# 18.s096 pset1

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# 1 18.s096 Problem Set 1

#### 1.1 Dimitris Koutentakis

#### 1.2 Problem 1

(a)

$$\hat{\beta} = (X^{T}X)^{-1}X^{T}\hat{y}$$

$$= ((QR)^{T}QR)^{-1}(QR)^{T}\hat{y}$$

$$= (R^{T}Q^{T}QR)^{-1}R^{T}Q^{T}\hat{y}$$

$$= (R^{T}R)^{-1}R^{T}Q^{T}\hat{y}$$

$$= R^{-1}(R^{T})^{-1}R^{T}Q^{T}\hat{y}$$

$$= R^{-1}Q^{T}\hat{y}$$
(1)

$$Cov(\hat{\beta}) = \sigma^{2}(X^{T}X)^{-1}$$

$$= \sigma^{2}X^{-1}(X^{T})^{-1}$$

$$= \sigma^{2}R^{-1}Q^{-1}(R^{T}Q^{T})^{-1}$$

$$= \sigma^{2}R^{-1}Q^{-1}(Q^{T})^{-1}(R^{T})^{-1}$$

$$= \sigma^{2}R^{-1}(QQ^{T})^{-1}(R^{T})^{-1}$$

$$= \sigma^{2}R^{-1}(R^{T})^{-1}$$

$$= \sigma^{2}R^{-1}(R^{T})^{-1}$$

$$= \sigma^{2}R^{-1}(R^{-1})^{T}$$
(2)

(b)

```
ldl
                                                 glu prog
     sex
          bmi map
                      tc
                                  hdl
                                       tch
                                           ltg
age
59
     1
          32.1
                101
                      157
                           93.2
                                  38
                                       4
                                            2.11 87
                                                       151
 48
     0
          21.6
                87
                      183
                           103.2
                                  70
                                       3
                                            1.69
                                                 69
                                                       75
 72
          30.5
               93
                      156
                           93.6
                                  41
                                            2.03 85
                                                       141
     1
                                       4
          25.3
               84
                           131.4 40
                                       5
                                            2.12 89
 24
     0
                      198
                                                       206
 50
     0
          23.0
               101
                      192
                           125.4
                                  52
                                       4
                                            1.86 80
                                                       135
 23
     0
          22.6
               89
                      139
                           64.8
                                       2
                                            1.82 68
                                                       97
                                  61
                                                 glu
                           ldl
          bmi
               map
                      tc
                                  hdl
                                       tch ltg
                                                      b
age
     sex
 59
     1
          32.1
               101
                      157
                           93.2
                                  38
                                       4
                                            2.11 87
                                                       1
 48
     0
          21.6
               87
                      183
                           103.2
                                 70
                                       3
                                            1.69
                                                 69
                                                       1
 72
          30.5 93
                      156
                           93.6
                                            2.03 85
    1
                                  41
                                       4
                                                       1
 24
    0
          25.3
               84
                      198
                           131.4
                                 40
                                       5
                                            2.12 89
                                                      1
                      192
 50
    0
          23.0
               101
                           125.4
                                  52
                                       4
                                            1.86
                                                 80
                                                      1
 23 | 0
          22.6
                      139
                           64.8
                                       2
                                            1.82 68
                                                      1
                89
                                  61
```

In [127]: R = qr.R(qr(X))

Q = qr.Q(qr(X))

y = diabetes["prog"]

y = as.matrix(y)

In [174]:  $b_hat = solve(R) %*\%t(Q) %*\%y$  $b_hat$ 

lm(prog ~~.,~diabetes)

prog
-0.03529284
-22.79232590
5.59548470
1.11589075
-1.08285741
0.73913778
0.36782732
6.54048459
157.17605916
0.28147926
-356.64395038

#### Call:

lm(formula = prog ~ ., data = diabetes)

#### Coefficients:

tc	map	bmi	sex	age	(Intercept)
-1.08286	1.11589	5.59548	-22.79233	-0.03529	-356.64395
	glu	ltg	tch	hdl	ldl
	0.28148	157.17606	6.54048	0.36783	0.73914

It can be easily seen that the coefficients are the same. (c) Let k=4, then:

age	sex	bmi	map	b		
59	1	32.1	101	1		
48	0	21.6	87	1		
72	1	30.5	93	1		
24	0	25.3	84	1		
50	0	23.0	101	1		
23	0	22.6	89	1		
tc	ldl	hdl	tch	ltg	glu	b
tc 157	ldl 93.2	hdl 38	tch 4	1tg 2.11	glu 87	b 1
157	93.2	38	4	2.11	87	1
157 183	93.2 103.2	38 70	4 3	2.11 1.69	87 69	1 1
157 183 156	93.2 103.2 93.6	38 70 41	4 3 4	2.11 1.69 2.03	87 69 85	1 1 1
157 183 156 198	93.2 103.2 93.6 131.4	38 70 41 40	4 3 4 5	2.11 1.69 2.03 2.12	87 69 85 89	1 1 1 1

age	sex	bmi	map	
-1056.53	-9.980789	-539.83925	-1946.48499	_
0.00	10.362618	15.20642	86.72943	
0.00	0.000000	156.34001	396.23297	
0.00	0.000000	0.00000	-300.79028	
age	sex	bmi	map	b
-1056.53	-9.980789	-539.83925	-1946.48499	-20.2975837
0.00	10.362618	15.20642	86.72943	0.4259637
0.00	0.000000	156.34001	396.23297	4.4402596
0.00	0.000000	0.00000	-300.79028	-1.7571613
0.00	0.000000	0.00000	0.00000	-2.6501186
-0.055843	20 0.04271	515 0.008	341459 0.048	889711
-0.045431	76 -0.0437	5774 -0.014	458531 -0.02	690179
-0.068147	63 0.03086	<b>-0.043</b>	3226943 0.083	377011
-0.022715	88 -0.0218	7887 0.085	517308 -0.02	592055
-0.047324	75 -0.0455	8098 -0.011	1862812 -0.05	830222
-0.021769	38 -0.0209	6725 0.071	426818 -0.06	696706

```
0.008341459
    -0.05584320
                0.04271515
                                          0.04889711
                                                       0.038788940
    -0.04543176 -0.04375774
                            -0.014458531 -0.02690179 -0.042795506
    -0.06814763
                0.03086410
                             -0.043226943 0.08377011
                                                       0.021600118
                             0.085517308
                                          -0.02592055 -0.046404163
    -0.02271588
                -0.02187887
    -0.04732475
                -0.04558098
                             -0.011862812
                                          -0.05830222 -0.003420753
    -0.02176938 -0.02096725 0.071426818
                                          -0.06696706 -0.049899608
In [197]: b_{t} = solve(R1)\%*\%t(Q1)\%*\%y
          y_hat1 = Q1\%*\%t(Q1)\%*\%y
          b_hat1
          head(y_hat1)
          prog
          0.1352584
     age
          -10.1578933
     sex
    bmi
          8.4845665
    map
          1.4344274
          -209.2226408
       b
    prog
    205.8315
    105.3316
    182.5391
    129.1750
    137.5625
    113.3035
   (d)
In [198]: b_hat1 = solve(R1)\%*\%t(Q1)\%*\%y
          b_hat1
          b_hat1b = lm(prog ~ age + sex + bmi + map, data = diabetes)
          b hat1b
          prog
     age
          0.1352584
          -10.1578933
     sex
          8.4845665
    bmi
    map
          1.4344274
          -209.2226408
      b
Call:
lm(formula = prog ~ age + sex + bmi + map, data = diabetes)
Coefficients:
(Intercept)
                      age
                                    sex
                                                  bmi
                                                                map
  -209.2226
                   0.1353
                              -10.1579
                                              8.4846
                                                            1.4344
```

### 2 Problem 2

```
(a)
In [266]: fcn.dqa0 \leftarrow function(x){
              x.n = length(x)
              x.mean = mean(x, na.rm = TRUE)
              x.missing = sum(is.na(x))
              x.unique = length(unique(x, na.rm = TRUE))
              x.standard_dev = sd(x, na.rm = TRUE)
              x.skew = sum((x-x.mean)^3, na.rm = TRUE)/(x.n*x.standard_dev^3)
              x.kurtosis = sum((x-x.mean)^4, na.rm = TRUE)/(x.n*x.standard_dev^4)
              x.median = median(x, na.rm = TRUE)
              x.iqr = IQR(x, na.rm = TRUE)
              x.q05 = quantile(x,prob = 0.05, na.rm = TRUE)
              x.q95 = quantile(x, prob = 0.95, na.rm = TRUE)
              stats=cbind(
              n=x.n,
              mean=x.mean,
              median = x.median,
              missing = x.missing,
              unique = x.unique,
              sd=x.standard_dev,
              skew=x.skew,
                kurtosis=x.kurtosis,
              iqr = x.iqr,
              q05 = x.q05,
              q95 = x.q95
            # cbind creates a 1-row numeric matrix with columns so-named
            return(stats)
          fcn.dqa0.matrix <- function(X){</pre>
            X.dqa0<-apply(X,2,fcn.dqa0)</pre>
            dimnames(X.dqa0)[[1]]<-dimnames(</pre>
              fcn.dqa0(X[,1]))[[2]]
            result <- (X.dqa0)
            return(result)
          }
In [270]: diabetes[1,1] <- NA</pre>
          fcn.dqa0.matrix(diabetes)
          round(fcn.dqa0.matrix(matrix(rnorm(5000),nrow=500,ncol=10)),
                digits=2)
```

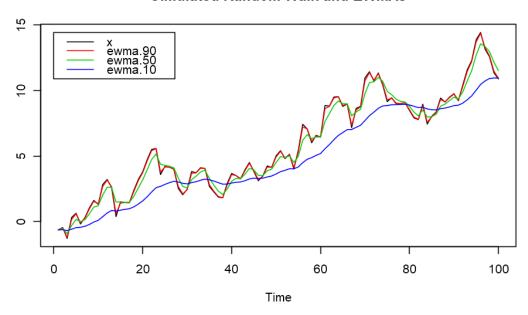
	age sex bmi			map		tc		ldl		hdl		
n	442.0000000 442.0000000		0 442.0	442.0000000 442.0		0000 442.0000000		) 442.0	00000	442.0000000		
mean	48.4943311 0.4683258		26.37	26.3757919		94.6466063 18		189.1402715		39140	49.7884615	
median	50.0000000 0.0000000		25.70	25.7000000 93.0000000		186.0000000		113.0	00000	48.0000000		
missing	1.000000	0 00	.0000000	0.000	00000	0.000000	00	0.0	000000	0.000	0000	0.0000000
unique	59.00000	000 2	.0000000	163.0	000000	100.0000000		141.0000000		302.0	00000	63.0000000
sd	13.1143	<b>776</b> 0	.4995612	4.418	31216	16 13.8319998		34.6080517		30.41	3081	12.9342022
skew	-0.22527	<b>74</b> 9 0	.1265212	0.594	0948	0.288639	92	0.3	755457	0.433	6633	0.7938385
iqr	21.0000000 1.0000000		6.075	0000	21.00000	000000 45.5000000		38.45	0000	17.5000000		
q05	25.00000	000 0	.0000000	20.20	000000	73.05000	000	136	5.0000000	69.00	0000	32.0000000
q95	68.00000	000 1	.0000000	34.30	000000	118.9500	0000	249	9.9500000	166.1	90000	70.9500000
n	500.00	500.00	500.00	500.00	500.00	500.00	500.	00	500.00	500.00	500.00	)
mean	-0.01	-0.04	0.04	0.03	0.03	-0.01	0.05		0.01	0.02	0.05	
median	-0.07	-0.04	0.04	0.02	-0.02	0.03	0.06		-0.01	0.07	0.04	
missing	0.00	0.00	0.00	0.00	0.00	0.00	0.00		0.00	0.00	0.00	
unique	500.00	500.00	500.00	500.00	500.00	500.00	500.	00	500.00	500.00	500.00	)
sd	0.94	0.95	0.97	1.03	0.96	0.97	1.03		1.00	0.99	0.97	
skew	0.18	0.03	0.10	0.05	0.16	-0.11	0.12		0.04	-0.11	0.03	
iqr	1.31	1.24	1.33	1.39	1.27	1.32	1.38		1.43	1.33	1.31	
q05	-1.46	-1.57	-1.45	-1.50	-1.49	-1.62	-1.61	l	-1.64	-1.67	-1.53	
q95	1.59	1.59	1.60	1.68	1.71	1.68	1.82		1.64	1.59	1.67	

# 3 Problem 3

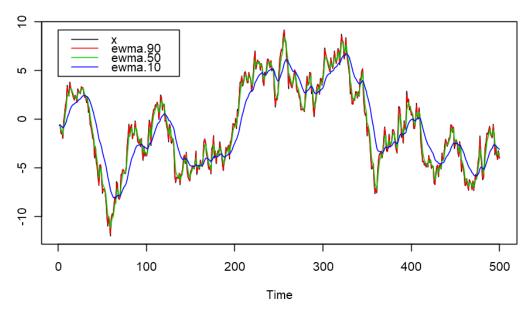
```
(a)
In [49]: ewma <- function(x, alpha) {</pre>
            n <- length(x)
            s <- rep(NA,n)
            s[1] <- x[1]
            if (n > 1) {
                 for (i in 2:n) {
                 s[i] \leftarrow alpha * x[i] + (1 - alpha) * s[i-1]
                 }
            }
            return(s)
          }
In [55]: set.seed(1)
          x=cumsum(rnorm(100))
         library(repr)
         options(repr.plot.width=8, repr.plot.height=5)
         library(microbenchmark)
          x.ewma.90 < -ewma(x,alpha=.90)
```

```
x.ewma.50 < -ewma(x,alpha=.50)
 x.ewma.10 < -ewma(x,alpha=.10)
 ts.plot(ymat0<-cbind(x=x,</pre>
     ewma.90=x.ewma.90,
     ewma.50=x.ewma.50,
     ewma.10=x.ewma.10), col=c(1:4),
     main="Simulated Random Walk and EWMAs")
 legend(x=0, y=max(as.vector(ymat0)),
     legend=dimnames(ymat0)[[2]],
     col=c(1:4),
     lty=rep(1,times=4))
 x=cumsum(rnorm(500))
options(repr.plot.width=8, repr.plot.height=5)
library(microbenchmark)
 x.ewma.90 < -ewma(x,alpha=.90)
 x.ewma.50 < -ewma(x,alpha=.50)
 x.ewma.10 < -ewma(x,alpha=.10)
 ts.plot(ymat0<-cbind(x=x,</pre>
     ewma.90=x.ewma.90,
     ewma.50=x.ewma.50,
     ewma.10=x.ewma.10), col=c(1:4),
     main="Simulated Random Walk and EWMAs")
 legend(x=0, y=max(as.vector(ymat0)),
     legend=dimnames(ymat0)[[2]],
     col=c(1:4),
     lty=rep(1,times=4))
```

#### Simulated Random Walk and EWMAs

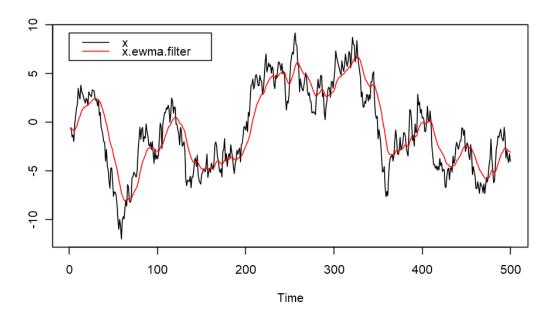


# Simulated Random Walk and EWMAs



```
return(result)
}

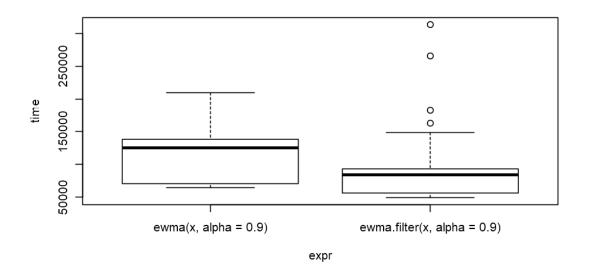
ts.plot(ymat<-cbind(
    x=x,
    x.ewma.filter=ewma.filter(x,0.1)),
col=c(1,2))
legend(x=0,
    y=max(as.vector(ymat)),
legend=dimnames(ymat)[[2]],
col=c(1:ncol(ymat)),
lty=rep(1,times=ncol(ymat)))
options(repr.plot.width=8, repr.plot.height=4.5)</pre>
```

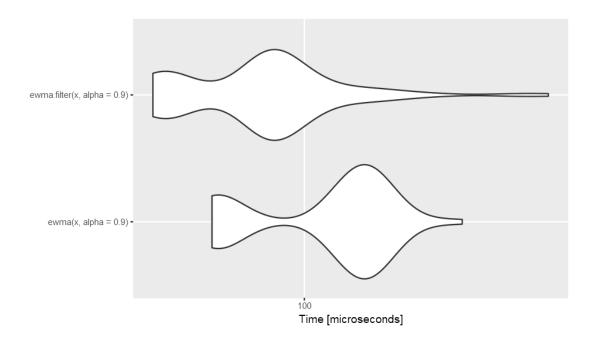


```
In [57]: all.equal(ewma.filter(x,alpha=.9), ewma(x,alpha=.9))
    TRUE
In [59]: microbm.1<-microbenchmark::microbenchmark(ewma(x,alpha=.9), ewma.filter(x,alpha=.9))
    # Read the help function for microbenchmark, and
    # print out/plot the results:
    print(microbm.1)
    plot(microbm.1)
    library(ggplot2)
    autoplot(microbm.1)</pre>
```

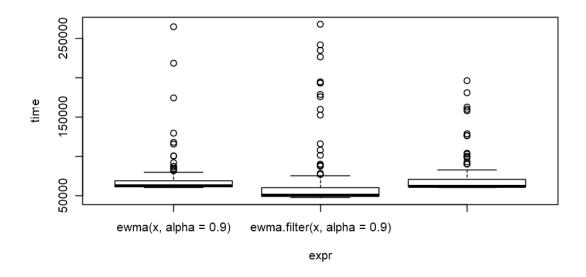
#### Unit: microseconds

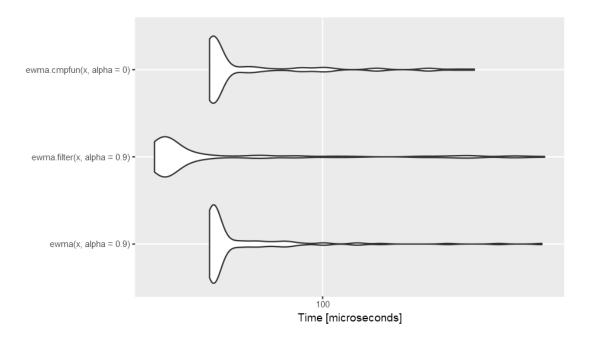
```
ewma(x, alpha = 0.9) 64.912 70.747 115.3611 125.4475 138.3935 209.323 ewma.filter(x, alpha = 0.9) 49.231 56.525 87.2923 84.6045 93.3565 313.254 neval 100 100
```





```
In [61]: ewma.cmpfun <- compiler::cmpfun(function(x, alpha) {</pre>
         n <- length(x)
         s <- rep(NA,n)
         s[1] <- x[1]
         if (n > 1) {
         for (i in 2:n) {
         s[i] \leftarrow alpha * x[i] + (1 - alpha) * s[i-1]
         }
         }
         return(s)
         })
In [63]: all.equal(ewma(x,alpha=.9), ewma.cmpfun(x,alpha=.9))
         all.equal(ewma.filter(x,alpha=.9), ewma.cmpfun(x,alpha=.9))
   TRUE
   TRUE
In [64]: microbm.2<-microbenchmark::microbenchmark(</pre>
         ewma(x,alpha=.9),
          ewma.filter(x,alpha=.9),
          ewma.cmpfun(x,alpha=.0))
In [67]: print(microbm.2)
         plot(microbm.2)
         library(ggplot2)
         autoplot(microbm.2)
Unit: microseconds
                                                 mean median
                                 \min
                                         lq
        ewma(x, alpha = 0.9) 60.536 61.266 72.09637 62.1770 68.9235 264.752
 ewma.filter(x, alpha = 0.9) 47.408 49.049 71.64050 50.8725 60.1715 268.035
   ewma.cmpfun(x, alpha = 0) 60.536 61.265 73.44931 61.9950 70.7465 196.194
neval
   100
   100
   100
```





# 4 Problem 4

# 4.1 R basics

R is a free, open source programming language very commonly used for data analysis. It has a very large set of packages and build in tools that are very useful for analyzing and visualizing

data.

# 4.2 Common operators and functions

In addition to most mathematical operators ("+", "-", "\*", "/") used to perform simple operations, a very common operator in r is the assignment operator, "<-" in order to assign values to variables, but the same can be done with the equals sign. The pound sign ("#") declares anything that follows it as a comment. Furthermore, the logical operators used are ">" for "greater that", ">=" for "greater than or equal to", "==" for "equal to" and "!=" for "not equal to".

One very important function is the help function, that is "help(f)". This function gives information on the function passed as the argument. Furthermore, one of the strong points of R is its ability to install and include extra packages. In order to do that, one must use "install.packages(x)" to install the package x and after that we have to use "libraries(x)" in order to include the package.

Other useful functions include:

- abs(x) absolute value
- c(a,b,c) combine arguments in a vector
- cat(x) prints arguments
- cbind(x) combines vectors by rows/columns
- length(x) number of elements in x
- seq(a,b,c) makes a squence from a to b in steps of c
- rev(x) prints x in revers
- sort(x) sorts the vector x
- unique(x) removes duplicates from x
- getwd() prints current working directory
- setwd() set woring directory
- sin(), cos(), tan(), acos(), atan(), asin() trigonometric functions
- plot(x) generate plot of x
- hist(x) generate histogram of x
- lm() fit linear model
- sd() standard deviation
- mean(x) mean of x
- median(x) median of x
- var(x) variance of x
- qqplot() quantile-quantile plot
- head(x) show the first few rows of a dataframe
- ls() prints all the current objects in memory

In order to define custom functions, the following syntax is used:

```
myfunction <- function(arg1, arg2, ...){
statements
return(object)
}</pre>
```

## 4.3 Data (types and importing)

Some of the main datatypes in R are: 1. integers - integer values 2. numerics - general number datatype (decimal) 3. complex - complex numbers with real and imaginary parts 4. logicals -

boolean variables 5. Characters - string characters 6. Vectors - arrays of numbers 7. lists - like vectors but can have many different datatypes 8. matrices - two dimensional vectors 9. data frame - table like object with headers; each column contains objects of a certain type

In order to import data from a csv file one can use the function read.csv(x). This function imports the data from the csv file into a dataframe variable.

#### 4.4 Environments

The most straightforward way to use R, is to just type commands into a terminal running R, or write whole scripts and then run them. RStudio is an integrated development environment (IDE) for R, which includes a console, syntax-highlighting editor that supports direct code execution, as well as tools for plotting, history, debugging and workspace management. RStudio is available on all major platforms and very easy to download.

An alternative that provides a lot of ease of use is runing R on Jupyter. Jupyter is an open-source web application that allows one to create and share documents that contain live code, equations, visualizations and narrative text. It was initially created for Python, but it can easily be used with R. A Jupyter Notebook contains multiple cells, each of which contains code that can be run independently of each other. Cells can also be used to display text written in markdown format in order to include text or equations on the same document as the code.

In order to install Jupyter with R, one must first download jupyter, by downloading the Anaconda suite which is free for any platform. After this, there are two more steps needed. First one should type the following into an R terminal:

```
install.packages(c('repr', 'IRdisplay', 'evaluate', 'crayon', 'pbdZMQ', 'devtools', 'uuid', 'd
devtools::install_github('IRkernel/IRkernel')
```

And secondly, input this command: IRkernel::installspec() in order to make available the installation to Jupyter. After that one can use Jupyter in order to perform all calulations necessary and include text and equations like on this submission.