−0.006
−0.002
0
20
40
60

Appendix A

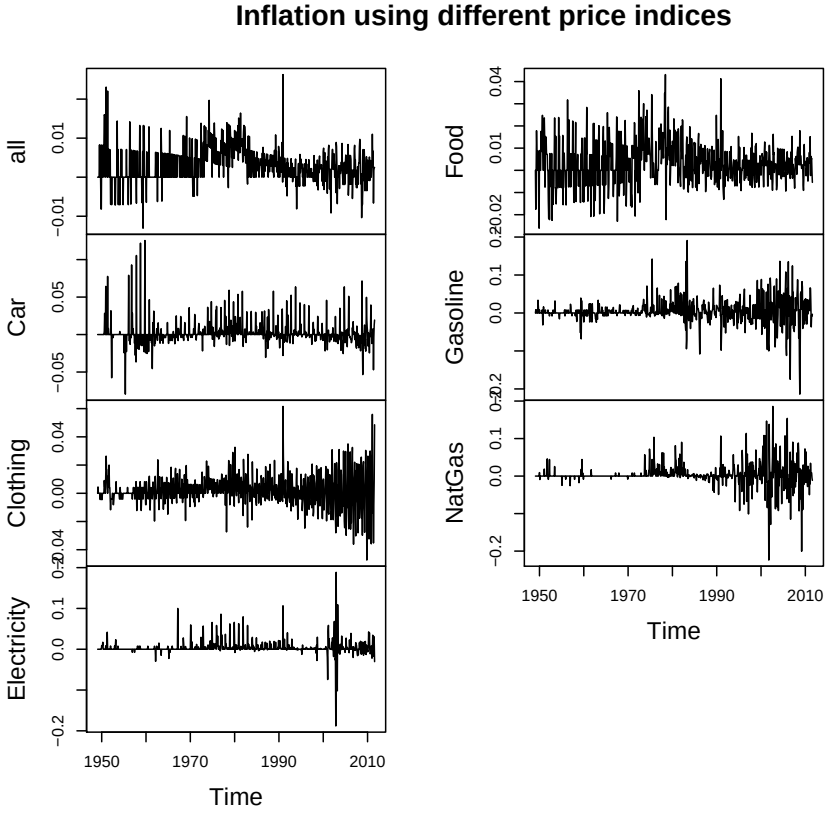
Solution to some Problems

A.1 Chapter 1

Exercise 1.2. *In order to do the exercise, you will need to load the data file "PriceIndex.rda", in which you'll find seven vectors of price index: all, Car, Clothing, Electricity, Food, NatGas and Gasoline. All vectors are monthly time series going from January 1949 to September 2011. This exercise makes you use what we have covered above and more. You may need to use Google, help() or help.search(). That is where the fun begins*

1. *Collect the data in a matrix of class "ts" with the correct starting date and frequency. You can then plot the data and compare the inflation of different items.*

```
> load("../../data/PriceIndex.rda")
> Nvar <- objects() # I only have the loaded variables in the workspace
> CPI <- get(Nvar[1]) # get the variable from its name
> for (i in 2:length(Nvar))
+         CPI <- cbind(CPI,get(Nvar[i]))
> colnames(CPI) <- Nvar
> CPI <- ts(CPI,freq=12,start=c(1949,1))
> INF <- diff(CPI)/lag(CPI,-1)
> colnames(INF) <- colnames(CPI)
> plot(INF, main="Inflation using different price indices")
```



2. *Build a table in which you have for each item, the average annual inflation, its standard deviation, its kurtosis and its skewness.*
   To compute annual inflation I first aggregate CPI using the average method (CPI in a given year is the average price during that period)

```
> ACPI <- aggregate(CPI,nfrequency=1)
> AINF <- diff(ACPI)/lag(ACPI,-1)
> colnames(AINF) <- colnames(CPI)
> S1 <- colMeans(AINF)
> S2 <- apply(AINF,2,sd)
> Momfct <- function(x, mom)
+         {
+         s <- sd(x)
+         mean((x-mean(x))^mom)/s^mom
+         }
> S3 <- apply(AINF,2,Momfct,mom=3)
> S4 <- apply(AINF,2,Momfct,mom=4)
```

```
> res <- cbind(S1,S2,S3,S4)
> colnames(res) <- c("Mean","S-dev","Skewness","Kurtosis")
> rownames(res) <- colnames(CPI)
> round(res,4)
```

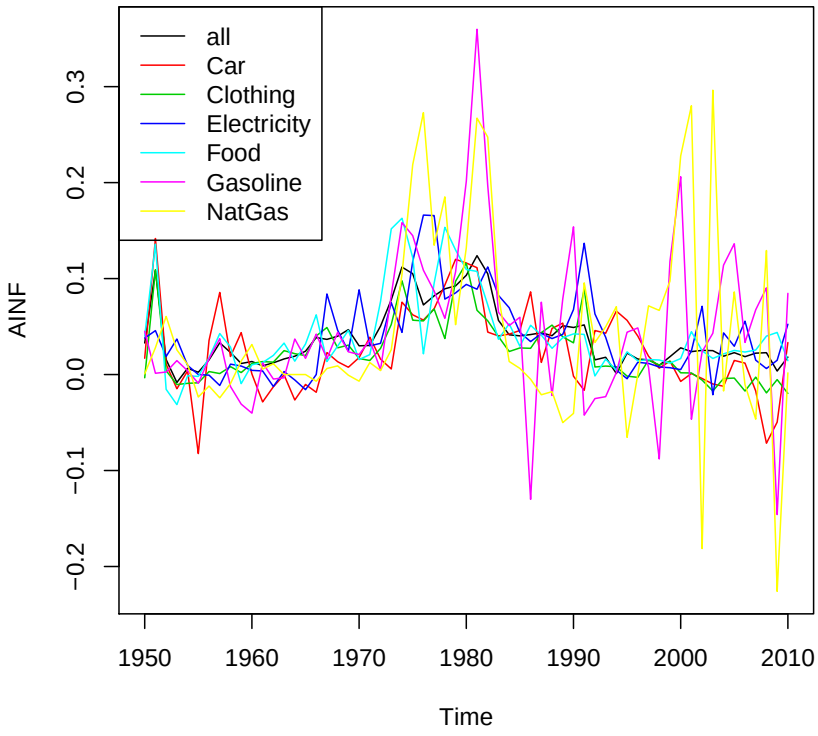
```
              Mean  S-dev Skewness Kurtosis
all         0.0382 0.0317   1.1385   3.3053
Car         0.0250 0.0439   0.3135   3.3084
Clothing    0.0238 0.0323   1.0523   3.5600
Electricity 0.0404 0.0428   1.0250   3.7015
Food        0.0406 0.0427   1.3418   4.1551
Gasoline    0.0453 0.0816   0.8823   5.5863
NatGas      0.0443 0.1008   0.6304   3.9948
```

3. *Create a matrix of annual data from your monthly series. An annual index is defined as the average monthly index.*

   Done in the previous question.

4. *Using the annual series, plot on the same graph the annual inflation series of all component of CPI and include a legend. Do you see a difference between the different items?*

```
> plot(AINF,plot.type="single",col=1:7)
> legend("topleft",colnames(AINF),col=1:7,lty=rep(1,7))
```



Exercises 1.4 to 1.7

I use the simplest way (for me) by creating objects. Here is the new constructor for consumers:

```
consumer <- function(name = NULL, par, Y = NULL, utility = c("Cobb",
    "Linear", "Leontief", "Subsistence", "CES", "Linear", "Concave")) {
    utility <- match.arg(utility)
    U <- get(utility)
    if (!U(par)$good)
        stop("The vector of parameters does not fit the selected utility function")
    cons <- list(name = name, par = par, Y = Y, utility = U,
        nameU = utility)
    class(cons) <- "consumer"
    return(cons)
}
```

I then create each utility function (notice what the function returns):

```
Cobb <- function(par) {
    names(par) <- NULL
    good = TRUE
    if (length(par) != 2)
        good <- FALSE
    par <- c(alpha = par)
    f <- expression(x1^alpha1 * x2^alpha2)
    X1 <- expression(alpha1 * Y/(p1 * (alpha1 + alpha2)))
    X2 <- expression(alpha2 * Y/(p2 * (alpha1 + alpha2)))
    Indif <- expression(U^(1/alpha2) * x1^(-alpha1/alpha2))
    fct <- paste("U = X1^", par[1], "*X2^", par[2], sep = "")
    ans <- list(Uexp = f, Sol = list(X1 = X1, X2 = X2), par = par,
        name = "Cobb Douglas", fct = fct, Indif = Indif, good = good)
    class(ans) <- "Utility"
    return(ans)
}

Leontief <- function(par) {
    names(par) <- NULL
    good = TRUE
    if (length(par) != 2)
        good <- FALSE
    par <- c(alpha = par)
    f <- expression(min(x1 * alpha1, x2 * alpha2))
    X1 <- expression(Y/(p1 + p2 * alpha1/alpha2))
    X2 <- expression(Y/(p2 + p1 * alpha2/alpha1))
    Indif <- function(U, par) {
        x1 <- U/par[1]
        x2 <- U/par[2]
        ylim <- c(0, 3 * x2)
        xlim <- c(0, 3 * x1)
        plot(c(x1, x1), c(x2, ylim[2]), xlab = "X1", ylab = "X2",
            bty = "n", xlim = xlim, ylim = ylim, type = "l",
            col = 2, lwd = 2)
        lines(c(x1, xlim[2]), c(x2, x2), col = 2, lwd = 2)
    }
    fct <- paste("U = Min(", par[1], "*X1, ", par[2], "*X2)",
        sep = "")
    ans <- list(Uexp = f, Sol = list(X1 = X1, X2 = X2), par = par,
        name = "Leontief", fct = fct, Indif = Indif, good = good)
    class(ans) <- "Utility"
```

```
    return(ans)
}

Subsistence <- function(par) {
    names(par) <- NULL
    good = TRUE
    if (length(par) != 4)
        good <- FALSE
    par <- c(alpha = par[1:2], x0 = par[3:4])
    f <- expression((x1 - x01)^alpha1 * (x2 - x02)^alpha2)
    X1 <- expression((alpha1 * Y + alpha2 * p1 * x01 - alpha1 *
        x02 * p2)/(p1 * (alpha1 + alpha2)))
    X2 <- expression((alpha2 * Y + alpha1 * p2 * x02 - alpha2 *
        x01 * p1)/(p2 * (alpha1 + alpha2)))
    Indif <- expression(x02 + U^(1/alpha2) * (x1 - x01)^(-alpha1/alpha2))
    fct <- paste("U = (X1-", par[3], ")^", par[1], "*(X2-", par[4],
        ")^", par[2], sep = "")
    ans <- list(Uexp = f, Sol = list(X1 = X1, X2 = X2), par = par,
        name = "Subsistence", fct = fct, Indif = Indif, good = good)
    class(ans) <- "Utility"
    return(ans)
}
```

The solve function would then be easy to write:

```
solve.consumer <- function(cons, p, print = T) {
    U <- cons$utility(cons$par)
    x1 <- eval(U$Sol$X1, as.list(c(U$par, Y = cons$Y, p = p)))
    x2 <- eval(U$Sol$X2, as.list(c(U$par, Y = cons$Y, p = p)))
    x <- c(x1, x2)
    V <- eval(U$Uexp, as.list(c(U$par, x = x)))
    if (print)
        cat("\n", cons$name, " will consume \n", x1, "X1 and ",
            x2, "X2 (U = ", V, ")\n") else return(list(x1 = x1, x2 = x2, V = V))
}
```

Lets try it with 3 different consumers:

```
> cons1 <- consumer("Pierre",c(.2,.8),2000,"Cobb")
> cons2 <- consumer("John",c(2,4),2000,"Leontief")
> cons3 <- consumer("Bill",c(.2,.8,10,20),2000,"Subsistence")
> p <- c(15,20)
> solve(cons1,p)
```

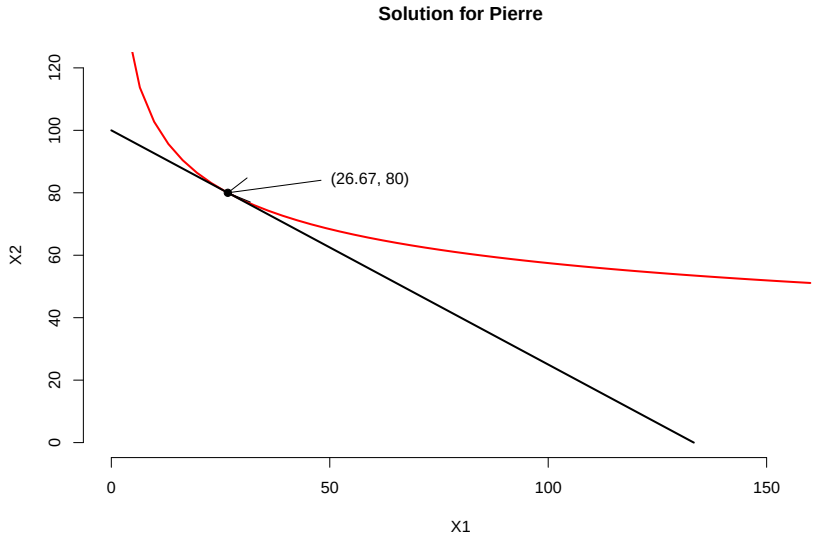
```
 Pierre  will consume
 26.66667 X1 and  80 X2 (U =  64.21932 )

> solve(cons2,p)

 John  will consume
 80 X1 and  40 X2 (U =  160 )

> solve(cons3,p)

 Bill  will consume
 29.33333 X1 and  78 X2 (U =  46.55901 )
```

The plot function would look like:

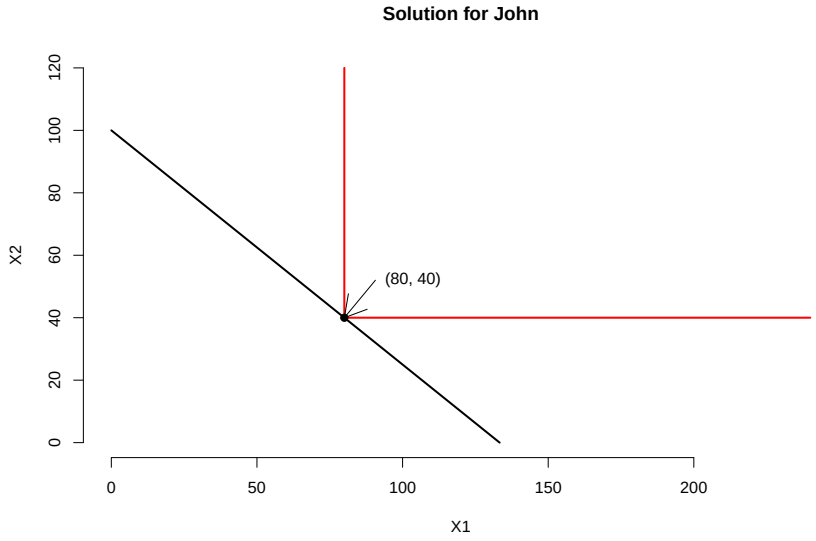
```
plot.consumer <- function(cons, p) {
    x <- solve(cons, p, print = FALSE)
    U <- cons$utility(cons$par)

    if (class(U$Indif) == "expression") {
        if (is.null(cons$Y))
            cons$Y <- eval(U$Y, as.list(c(U$par, p = p)))
        ylim <- c(0, 1.2 * cons$Y/p[2])
        xlim <- c(0, 1.2 * cons$Y/p[1])
        ux1 <- xlim[1]
        ux2 <- xlim[2]
        ux <- seq(ux1, ux2, len = 50)
        uy <- vector()
        for (i in 1:length(ux)) uy[i] <- eval(U$Indif, as.list(c(U$par,
            U = x$V, x1 = ux[i])))

        plot(ux, uy, xlim = xlim, ylim = ylim, xlab = "X1", ylab = "X2",
            type = "l", col = 2, lwd = 2, bty = "n")
    } else U$Indif(x$V, U$par)
    bx <- seq(0, cons$Y/p[1], len = 10)
    by <- cons$Y/p[2] - p[1] * bx/p[2]
    lines(bx, by, lwd = 2)
    points(x$x1, x$x2, pch = 21, bg = 1)
    title(paste("Solution for ", cons$name, sep = ""))
    ax <- x$x1 + (cons$Y/p[1] - x$x1) * 0.2
    ay <- x$x2 + (cons$Y/p[2] - x$x2) * 0.2
    mes <- paste("(", round(x$x1, 2), ", ", round(x$x2, 2), ")",
```

```
        sep = "")
    text(ax, ay, mes, pos = 4)
    arrows(ax, ay, x$x1, x$x2)
}
```

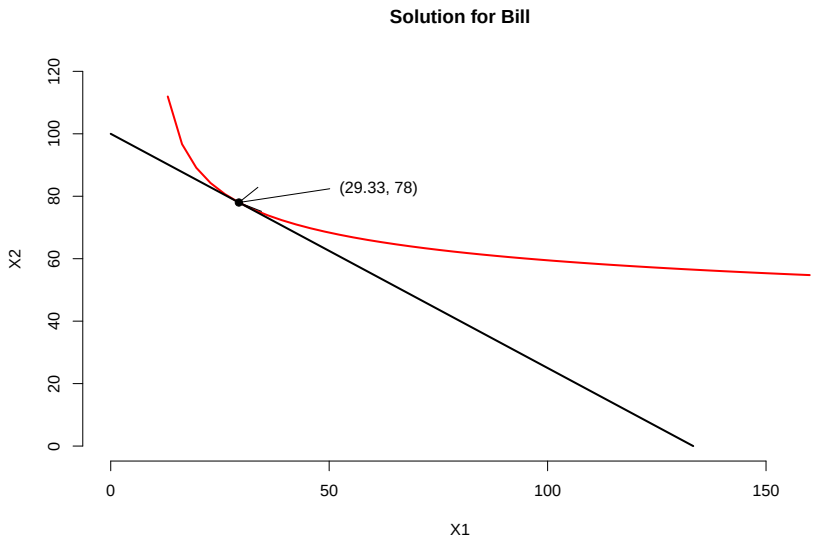
```
> plot(cons1,p)
```




```
> plot(cons2,p)
```



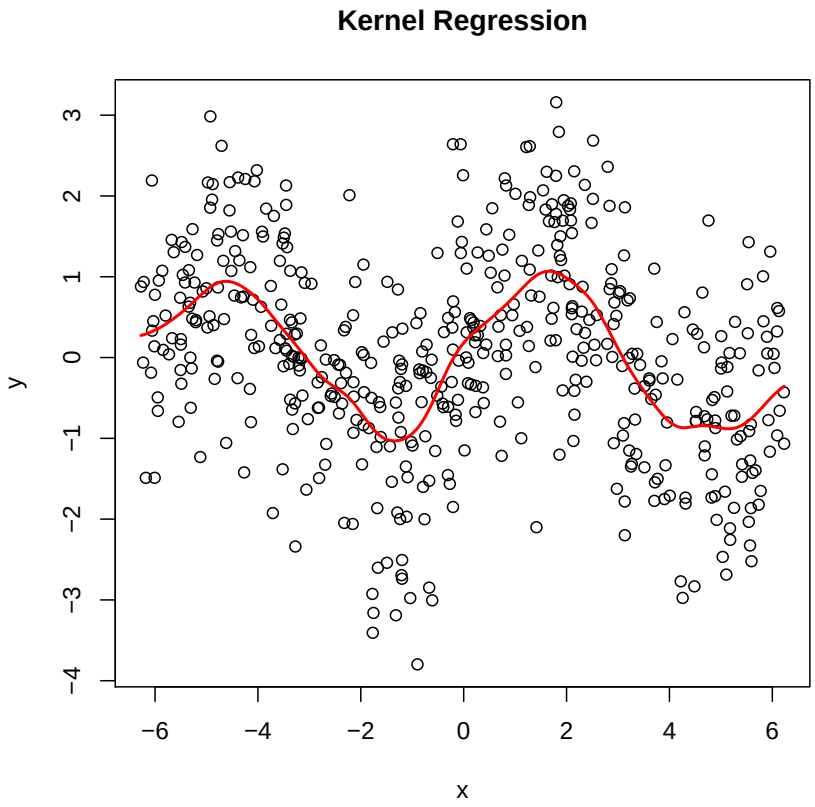
```
> plot(cons3,p)
```



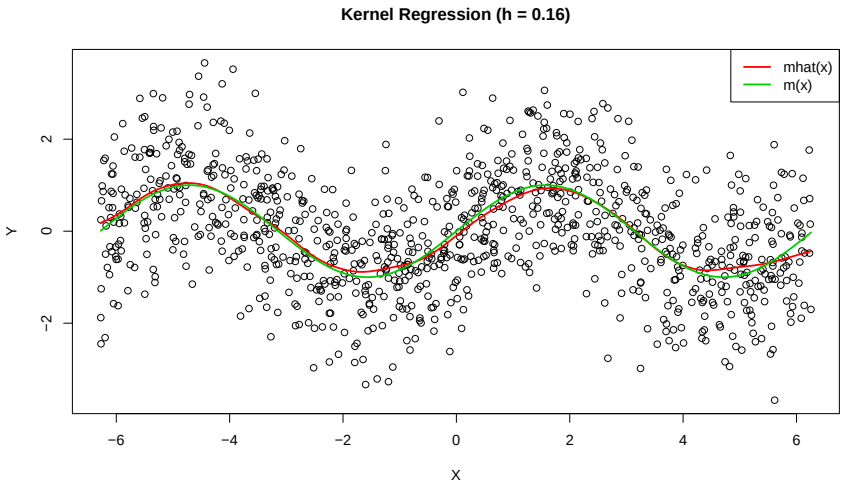
Here is the function for the Engel curve:

```
Engel <- function(cons, p) {
    Y <- seq(cons$Y * 0.5, cons$Y * 1.5, len = 40)
    X1 <- vector()
    X2 <- vector()
    cons1 <- cons
    for (i in 1:length(Y)) {
        cons1$Y <- Y[i]
        res <- solve(cons1, p, FALSE)
        X1[i] <- res$x1
        X2[i] <- res$x2
    }
    ylim <- c(min(c(X1, X2)), max(c(X1, X2)))
    plot(Y, X1, type = "l", xlab = "Income", ylab = "X", ylim = ylim,
        bty = "n", lwd = 2)
    lines(Y, X2, col = 2, lwd = 2)
    legend("topleft", c("X1", "X2"), col = 1:2, lty = c(1, 1))
    title(paste("Engel Curve for ", cons$name, sep = ""))
}
```

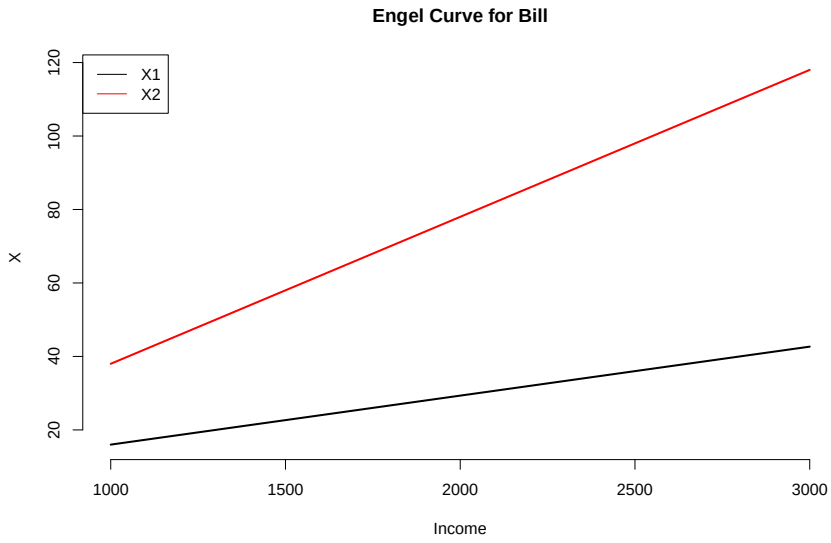
```
> Engel(cons1,p)
```




```
> Engel(cons2,p)
```




```
> Engel(cons3,p)
```


Engel Curve for Bill
X1
X2
120
100
80
60
40
20
X
1000
1500
2000
2500
3000
Income

Appendix B

Sweave

In this section, we want to give a small introduction to Sweave of [Leisch 2002], which allows to produce documents using LaTeX 2_ε. In the first section, we give an introduction to LaTeX 2_ε, and in the second section we show how to incorporate R codes in your document. The best way to get help is through Google, but it is recommended to go though the manuals: http://en.wikibooks.org/wiki/LaTeX and http://www.stat.uni-muenchen.de/~leisch/Sweave/.

B.1 Latex

LaTeX 2_ε is an environment for producing scientific documents. The current version exists since 1994 and is widely used in academia. There exists no better alternative for producing documents with lots of equations. Once you get used to it, you never want to go back to software such as MS Word. Nowm I use it even to write small letters. However, there is a fix cost of switching from a WYSIWYG software to one that requires coding. But what better place then in a numerical method course to learn another computer language.

If you have a MAC or a PC running Windows, you can install LaTeX 2_ε for free on the MikeTex web page: http://miktex.org/. You just need to follow the instructions. If you are running Linux, it is in general installed automatically. Once installed, you have the tools for producing documents but not the editor. The latter is not required but it makes your life much easier. There are many LaTeX 2_ε editors, so you can search for it and pick the one you like the most. My suggestion is Texmaker. It is open source and can be downloaded at http://www.xm1math.net/texmaker/ for free. Once installed, you may need to modify a little the configuration for Sweave and pdf-Latex. For Sweave, you go to the menu "option"-"Configure Texmaker", and locate R Sweave (usually the last slot). You should put the path to R.exe instead of just R before CMD. You can now click on quick build, choose "user" and use the wizard to select first Sweave and then pdf-Latex. Once the command is created in the text box, replace everything between | and %.tex by the path to R.exe followed by "CMD texify". In my experience, it never works at the first attempt. I can provide help for configuration if you need assistance.

Once installed, you are go to go. A Latex file must end with the .tex. For example,

you may create the file test.tex and put the following in it:

```
\documentclass[12pt,letterpaper]{article}
\usepackage{amsthm}
\usepackage[hmargin=3cm,vmargin=3.5cm]{geometry}
\usepackage[utf8x]{inputenc}
\usepackage[active]{srcltx}
\usepackage{amsmath}
\usepackage{verbatim}
\usepackage{amsfonts}
\usepackage{amssymb}
\usepackage{graphicx}
\newcommand\R{ \mathbb{R} }
\newcommand\N{ \mathbb{N} }
\newcommand\C{ \mathbb{C} }
\newcommand\Q{\mathbb{Q}}

\author{Pierre Chauss\'e \footnote{Department of Economics,
University of Waterloo, Ontario,
Canada (pchausse@uwaterloo.ca)} }
\title{\textbf A Template for \LaTeXe{}}
\date{\today}

\usepackage{Sweave}
\begin{document}
\maketitle
\section{Introduction}
This is my introduction...
\end{document}
```

For most of you first documents, you just copy the above code in a .tex file and run pdf-Latex (F6 in Texmaker and F7 to see the pdf). You just need to write your document between the \begin{document} and \end{document}. Try the above codes in a file and modify the title, author, and section title. You can also start writing stuff in the section. The main part are divided in section{} subsection{}, and subsubsection{}. By default, the sections, and subsections are numbered. If you do not want numbered sections, you add a * to the type of section (try all the codes bellow to make sure you understand what they do):

```
% With number
%%%%%%%%%%%%%%
\section{Section 1}
blabla
\subsection{my first subsection}
blabla
\subsubsection{Why not another one}}
blabla
\section{Section 2}
end of my blabla

% Without number
%%%%%%%%%%%%%%
\section*{Section 1}
blabla
\subsection*{my first subsection}
blabla
\subsubsection*{Why not another one}}
blabla
\section*{Section 2}
end of my blabla
```

Of course, you do not need to use sections. You can use the following fonts to initiate sections like a **Question 1:** in an assignment (here I give you many different fonts that you can also produce by using the automatic format builder in Texmaker):

```
\textbf{Bold}
\textit{Italic}
\large{a little large}
\Large{a little larger}
\LARGE{even larger}
```

You can also use the following environment (which do not require explanation):

```
\begin{Huge}
Huge text
\end{Huge}
\begin{center}
Something in the middle
\end{center}
\begin{itemize}
\item item 1
\item item 2
\end{itemize}
\begin{enumerate}
\item with number instead of bullets
\item[a)] I prefer a letter
\end{enumerate}
```

And all of these environment can be combined:

```
\begin{center}
\begin{Huge}
Huge text in the middle
\end{Huge}
\end{center}
\begin{enumerate}
\item[a)] I want to itemize each enumeration
\begin{itemize}
\item item 1 of a)
\item item 2 of a)
\end{itemize}
\item[b)]
\begin{itemize}
\item item 1 of b)
\item item 2 of b)
\end{itemize}
\end{enumerate}
```

All of the above allows you to write your document. However, there are hundreds of other commands to enhance your documents. You can go through the manual to find out about them or simply look for what you need (a Google search) while you are writing your document. It is up to you.

We can experience how powerful is LaTeX 2_ε when we start writing equations. You can insert equations (in fact you must) inside your text by using $$. For example, the sentence: "The valiable X is a random variable distributed as $N(\mu, \sigma^2)$", is produced by writing:

```
The valiable $X$ is a random variable distributed as
$N(\mu,\sigma^2)$.
```

If you forget the $$ especially with command such as \sigma, pdf-Latex will return an error message. It is often the first source of errors. If you want to write an equation on a single line, you can use the environment equation, for numbered equations, and equation* for unnumbered equations. The latter has a shortcut as you can see in the following examples. The following:

$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-0.5(x-\mu)^2/\sigma^2} \tag{B.1}$$

$$\int_{-\infty}^{\infty} f(x)dx = 1$$

$$\int_{-\infty}^{\infty} x \left(\frac{1}{\sqrt{2\pi\sigma^2}} e^{-0.5(x-\mu)^2/\sigma^2} \right) dx = \mu$$

$$\begin{aligned}\sum_{i=0}^{n} a^i = & \quad 1 + a + a^2 + \cdots + a^n \\ = & \quad \frac{1-a^{n+1}}{1-a}\end{aligned}$$

was produced using the following commands:

```
\begin{equation}
f(x) = \frac{1}{\sqrt{2\pi\sigma^2}}e^{-0.5(x-\mu)^2/\sigma^2}
\end{equation}
\begin{equation*}
\int_{-\infty}^{\infty} f(x) dx = 1
\end{equation*}
\[
\int_{-\infty}^{\infty} x\left(\frac{1}{\sqrt{2\pi\sigma^2}}
e^{-0.5(x-\mu)^2/\sigma^2}\right)  dx = \mu
\]
\begin{eqnarray*}
\sum_{i=0}^n a^i  = & 1 + a + a^2 + \cdots + a^n\\
 = & \frac{1-a^{n+1}}{1-a}
\end{eqnarray*}
```

I will let you understand the commands based on the result. Notice the left-right environment. It can be used with (), [], ||, and {}. You can also write matrices:

$$\Sigma = \begin{pmatrix} \sigma_{11} & \sigma_{12} & \sigma_{13} \\ \sigma_{21} & \sigma_{22} & \sigma_{23} \\ \sigma_{31} & \sigma_{32} & \sigma_{33} \end{pmatrix}$$

which is produced with

```
\[
\Sigma = \begin{pmatrix}
\sigma_{11} & \sigma_{12} & \sigma_{13}\\
\sigma_{21} & \sigma_{22} & \sigma_{23}\\
\sigma_{31} & \sigma_{32} & \sigma_{33}\\
\end{pmatrix}
\]
```

We can also have only one side parenthesis:

$$y = \begin{cases} 1 + x & \text{if} \quad -1 \leq x \leq 0 \\ 1 - x & \text{if} \quad 0 \leq x \leq 1 \\ 0 & \text{otherwise} \end{cases}$$

produced by

```
\[
y = \left\{
```

```
\begin{array}{ccc}
1+x & \mbox{if} & -1 \leq x \leq 0\\
1-x & \mbox{if} & 0 \leq x \leq 1\\
0 & \mbox{otherwise} &
\end{array} \right.
\]
```

I could write pages with examples. This is something you have to discover by yourself. One last thing I want to show you is how to build tables:

Table B.1: My first table means absolutely nothing

	Var1	Var2	Var3	Var4
Speed	0.8175	0.6336	0.3590	0.4684
Variance	0.4194	0.8996	0.9569	0.8990
Mean	0.7047	0.2999	0.4654	0.2105

Was produced using the following:

```
\begin{table}[ht]
\begin{center}
\caption{My first table means absolutely nothing}
\begin{tabular}{rrrrr}
  \hline
 & Var1 & Var2 & Var3 & Var4 \\
  \hline
Speed & 0.8175 & 0.6336 & 0.3590 & 0.4684 \\
  Variance & 0.4194 & 0.8996 & 0.9569 & 0.8990 \\
  Mean & 0.7047 & 0.2999 & 0.4654 & 0.2105 \\
   \hline
\end{tabular}
\end{center}
\end{table}
```

There is a whole Wiki for tables. I invite you to consult it when needed at http://en.wikibooks.org/wiki/LaTeX/Tables.

B.2 Sweave

Sweave is just an R command that generate a .tex file from an .Rnw file in which we can insert R codes. The .Rnw file is a tex file in which we add R commands. There are two ways on inserting codes: in the text or in a chunk. The .Rnw file must be executed first with "R CMD Sweave file name". That command creates a .tex file. Once created, we can run pdflatex on it to create the pdf file. That's what Texmaker will do for you once correctly configured (the quick build does both at the same time). So in this section,

you will create an .Rnw file and copy the .tex template I gave you at the beginning of the previous section. You can add what you will learn in this section.

As a first example, you can write the following sentence: "The square root of 7 is approximately equal to 2.6458." by writing the following: "The square root of 7 is approximately equal to \Sexpr{round(sqrt(7),4)}.". You can write any R codes inside \Sexpr{} and it will print the result. This is of course only useful to print a single number. Most of the time, R codes are written inside chunks. A chunk is several R commands written between <<>>= and @. For example, you can generate x, y, run a regression $y_i = \alpha + \beta x_i + e_i$, and print the results using the following:

```
<<>>=
set.seed(123)
x <- rnorm(100)
y <- -1 + 2 * x + rnorm(100)
res <- lm(y ~ x)
summary(res)
@
```

which would produce

```
> set.seed(123)
> x <- rnorm(100)
> y <- 1+2*x+rnorm(100)
> res <- lm(y~ x)
> summary(res)

Call:
lm(formula = y ~ x)

Residuals:
    Min      1Q  Median      3Q     Max
-1.9073 -0.6835 -0.0875  0.5806  3.2904

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.89720    0.09755   9.197 6.69e-15 ***
x            1.94753    0.10688  18.222  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.9707 on 98 degrees of freedom
Multiple R-squared: 0.7721,        Adjusted R-squared: 0.7698
F-statistic:   332 on 1 and 98 DF,  p-value: < 2.2e-16
```

You can even use those results in your text: The standard deviation of β is 0.106878616528031 and the t-statistics is 18.2218712105241. Here, the object "res" is kept in memory throughout the document so we can always reuse it (try to do it). If you do not want us to see the codes, but only the results, you can add the option echo=false:

$<< echo = false >>=$
$set.seed(123)$
$x < -rnorm(100)$
$y < -1 + 2 * x + rnorm(100)$
$res < -lm(y \sim x)$
$summary(res)$
@

would produce

```
Call:
lm(formula = y ~ x)
```

```
Residuals:
    Min      1Q  Median      3Q     Max
-1.9073 -0.6835 -0.0875  0.5806  3.2904

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.89720    0.09755   9.197 6.69e-15 ***
x            1.94753    0.10688  18.222  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9707 on 98 degrees of freedom
Multiple R-squared: 0.7721,        Adjusted R-squared: 0.7698
F-statistic:   332 on 1 and 98 DF,  p-value: < 2.2e-16
```

There is also a nice R package that produces Latex tables from R matrices or other objects. For example the following
$<< echo = false, results = tex >>=$
$library(xtable)$
$set.seed(123)$
$x < -rnorm(100)$
$y < -1 + 2 * x + rnorm(100)$
$res < -lm(y \sim x)$
$xtable(summary(res), digit = 4)$
@

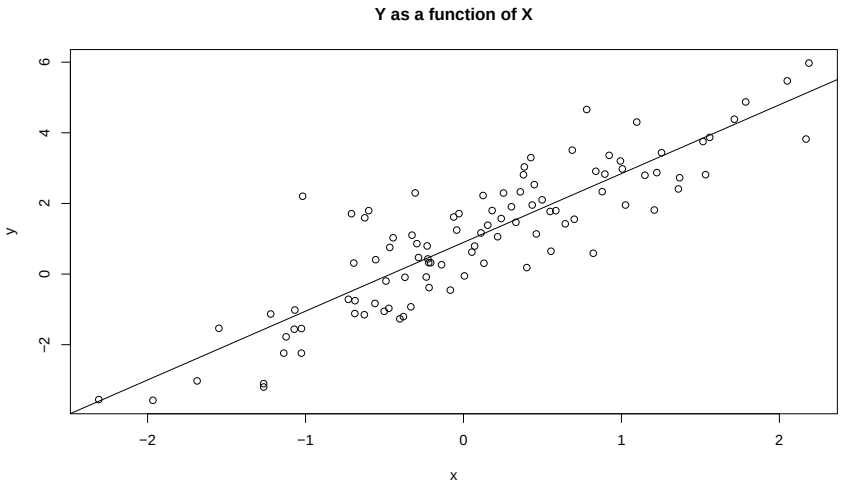
Would produce this nice result: You can also produce graphs with the option fig=true

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	0.8972	0.0976	9.1972	0.0000
x	1.9475	0.1069	18.2219	0.0000

(be careful not to put that option without plotting anything. It creates a fatal error) The following:

$<< echo = false, fig = true >>=$
$set.seed(123)$
$x < -rnorm(100)$
$y < -1 + 2 * x + rnorm(100)$

$res <- lm(y \sim x)$
$plot(x, y, title = "Y\ as\ a\ function\ of\ X")$
$abline(res)$
@



You can do everything that is allowed by R in these chunks. You can write a bunch of functions, save them in one file and use source() in a chunk at the beginning so that all functions can be used in the main document. It is all you need to know about Sweave. Once you know R, which is the hardest part to learn along with LaTeX 2_ε, it is a very convenient way of producing your documents.

Appendix C

Using foreign languages within R

C.1 The motivation

In this section, we present briefly how to call functions that are written in another language such as C or Fortran. The main reason for writing codes in C is to increase the speed. For example, we saw that adding the elements of a vector using loops is very slow in R. You could instead write the loop in C, and call the function from R. The C function would look like (in a file mySum.c):

```
#include <R.h>
#include <Rmath.h>

void mySum(double *x, int *n, double *sum)
{
     int i;
     double sum1 = 0.0;
     for (i=0; i< *n; i++) {
          sum1 += x[i];
          }
     *sum = sum1;
}
```

Once you have compiled the .c file, you can create an R function mySum() as follows:

```
mySum_C <- function(x)
        {
        res <- .C("mySum",as.double(x), as.integer(length(x)),as.double(0.0))
        res[[3]]}
```

Then, the function would simply be used as any R function. Here is an example:

```
dyn.load("src/mySum.so")
set.seed(222)
x <- rnorm(500000)
ans1 <- mySum_C(x)
ans2 <- sum(x)
ans1
```

```
## [1] -224.6011

ans2

## [1] -224.6011
```

We can compare the speed of loops in R and C just to see why it is better to use the latter:

```
mySum_R <- function(x)
        {
        s <- 0
        for (i in 1:length(x))
                s <- s + x[i]
        s}
```

```
system.time(mySum_R(x))

##    user  system elapsed
##   0.152   0.000   0.155

system.time(mySum_C(x))

##    user  system elapsed
##   0.004   0.000   0.003
```

As we see, it is about 100 times faster for the same loop. This is particularly useful when loops are unavoidable and that you need to evaluate the function several times. For example, suppose you want to estimate an MA(1) process $X_t = \theta\varepsilon_{t-1} + \varepsilon_t$. The log-likelihood is:

$$l(\theta, \sigma^2) = -\frac{n-1}{2}\log(2\pi\sigma^2) - \frac{1}{\sigma^2}\sum_{i=1}^{n}\varepsilon_t^2$$

with

$$\varepsilon_t = x_t - \theta x_{t-1} + \theta^2 x_{t-2} - ... \pm \theta^{t-1}x_1$$

The C code would look like the following:

```
#include <R.h>
#include <Rmath.h>

void ll(double *x, int *n, double *theta, double *sigma2, double *
    loglik)
```

```
{
    int i;
    double llik, pi, Cst, eps;
    pi = 4.0*atan(1.0);
    Cst = -0.5*log(2 * pi * *sigma2);
    eps = x[0];
    llik = Cst - 0.5*pow(eps,2) / *sigma2;
    for (i=1; i< *n; i++) {
        eps = x[i] - *theta * eps;
        llik += Cst - 0.5*pow(eps,2) / *sigma2;
        }
    *loglik = llik;
}
```

and the R function as:

```
myMa_ll <- function(beta, x)
        {
        theta <- beta[1]
        sigma2 <- beta[2]
        res <- .C("ll",as.double(x), as.integer(length(x)),
                  as.double(theta), as.double(sigma2), as.double(0.0))
        -res[[5]]
        }
```

Lets now try it:

```
dyn.load("src/ll.so")
x <- arima.sim(n=5000, model=list(ma=.9))
t1 <- system.time(res <- optim(c(.5,.5),myMa_ll, x=x))
t1

##    user  system elapsed
##   0.008   0.000   0.005

res$par

## [1] 0.9137083 0.9956378
```

To see that relying on C makes a big difference here, lets redo the estimation in R only.

```
myMa_ll2 <- function(beta, x)
    {
        theta <- beta[1]
        sigma2 <- beta[2]
        Cst <- -0.5*log(2*pi*sigma2)
        eps = x[1]
        llik = Cst - 0.5*eps^2 / sigma2
        for (i in 2:length(x))
            {
                eps <- x[i] - theta * eps
                llik <- llik + Cst - 0.5*eps^2 / sigma2
            }
        -llik
    }
```

```
t2 <- system.time(res2 <- optim(c(.5,.5),myMa_ll2, x=x))
t2

##    user  system elapsed
##   2.356   0.000   2.358

res2$par

## [1] 0.9137083 0.9956378
```

For this example, it is 472 times faster to use the C function. Of course, the ratio would be much higher if the function had more coefficients and that the optim() algorithm took many more iterations to converge (Try with an ARMA(2,2)+GARCH(1,1)). If I failed to convince you, stop reading. Otherwise, the next section explains are to proceed.

C.2 Brief How To

Here, I explain how to proceed if you are using either a Linux OS or a MAC. I don't know how it works in a Windows environment and I cannot test it since I do not have computers with Windows. The only think that you need is a compiler for either C or Fortran. It is installed on most Linux distributions and for MAC you need to install Xcode that can be downloaded from the Apple developer website for free once you register. I am explaining the procedure for C only since I am more familiar with that language. For more details see http://dirk.eddelbuettel.com/bio/presentations.html

, http://www.cran.r-project.org/doc/manuals/r-release/R-exts.pdf or, if you want a book, Statistical Computing in C++ and R.

The main steps are (1) write your C or C++ codes in a file, (2) run R CMD SHLIB your_file, (3) put dyn.load("your_file.so") at the beginning of the R script file, (4) write an R function that calls the C or C++ function. There are three ways (maybe more) of calling a C function in R: .C(), .Call(), or .External(). I will explain the first two. You have to understand first that it is recommended in the main R manual to do it in pure R first, then using .C() and finally .Call() if you are still unsatisfied. The main difference between .C() and .Call() is that the latter allows to use R functions within the C codes. It is much newer than the .C() and therefore should be used with caution (See the above manual for more details).

The C functions included in the .c file should not return any value. Therefore, it should be of the form

```
void myfct(arguments){
...
}
```

The arguments of the functions are pointers (here I am assuming you know what it means; it points to the address in the memory where is stored the argument) and it is the values associated with these pointers that are returned by .C() in a list format. Since they are pointers, modifying their values inside the function will automatically change the values returned by .C(). If we go back to the MySum() function:

```
#include <R.h>
#include <Rmath.h>

void mySum(double *x, int *n, double *sum)
{
    int i;
    double sum1 = 0.0;
    for (i=0; i< *n; i++) {
        sum1 += x[i];
        }
    *sum = sum1;
}
```

we can see that there are 3 arguments: the vector x, the length of x, and the pointer that will store the sum. The star indicates that these are pointers. Also, you have to specify the type of variable associated with each argument. The main type that we will use are integers (int) or double precision floating numbers (double). For a vector, the pointer points to the address of the first element (x[0]), and the others can be obtained using x[i]. For the integer types, to access their values by adding a star. So in the loop setup, I use ";i<*n;", not ";i<n;". Notice that most of the time, you only need to load the libraries R.h and Rmath.R. You therefore need at least the first two lines in each

of your .c files. You have the choice between writing several functions inside the same file or to have a different file for each function. It is up to you.

If we look at the R function that calls it:

```
mySum_C

## function(x)
##  {
##  res <- .C("mySum",as.double(x), as.integer(length(x)),as.double(0.0))
##  res[[3]]}
```

we can see that we first have to make sure the arguments are of the right type. For the third argument that will point to the answer, I just give an arbitrary value. I then return the third element of the list generated by .C(). In order to be able to run that function, we need to load the object containing the C function. That object is the output we get by compiling our .c file. You could do it manually using gcc, but you would have to specify the location of the R libraries. It is easier to use R. Just open a terminal, go to the directory in which mySum.c is and type "R CMD SHLIB mySum.c". This will create a file "mySum.so". Place that file in the working directory of R, open R, and type

```
dyn.load("mySum.so")
```

You can now use the R function mySum(). Notice that the name of the functions are the same in R and C. It does not matter before the C function can only be run through .C().

As another example, suppose you want to do a kernel regression to estimate $Y_i = m(X_i) + \varepsilon_i$. The estimated function $\hat{m}(x)$ is defined as:

$$\hat{m}(x) = \frac{\sum_{i=1}^{n} K_h(X_i - x)Y_i}{\sum_{i=1}^{n} K_h(X_i - x)}$$

where

$$K_h(x) = \frac{1}{\sqrt{2\pi h}} e^{-\frac{1}{2h}x^2}$$

This is a pretty intensive method because the sum must be obtained for each point x. Also, the bandwidth h (this is one possibler method) is obtained by minimizing the following cross-validation criterion:

$$CV = \sum_{i=1}^{n} (Y_i - \hat{m}^{-i}(X_i))^2$$

where $\hat{m}^{-i}(X_i)$ is the prediction of Y_i obtained by removing the i^{th} observation. The kernel.c file shown below. Notice that I decided, as I usually do in R. to write small functions. The ones that are called by other C functions can return something. For example, the gaussian() function returns a number of type double. It is the same with kernel_lou() which returns the kernel estimate leaving one observation out of the sample (lou = leave-one-out).

```
#include <R.h>
#include <Rmath.h>
double gaussian(double x, double h) {
        double pi, ans;
        pi = 4.0*atan(1.0);
        ans = exp(-0.5*pow(x,2)/h)/sqrt(2*pi*h);
        return ans;
        }
double kernel_lou(double *y, double *x, int n, double xi, double h,
    int leaveout) {
        int i;
        double m=0.0, k=0.0, k1;
        for (i=0; i<n; i++) {
                if (i != leaveout) {
                        k1 = gaussian(xi-x[i], h);
                        k += k1;
                        m += k1*y[i];
                        }
                }
        m = m/k;
        return m;
        }
void kernel(double *y, double *x, int *n, double *h, double *xi,
    double *mhat) {
        int i;
        double m=0.0, k=0.0, k1;
        for (i=0; i < *n; i++) {
                k1 = gaussian(*xi-x[i], *h);
                k += k1;
                m += k1*y[i];
                }
        *mhat = m/k;
        }
void crossval(double *y, double *x, int *n, double *h, double *cv) {
        int i;
        double cv2=0.0,yhat;
        for (i=1; i < *n; i++){
                yhat = kernel_lou(y, x, *n, x[i], *h, i);
                cv2 += pow(y[i]-yhat,2);
                }
        *cv = cv2;
        }
```

and my R functions are:

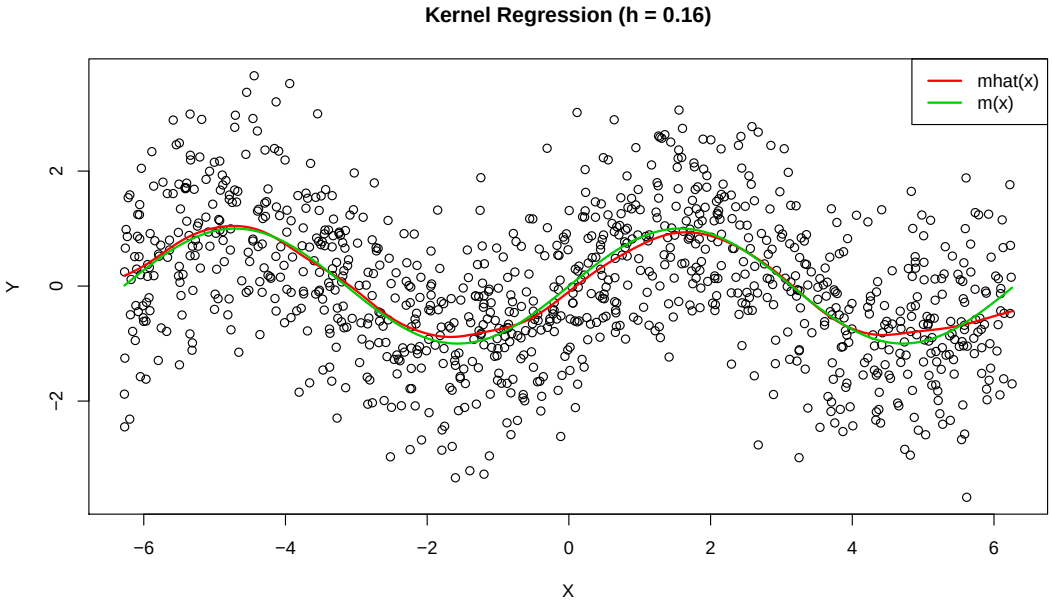
```
CV <- function(h, data)
    .C("crossval", as.double(data$y), as.double(data$x),
           as.integer(length(data$x)), as.double(h), as.double(0.0))[[5]]
getKernel <- function(x, data, h)
    sapply(x, function(i) .C("kernel", as.double(data$y), as.double(data$x),
                             as.integer(length(data$x)), as.double(h),
                             as.double(i), as.double(0.0))[[6]])
```

Lets try is with a sample of 1000 observations.

```
dyn.load("src/kernel.so")
set.seed(1222)
x <- runif(1000, -2*pi, 2*pi)
y <- sin(x) + rnorm(1000)
system.time(h <- optimize(CV, c(.0001,1),data=list(x=x,y=y))$minimum)

##    user  system elapsed
##   0.432   0.000   0.429

system.time(mhat <- getKernel(sort(x), list(x=x,y=y),h))

##    user  system elapsed
##   0.044   0.000   0.045
```

This is a very good example that shows the gain we get from writing out codes in C. The leave-one-out cross-validation requires to estimate $\hat{m}^{-i}(X_i)$ for all n observations every time we change the value of h. Try to do it in pure R. On my computer, it took 66 seconds to get h and 4.5 seconds to get mhat. Of course, cross-validation codes should be parallelized, which would make R codes faster. The same thing is true also with the C codes. We can then plot the solution:

```
plot(x,y,main=paste("Kernel Regression (h = ",round(h,2),")",sep=""),
     xlab="X", ylab="Y")
lines(sort(x), mhat,col=2,lwd=2)
lines(sort(x),sin(sort(x)),col=3,lwd=2)
legend("topright",c("mhat(x)","m(x)"),col=2:3,lty=1,lwd=2)
```



Almost everything can be computed using C codes and then called by R. However, it is a problem when it comes to working with matrices. C does not deal directly with matrices. R is much better designed to do matrix operations and it is highly optimized. There would therefore be no much gain by writing you own C library.

A new approach that has recently been developed is to use R functions into the C codes. Such a function is called by R using .Call() instead of .C(). To give you an example, here is a modified version of the C codes for adding elements of a vector.

```
#include <R.h>
#include <Rmath.h>
#include <Rinternals.h>

SEXP mySum3(SEXP x)
{
    int i, n;
    double *p_sum1;
    SEXP sum1;
    sum1 = PROTECT(sum1 = allocVector(REALSXP,1));
    p_sum1 = REAL(sum1);
    *p_sum1 = 0.0;
    n = length(x);
    for (i=0; i < n; i++) {
        *p_sum1 += REAL(x)[i];
        }
    UNPROTECT(1);
    return sum1;
}
```

You need to load the library Rinternals.h in which new functions and variable types are defined. The main difference is that all variables are defined as being of type SEXP which stands for "Simple EXPression" (A complete presentation of all R internals can be found at http://cran.r-project.org/doc/manuals/R-ints.html). The coding is somehow confusing at first but is relatively simpler when we get used to it. Notice that a variable of type SEXP does not really have a type. The type must me defined in the function. The line "sum1 = allocVector (REALSXP ,1)" defines the variable sum1 as being a one dimensional vector of type double. The main types are: double (REALSXP), integers (INTSXP), logical (LGLSXP), complex (CPLXSXP), and character (STRSXP). In the above example, I created a pointer (p_sum1) and the value attached to it is updated in the loop, which also updates sum1. Noltice that we do not need to provide the length of the vector. The function length() is available. Also, since the function returns the answer, we do not need to have an argument in which to store the answer. Finally, we need to use PROTECT() and UNPROTECT() when we create new variables to make sure the memory is not used elsewhere. Lets try it and compare it with the previous function.

```
mySum_SEXP <- function(x)
    .Call("mySum3",x)
```

```
dyn.load("src/mySum3.so")
set.seed(222)
x <- rnorm(500000)
system.time(ans1 <- mySum_C(x))

##    user  system elapsed
##   0.000   0.000   0.002

system.time(ans2 <- mySum_SEXP(x))

##    user  system elapsed
##   0.000   0.000   0.001

c(ans1,ans2)

## [1] -224.6011 -224.6011
```

It seems to be a little faster but I cannot tell why. Here is the modified codes using SEXP type variable and Rinternals. Notice that I wrote the code in a way that we

do not have to use sapply() in the kernel function. All points are obtained by the C function.

```
#include <R.h>
#include <Rmath.h>
#include <Rinternals.h>

double gaussian(double x, double h) {
        double pi, ans;
        pi = 4.0*atan(1.0);
        ans = exp(-0.5*pow(x,2)/h)/sqrt(2*pi*h);
        return ans;
        }
double kernel_lou(double *y, double *x, int n, double xi, double h,
    int leaveout) {
        int i;
        double m=0.0, k=0.0, k1;
        for (i=0; i<n; i++) {
                if (i != leaveout) {
                        k1 = gaussian(xi-x[i], h);
                        k += k1;
                        m += k1*y[i];
                        }
                }
        m = m/k;
        return m;
        }
SEXP kernel_SEXP(SEXP y, SEXP x, SEXP h, SEXP xvec) {
        int i, j, nx, nxvec;
        double *m_p, k, k1;
        SEXP m;
        y = coerceVector(y,REALSXP);
        x = coerceVector(x,REALSXP);
        xvec = coerceVector(xvec,REALSXP);
        h = coerceVector(h,REALSXP);
        nx = length(x);
        nxvec = length(xvec);
        PROTECT(m = allocVector(REALSXP,nxvec));
        m_p = REAL(m);
        for (j=0; j < nxvec; j++)
                {
                k = 0.0;
                m_p[j] = 0.0;
                for (i=0; i < nx; i++) {
                        k1 = gaussian(REAL(xvec)[j]-REAL(x)[i], REAL(
                            h)[0]);
                        k += k1;
                        m_p[j] += k1 * REAL(y)[i];
                        }
                m_p[j] = m_p[j] / k;
```

```
                }
        UNPROTECT(1);
        return m;
        }

SEXP crossval_SEXP(SEXP y, SEXP x, SEXP h) {
        int i, n;
        double *cv_p,yhat;
        SEXP cv;
        y = coerceVector(y,REALSXP);
        x = coerceVector(x,REALSXP);
        h = coerceVector(h,REALSXP);
        n = length(x);
        PROTECT(cv = allocVector(REALSXP,1));
        cv_p = REAL(cv);
        *cv_p = 0.0;
        for (i=1; i < n; i++){
                yhat = kernel_lou(REAL(y), REAL(x), n, REAL(x)[i],
                    REAL(h)[0], i);
                *cv_p += pow(REAL(y)[i]-yhat,2);
                }
        UNPROTECT(1);
        return cv;
        }
```

```
dyn.load("src/kernel_SEXP.so")
CV_SEXP <- function(h, data)
    .Call("crossval_SEXP", data$y, data$x, h)
getKernel_SEXP <- function(x, data, h)
    .Call("kernel_SEXP", data$y, data$x, h, x)
set.seed(1222)
x <- runif(1000, -2*pi, 2*pi)
y <- sin(x) + rnorm(1000)
system.time(h <- optimize(CV_SEXP, c(.0001,1),data=list(x=x,y=y))$minimum)

##    user  system elapsed
##   0.424   0.000   0.426

system.time(mhat <- getKernel_SEXP(sort(x), list(x=x,y=y),h))

##    user  system elapsed
##    0.04    0.00    0.04
```

Notice that the gain from using C instead of sapply is very small. We can compare more precisely the performance usinf the package rbenchmark:

```
library(rbenchmark)
f <- function()
    getKernel(sort(x), list(x=x,y=y),h)
f_SEXP <- function()
    getKernel_SEXP(sort(x), list(x=x,y=y),h)
benchmark(f(), f_SEXP(), replications=50,
          columns=c("test", "replications", "elapsed", "relative"))

##       test replications elapsed relative
## 1      f()           50   2.340    1.192
## 2 f_SEXP()           50   1.963    1.000
```

There is a small gain which is probably due to the use of C instead of sapply() rather than the use of SEXP type. The latter is just another way of programing. It is not meant to be more efficient. We can compare them with a modified function that uses mclapply.

```
getKernel_MC <- function(x, data, h)
    {
        res <- mclapply(x, function(i) .C("kernel", as.double(data$y),
                                          as.double(data$x),
                                          as.integer(length(data$x)),
                                          as.double(h),
                                          as.double(i),
                                          as.double(0.0))[[6]], mc.cores=8)
        simplify2array(res)
    }
f_MC <- function()
    getKernel_MC(sort(x), list(x=x,y=y),h)
```

```
library(parallel)
benchmark(f(), f_SEXP(), f_MC(), replications=50,
          columns=c("test", "replications", "elapsed", "relative"))

##       test replications elapsed relative
## 1      f()           50   2.321    1.672
## 3   f_MC()           50   1.388    1.000
## 2 f_SEXP()           50   1.964    1.415
```

Not surprisingly, the mcapply() approach wins. It is even faster than the method that uses only C. It is sometimes necessary to try different methods in order to find the most efficient one.

There is an even easier way of running C and C++ codes using the Rcpp package of [Eddelbuettel & Francois 2011]. Many detailed tutorials are available at http://dirk.eddelbuettel.com/code/rcpp.html. The main goal of the package is to help package developers to insert C++ codes in their package. You can write your code in a .cpp file and use R CMD SHLIB as for the above examples, but it is not recommended. An easy way to use the Rcpp package is through the inline package of [Sklyar *et al.* 2013]. As a very simple example, the function to compute the sum of the elements of a vector could be written as follows.

```
library(Rcpp)
library(inline)
src = 'Rcpp::NumericVector xx(x);
   int i;
   Rcpp::NumericVector sum(1);
   sum[0] = 0.0;
   for (i=0; i<xx.size(); i++)
    sum[0] += xx[i];
    return sum;'
mySum_Rcpp <- cxxfunction(signature(x = "numeric"), src , plugin = "Rcpp")
```

We can then compare it with the others:

```
x <- rnorm(500000)
benchmark(mySum_C(x), mySum_R(x), mySum_SEXP(x), mySum_Rcpp(x), replications=10,
          columns=c("test", "replications", "elapsed", "relative"))

##            test replications elapsed relative
## 1    mySum_C(x)           10   0.031    2.214
## 4 mySum_Rcpp(x)           10   0.017    1.214
## 2    mySum_R(x)           10   1.523  108.786
## 3 mySum_SEXP(x)           10   0.014    1.000
```

But we could improve it in the following way:

```
src = 'Rcpp::NumericVector xx(x);
return wrap( std::accumulate( xx.begin(), xx.end(), 0.0));'
mySum_Rcpp2 <- cxxfunction(signature(x = "numeric"), src , plugin = "Rcpp")
benchmark(mySum_C(x), mySum_R(x), mySum_SEXP(x), mySum_Rcpp(x),
```

```
          mySum_Rcpp2(x), replications=10,
          columns=c("test", "replications", "elapsed", "relative"))

##             test replications elapsed relative
## 1     mySum_C(x)           10   0.031    2.583
## 5 mySum_Rcpp2(x)           10   0.012    1.000
## 4  mySum_Rcpp(x)           10   0.017    1.417
## 2     mySum_R(x)           10   1.525  127.083
## 3  mySum_SEXP(x)           10   0.014    1.167
```

The development of packages that facilitate the use of C and C++ codes has exploded in the last years. On nice package is RcppAmadillo from [Eddelbuettel & Sanderson 2013], which allows matrix operations. Here is an example taken from http://dirk.eddelbuettel.com/code/rcpp.armadillo.html. It estimates a linear model using OLS.

```
src <- '
   Rcpp::NumericVector yr(y);
   Rcpp::NumericMatrix Xr(X);
   int n = Xr.nrow(), k = Xr.ncol();
   arma::mat X(Xr.begin(), n, k, false);
   arma::colvec y(yr.begin(), yr.size(), false);
   arma::colvec coef = arma::solve(X, y);
   arma::colvec fitted = X*coef;
   arma::colvec resid = y - fitted;
   double sig2 = arma::as_scalar( arma::trans(resid)*resid/(n-k) );
   arma::mat vcov  = sig2 * arma::inv(arma::trans(X)*X);
   return Rcpp::List::create(
        Rcpp::Named("coefficients") = coef,
        Rcpp::Named("vcov")       = vcov,
        Rcpp::Named("fitted")       = fitted,
        Rcpp::Named("residuals")       = resid);'
lm_Rcpp <- cxxfunction(signature(y = "numeric", X = "numeric"), src ,
                       plugin = "RcppArmadillo")
x <- matrix(rnorm(500000), 5000,100)
y <- rnorm(5000)
benchmark(lm(y~x), lm_Rcpp(y,x), replications=10,
          columns=c("test", "replications", "elapsed", "relative"))

##            test replications elapsed relative
```

```
## 2 lm_Rcpp(y, x)           10   0.731    1.000
## 1     lm(y ~ x)           10   0.779    1.066
```

Many packages are build with Rcpp. They are usually meant to be more efficient.

C.3 Fortran

In the past years, I have used Fortran more than C because I find it much easier when it comes to doing matrix operations. For basic functions, is very much like C, except that the functions would be saved in a file with the extension .f. The .so file is generated the same way by typing R CMD SHLIB file.f. If we start with the simple example of adding the elements of a vector, the function in the ex.f file is

```
      subroutine mysumf(x, n, sum)
      integer i, n
      double precision x(n), sum

      sum = 0.0d0
      do  i = 1,n
         sum = sum+x(i)
      end do
      end
```

An important rule to remember is that you cannot write codes on the first 6 spaces of a line. In Fortran, you do not need to make a distinction between pointers and variable names as in C and the first element of a vector is x(1) not x(0). Calling the function in R is similar.

```
dyn.load("src/ex.so")
```

```
myFsum <- function(x)
    .Fortran("mysumf", as.double(x), as.integer(length(x)), sum=double(1))$sum
```

```
myFsum(rnorm(100))

## [1] 13.15439
```

It is also possible to use functions from the linear algebra libraries BLAS and LAPACK. A list of functions with descriptions and source codes are available on Netlib (www.netlib.org. A simple Google search with the function name will lead you directly to help page of that function. In order to create the .so file with the R CMD SHLIB

command, you need to tell the compiler that you are using functions from the BLAS and LAPACK libraries. R does import some functions, but there are many more available. To specify the libraries to R, you need to create a file Makevars with no extension and write the following in it:

```
PKG_LIBS = ${LAPACK_LIBS} ${BLAS_LIBS}
```

It is relatively easy to guess the names of the functions. Functions applied to complex numbers start with a c, and they start with a d for double precision numbers. For example, the dgeqrf, is a QR factorization of a double general matrix. It is a little tricky to do linear algebra with the LAPACK library, but once you get used to it and you have some notions of numerical methods, it becomes relatively intuitive.

In the next example, we want to compute the following:

$$V = \sum_{i=1}^{n} Z_{1i}' \Sigma^{-1} Z_{2i},$$

where Z_{1i} is $T \times k_1$, Z_{2i} is $T \times k_2$ and Σ is $T \times T$. This is one component that we need to compute in order to obtain the covariance matrix of the estimator in a system of equations (for more details take ECON 721). The best strategy here is to avoid inverting Σ n times. Since it is symmetric and positive definite, we want to do the Cholesky decomposition $\Sigma = PP'$, where P is lower triangular, and solve $PP'x = Z_{2i}$ using successively a forward and backward method for triangular systems. The function that I need is dpotrf for the Cholesky factorization (d: double, po: positive definite, trf: triangular factorization), and dpotrs which solve $Ax = b$ when A is positive definite. We have to provide not A but the P matrix computed by dpotrf. We then simply use dgemm to multiply Z_{1i}' and $(\Sigma^{-1} Z_{2i})$. Here is the Fortran function:

```
      subroutine sumquadra(z1, z2, sig, n, t, k1, k2, s)
      integer n, t, k1, k2, i, info
      double precision z1(t,k1,n), z2(t, k2, n), sig(t,t), s(k1,k2)
      double precision tmp(k1,k2), beta, alpha
      call dpotrf('U', t, sig, t, info)

      beta = 0.0d0
      alpha = 1.0d0
      s(:,:) = 0.0d0
      do i=1,n
         call dpotrs('U', t, k2, sig, t, z2(:,:,i), t, info)
         call dgemm('T', 'N', k1, k2, t, alpha, z1(:,:,i), t,
     *        z2(:,:,i), t, beta, tmp, k1)
         s(:,:) = s(:,:)+tmp(:,:)
      end do
      end
```

Notice that the variable sig is replaced by the cholesky factorization and that $z2[,,i]$ is replaced by $\Sigma^{-1}Z_{2i}$. Here is an example:

```
z1 <- array(rnorm(10*4*1000), c(10,4,1000))
z2 <- array(rnorm(10*5*1000), c(10,5,1000))
sig <- crossprod(matrix(rnorm(100),10,10)) # make sure it is pos. def.
quadraSum <- function(z1, z2, sig)
    {
        k1 <- dim(z1)[2]
        k2 <- dim(z2)[2]
        t <- dim(z1)[1]
        n <- dim(z1)[3]
        res <- .Fortran('sumquadra', as.double(z1), as.double(z2),
                        as.double(sig), as.integer(n), as.integer(t),
                        as.integer(k1), as.integer(k2), S=double(k1*k2))
        S <- matrix(res$S, k1, k2)
        }
```

Notice that even if the variable z2 is changed in the process, it is only changed in the function quadraSum. z2 remains unchanged outside the function. Lets compare the Fortran function with a naive R one:

```
quadraSumR <- function(z1, z2, sig)
    {
        S <- matrix(0, dim(z1)[2], dim(z2)[2])
        for (i in 1:dim(z1)[3])
            S <- S+t(z1[,,i])%*%solve(sig, z2[,,i])
        S
        }
benchmark(quadraSum(z1,z2,sig), quadraSumR(z1,z2,sig), replications=10,
          columns=c("test", "replications", "elapsed", "relative"))

##                     test replications elapsed relative
## 2 quadraSumR(z1, z2, sig)           10   0.240       15
## 1  quadraSum(z1, z2, sig)           10   0.016        1
```

C.3.1 Example: The shooting method

First, I reproduce the graph of Chapter 8 for the life cycle model. For that, we need to write a RK4 in Fortran:

```
      subroutine rk4(f, parf, nparf, n, k, a, b, y0, x, y, h)
      integer n, i, k, nparf
      double precision a, b, y0(k), h, x(n+1), y(n+1,k)
      double precision f1(k), f2(k), f3(k), f4(k), parf(nparf)
      external f

      h = (b-a)/n
      y(1,:) = y0
      x(1) = a
      do i=2,(n+1)
         x(i) = a+h*(i-1)
         call f(x(i-1), y(i-1,:),parf,f1)
         call f(x(i-1)+h/2,y(i-1,:)+h*f1/2, parf, f2)
         call f(x(i-1)+h/2,y(i-1,:)+h*f2/2, parf, f3)
         call f(x(i), y(i-1,:)+h*f3, parf, f4)
         y(i,:) = y(i-1,:) + h*(f1+2*f2+2*f3+f4)/6
      end do
      end
```

I make use of the command "external" so that the rk4 function can be used for any function f. A also need the lifecycle function that returns the first derivatives:

```
      subroutine lifecycle(x, y, par, dy)
      double precision par(5), x, y(2), dy(2)
      double precision rho, r, gamma, mi, mf, w
      rho = par(1)
      r = par(2)
      gamma = par(3)
      mi = par(4)
      mf = par(5)
      if (x<=mf .and. x>=mi) then
         w=1.0d0
      else
         w=0.0d0
      end if
      dy(2) = r*y(2)+w-y(1)
      dy(1) = (rho-r)*y(1)/gamma
      end
```

and the function that will be called by R:

```
      subroutine getlifecycle(n, rho, gamma, mi, mf, r, a, b, y0, x,
          y,
     * h)
      integer n
      double precision rho, gamma, mi, mf, r, a, b, y0(2), x(n+1)
      double precision y(n+1,2), par(5), h
      external lifecycle
      par(1) = rho
```

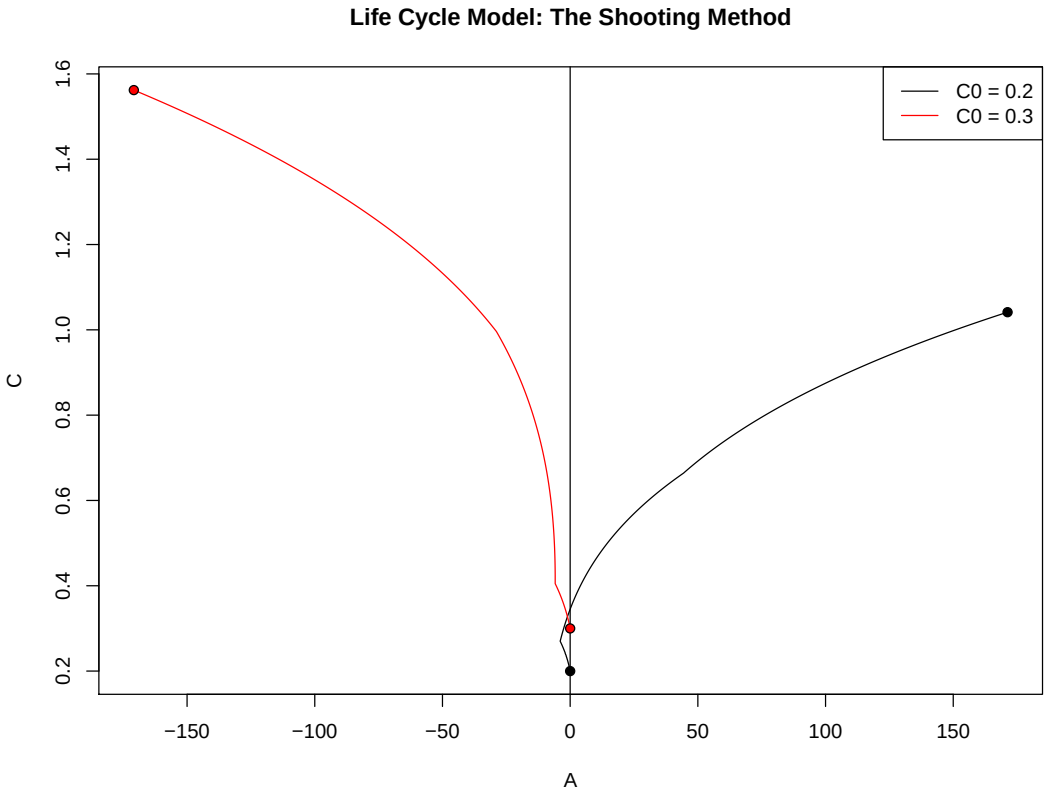
```
      par(2) = r
      par(3) = gamma
      par(4) = mi
      par(5) = mf
      call rk4(lifecycle, par, 5, n, 2, a, b, y0, x, y, h)
      end
```

The following R function will generate the solution of the differential equation:

```
getLifeCycle <- function(y0,n,a=0,b=55,rho=.04,r=.1,M=10,R=40,gamma=-2)
    {
        res <- .Fortran('getlifecycle', as.integer(n), as.double(rho),
                        as.double(gamma), as.double(M), as.double(R),
                        as.double(r), as.double(a), as.double(b), as.double(y0),
                        x=double(n+1), y=double(2*n+2), h=double(1))
        list(x=res$x, y=matrix(res$y, ncol=2), h=res$h)
    }
```

We can then reproduce the graph of Chapter 8 for two different values of c_0.

```
h <- .01
n <- floor(55/h)
s <- getLifeCycle(c(.2,0),n)
s2 <- getLifeCycle(c(.3,0),n)
```


Life Cycle Model: The Shooting Method
C0 = 0.2
C0 = 0.3
C
A
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
−150
−100
−50
0
50
100
150

Bibliography

[Eddelbuettel & Francois 2011] D. Eddelbuettel and R. Francois. *Rcpp: Seamless R and C++ Integration*. Journal of Statistical Software, vol. 40, no. 8, pages 1–18, 2011. (Cited on page 228.)

[Eddelbuettel & Sanderson 2013] Dirk Eddelbuettel and Conrad Sanderson. *RcppArmadillo: Accelerating R with high-performance C++ linear algebra*. Computational Statistics and Data Analysis, vol. in press, 2013. (Cited on page 229.)

[Genz *et al.* 2011] A. Genz, F. Bretz, T. Miwa, X. Mi, F Leisch, F. Scheipl and T. Hothorn. *mvtnorm: Multivariate Normal and t Distributions*. R Foundation for Statistical Computing, Vienna, Austria, 2011. R package version 0.9-9991. (Cited on page 6.)

[Goldberg 1991] D. Goldberg. *What every Computer Scientist Should Know About Floating-Point Arithmetic*. ACM Computing Surveys, vol. 23, no. 1, pages 5–48, 1991. (Cited on page 49.)

[Golub & Ortega 1992] G.H. Golub and J.M. Ortega. Scientific computing and differential equations. Academic Press, 1992. (Cited on page 185.)

[Hasselman 2012] Berend Hasselman. *nleqslv: Solve systems of non linear equations*, 2012. R package version 1.9.3. (Cited on page 133.)

[Hull 2011] J.C. Hull. Options, futures, and other derivatives. Prentice Hall, 2011. (Cited on page 189.)

[Judd 1998] K.L. Judd. Numerical methods in economics. The MIT Press, 1998. (Cited on page 57.)

[Leisch 2002] F. Leisch. Dynamic generation of statistical reports using literate data analysis. Compstat, 2002. (Cited on page 205.)

[Press *et al.* 2007] W.H. Press, S.A. Teukolsky, W.T. Vetterling and B.P. Flannery. Numerical recipes, third edition. Cambridge University Press, 2007. (Cited on pages 88 and 109.)

[Sklyar *et al.* 2013] Oleg Sklyar, Duncan Murdoch, Mike Smith, Dirk Eddelbuettel and Romain Francois. *inline: Inline C, C++, Fortran function calls from R*, 2013. R package version 0.3.12. (Cited on page 228.)

[Smyth *et al.* 2011] Gordon Smyth, Yifang Hu, Peter Dunn and Belinda Phipson. *statmod: Statistical Modeling*, 2011. R package version 1.4.14. (Cited on page 143.)

[Spence 1974] M.A. Spence. *Competitive and optimal responses to signals: An analysis of efficiency and distribution.* Journal of Economic Theory, vol. 7, no. 3, pages 296–332, 1974. (Cited on page 165.)

[Urbanek 2011] Simon Urbanek. *multicore: Parallel processing of R code on machines with multiple cores or CPUs*, 2011. R package version 0.1-7. (Cited on page 46.)

[Wuertz *et al.* 2009] Diethelm Wuertz, many others and see the SOURCE file. *fUnitRoots: Trends and Unit Roots*, 2009. R package version 2100.76. (Cited on page 13.)