# 統計模擬 作業三

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1. Given the following data, use the orthogonalization methods such as Cholesky or QR to perform regression analysis, including the parameter estimates and their standard errors via the sweep operator. Note that, to solve the linear equation, you may use the Gauss elimination or use the function "*lm*" or "*glm*" in R.

| $x_1$ Reactor temperature (°C) | $x_2$ Ratio of $H_2$ to n-heptane (mole ratio) | $x_3$ Contact time (sec.) | y Conversion of n-heptane to acetylene(%) |
|---|---|---|---|
| 1300 | 7.5 | 0.0120 | 49.0 |
| 1300 | 9.0 | 0.0120 | 50.2 |
| 1300 | 11.0 | 0.0115 | 50.5 |
| 1300 | 13.5 | 0.0130 | 48.5 |
| 1300 | 17.0 | 0.0135 | 47.5 |
| 1300 | 23.0 | 0.0120 | 44.5 |
| 1200 | 5.3 | 0.0400 | 28.0 |
| 1200 | 7.5 | 0.0380 | 31.5 |
| 1200 | 11.0 | 0.0320 | 34.5 |
| 1200 | 13.5 | 0.0260 | 35.0 |
| 1200 | 17.0 | 0.0340 | 38.0 |
| 1200 | 23.0 | 0.0410 | 38.5 |
| 1100 | 5.3 | 0.0840 | 15.0 |
| 1100 | 7.5 | 0.0980 | 17.0 |
| 1100 | 11.0 | 0.0920 | 20.5 |
| 1100 | 17.0 | 0.0860 | 29.5 |

It is anticipated that an equation of the following form would fit the data

$$E(Y) = \beta_0 + \sum \beta_i X_i + \sum \beta_{ii} X_i^2 + \sum_{i<j} \beta_{ij} X_i X_j \text{, and } Var(Y) = \sigma^2$$

令 $X$ 是資料矩陣，包含所有一次、二次與交互作用項，則透過 Cholesky 可以求得迴歸係數，

$$LL'\hat{\beta} = X'y, \text{ where } LL' \text{ is cholesky decomposition of } X'X.$$

而爲了去估計係數 $\hat{\beta}$ 的標準誤，需透過 sweep operator 去估計，過程如下

$$SSCP = \begin{pmatrix} X'X & X'y \\ y'X & y'y \end{pmatrix} \xrightarrow{\text{sweep colume 1 to p}} \begin{pmatrix} -(X'X)^{-1} & \hat{\beta} \\ \hat{\beta}' & RSS \end{pmatrix}$$

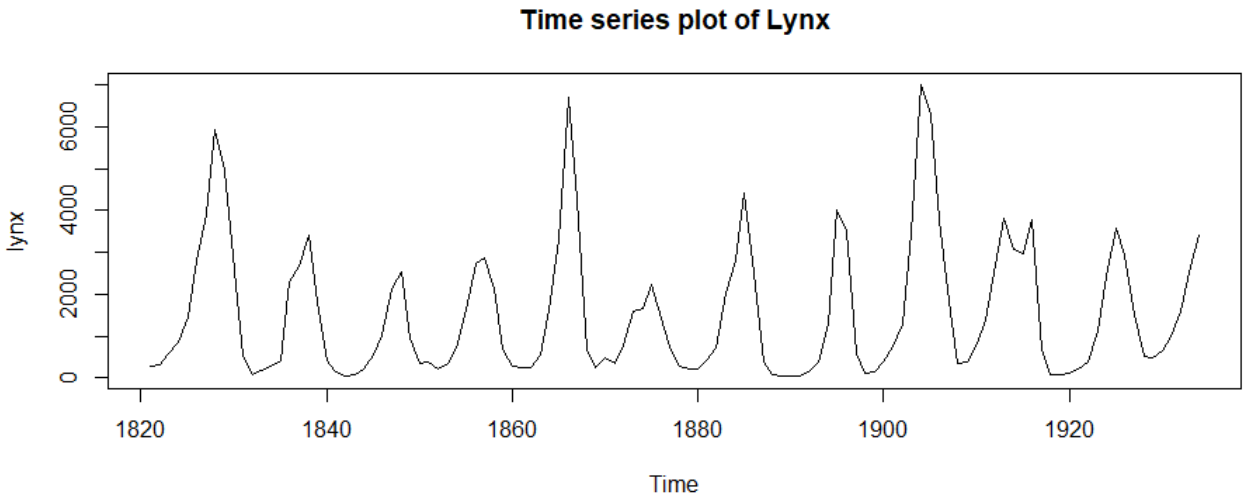
又 $Var(\hat{\beta}) = \sigma^2 (X'X)^{-1}$, where $\sigma^2 = RSS/(n-p)$.

有了以上定義，計算出的係數估計列出如下表格，並一併與 `lm()` 函數進行比較。

| | Cholesky | sweep | lm | lm |
|---|---|---|---|---|
| | $\hat{\beta}$ | $se(\hat{\beta})$ | $\hat{\beta}$ | $se(\hat{\beta})$ |
| Intercept | -3617.23 | 3136.04 | -3617.23 | 3136.04 |
| x1 | 5.32 | 4.88 | 5.32 | 4.88 |
| x2 | 19.24 | 4.30 | 19.24 | 4.30 |
| x3 | 13766.32 | 10448.32 | 13766.32 | 10448.32 |
| x1^2 | 0.00 | 0.00 | 0.00 | 0.00 |
| x2^2 | -0.03 | 0.01 | -0.03 | 0.01 |
| x3^2 | -11581.68 | 7698.61 | -11581.68 | 7698.61 |
| x1*x2 | -0.01 | 0.00 | -0.01 | 0.00 |
| x1*x3 | -10.58 | 8.24 | -10.58 | 8.24 |
| x2*x3 | -21.03 | 9.24 | -21.03 | 9.24 |

2. Figure a way to find the parameters of AR(1) and AR(2) models for the data "lynx" in R. Also, apply statistical software such as R, SAS, SPSS, and Minitab to get estimates for the AR(1) and AR(2) model and compare them to those from your program.

Lynx 資料時間序列圖如下，




AR(p)過程的定義如下:

$\{X_n: n = 0, \pm1, \pm2, \dots\}$ 爲一時間序列，滿足對 $\forall n \in Z$

$$X_n = a_0 + a_1 X_{n-1} + a_2 X_{n-2} + \cdots + a_p X_{n-p} + \epsilon_n,$$

$\{\epsilon_n: n = 0, \pm1, \pm2, \dots\}$ 爲誤差序列且$Var(\epsilon_n) = \sigma^2$。

有了以上定義，我們可以在 SAS 裡頭寫個線性估計式，與透過 R 的 `ar.ols()`的結果差不多，但截距項有些差異。

```
#SAS#
proc model data=lynx;
  parms p0 p1;
  x = p0 + p1* lag1(x);
  fit x;
proc model data=lynx;
  parms p0 p1 p2;
  x = p0 + p1* lag1(x) + p2 * lag2(x);
  fit x;
run;
#R#
ar.ols(lynx, order = 1)
ar.ols(lynx, order = 2)
```

| | | SAS | R |
|---|---|---|---|
| AR(1) | a0 | 454.15 | 23.060 |
| | a1 | 0.7197 | 0.7197 |
| AR(2) | a0 | 710.10 | 12.140 |
| | a1 | 1.1524 | 1.1524 |
| | a2 | -0.6062 | -0.6062 |

3. Singular Value Decomposition (SVD) and Principal Component Analysis (PCA) both can be used to reduce the data dimensionality. Please go to the webpage of Ministry of Interior and download Taiwan mortality data,17 five-age groups for ages 0~4, 5~9, …, 80~84 in 1991-2015, and use these data to demonstrate how these two methods work. The data of the years 1991-2010 are used as the "training" (in-sample) data and the years 2010-2015 are used as the "testing" (out-sample) data. Comments on your findings.

首先以下是子是用來估計死亡人數的模型

$$\ln(m_{xt}) = \alpha_x + \beta_x \kappa_t + \epsilon_{xt}$$

其中，$\alpha_x$ 表示每個年齡層的平均死亡人數；$\beta_x$ 表示隨著年齡層增加的死亡人數增加率；$\kappa_t$ 表示隨年增加的死亡人數增加率。爲了估計 $\beta_x$ 和 $\kappa_t$，我們對 $\ln(m_{xt}) - \alpha_x$ 做 SVD 拆解，意謂

$$\ln(m_{xt}) - \alpha_x = (UD)V' = \left(\widehat{\beta_x}\right)\widehat{\kappa_t}'$$

於是根據 1992~2010 的資料，我們做了 SVD 後，分別得到相對應的 $\widehat{\beta_x}$ 和 $\widehat{\kappa_t}$ 。爲了預測往後 2011~2015 年的死亡人數，我們透過 AR(1)模型預測了 $\widehat{\kappa_{t'}}$ 模型如下:

$$\widehat{k_{t'}} = 0.1561 + 1.0101\ \widehat{k_{t'-1}}$$

並透過以下模型預測，

$$\ln(m_{xt'}) = \alpha_x + \widehat{\beta_x}\widehat{\kappa_{t'}}$$

預測結果如下

```
> round(xnew.appr, 2)
       [,1]  [,2]  [,3]  [,4]  [,5]  [,6]  [,7]  [,8] [,9] ... [,17]
2011 -0.62 -0.60 -0.69 -0.74 -0.49 -0.29 -0.23 -0.09 0.09 ... 0.46
2012 -0.68 -0.67 -0.77 -0.82 -0.54 -0.32 -0.25 -0.10 0.10 ... 0.51
2013 -0.74 -0.73 -0.84 -0.90 -0.59 -0.35 -0.27 -0.11 0.11 ... 0.56
2014 -0.81 -0.79 -0.91 -0.98 -0.64 -0.39 -0.30 -0.12 0.12 ... 0.61
2015 -0.88 -0.86 -0.99 -1.06 -0.69 -0.42 -0.32 -0.13 0.13 ... 0.66
```

很可惜與眞實資料的對數死亡人數差距有 20.84，說明降維拿來做預測估計沒有很好。

```
> sum((xnew - xnew.appr)^2)
[1] 20.84244
```

❖ PCA 降維待補 !!

4. (a) Write a small program to perform the "Permutation test" and test your result on the correlation of DDT vs. eggshell thickness in class, and the following data:

| X | 585 | 1002 | 472 | 493 | 408 | 690 | 291 |
|---|---|---|---|---|---|---|---|
| Y | 0.1 | 0.2 | 0.5 | 1.0 | 1.5 | 2.0 | 3.0 |

Check your answer with other correlation tests, such as regular Pearson and Spearman correlation coefficients.

(b) Simulate a set of two correlated normal distribution variables, with zero mean and variance 1. Let the correlation coefficient be 0.2 and 0.8. (Use Cholesky!) Then convert the data back to Uniform(0,1) and record only the first decimal number. (亦即只取小數第一位，0至9的整數) Suppose the sample size is 10. Apply the permutation test, Pearson and Spearman correlation coefficients, and records the p-values of these three methods. (10,000 simulation runs)

(a) 此題有兩筆資料要進行相關性分析, 首先是 DDT 與 egg 資料, 此資料可以目測出呈現若相關, 因此若此資料算出的 $\sum x_i y_i$ 小於 permutations 亂數算出的 $\sum x_i y_i$ 的個數夠少, 才能說此負相關顯著的。執行結果告訴我們拒絕虛無假設。

```
> length(which(DDT2 %*% sort(egg) <= sum(DDT * egg)))/nrow(DDT2)
[1] 0.03333333
```

但 Pearson 和 Spearman 的相關係數估計結果都是不顯著的。

```
> cor.test(DDT, egg, method = "pearson")
...
t = -1.5343, df = 3, p-value = 0.2225
> cor.test(DDT, egg, method ="spearman")
...
S = 37.442, p-value = 0.05385
```

另外一筆資料是題目給的(X, Y)，結果如下;

```
> #Permutations test
> length(which(x2 %*% sort(y) <= sum(x * y)))/nrow(x2)
[1] 0.07757937
> cor.test(x, y, method="pearson")
...
t = -1.5083, df = 5, p-value = 0.1919
> cor.test(x, y, method="spearman")
...
S = 86, p-value = 0.2357
```

(b)首先生成兩筆 N(0, 1)資料，對其進行 Cholesky 職轉換後，再將其轉爲 uniform ，並取小數點後第一位，最後在檢定其相關性是否仍顯著存在。函數撰寫如下:

```
choln2u <- function(rho = 0.2){
  A <- matrix(c(1, rho, rho, 1), ncol=2)
  B <- t(chol(A))
  t1 <- NULL
  t2 <- NULL
  t3 <- NULL
  for (i in 1:100) {
    x1 <- rnorm(10)
    y1 <- rnorm(10)
    xy1 <- rbind(x1, y1)
    xy <- B %*% xy1
    xy.unif <- floor(10*pnorm(xy))
    z1 <- cor.test(xy.unif[1, ], xy.unif[2, ], method =
"pearson")$p.value
    z2 <- cor.test(xy.unif[1, ], xy.unif[2, ], method =
"spearman")$p.value
    t1 <- c(t1, z1)
    t2 <- c(t2, z2)
    t <- NULL
    z0 <- sum(x1*y1)
    for (j in 1:1000) {
      x0 <- sample(x1, 10, F)
      y0 <- sample(y1, 10, F)
      t <- c(t, sum(x0*y0))
    }
    z3 <- sum(t >= z0)/1000
    t3 <- c(t3, z3)
  }
  print(paste('pearson p<0.05 個數:', length(t1[t1<0.05])))
  print(paste('spearman p<0.05 個數:', length(t2[t2<0.05])))
  print(paste('permutation test p<0.05 個數:', length(t2[t2<0.05])))
}
```

設定 rho=0.2 和 0.8，分別執行 100 次的結果如下:

```
> choln2u(0.2)
[1] "pearson p<0.05 個數: 5"
[1] "spearman p<0.05 個數: 5"
[1] "permutation test p<0.05 個數: 5"
```

```
> choln2u(0.8)
[1] "pearson p<0.05 個數: 85"
[1] "spearman p<0.05 個數: 78"
[1] "permutation test p<0.05 個數: 78"
```

發現當相關性很高時，轉換過後的數值被認爲是顯著相關的次數也會增加。

5. Using simulation to construct critical values of the Mann-Whitney-Wilcoxon test in the case that $2 \le n_1, n_2 \le 10$, where $n_1$ and $n_2$ are the number of observations in two populations. (Note: The number of replications shall be at least 10,000.)

❖ 待補 !!

6. Similar to what Efron did in the Law school data example, compute the bootstrap simulation for 50, 100, …, 10,000 replications. But, instead of using the original 15 observations, we want to know if the number of observations plays an important role. Randomly select 10, 15, 20, and 25 observations and then see if the bootstrap variance converges as the number of replications increases. (Note: You also need to compare your results with that of population.)

| school | LSAT | GPA | school | LSAT | GPA | school | LSAT | GPA | school | LSAT | GPA |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 622 | 3.23 | 22 | 614 | 3.19 | 43 | 573 | 2.85 | 63 | 572 | 3.08 |
| 2 | 542 | 2.83 | 23 | 628 | 3.03 | 44 | 644 | 3.38 | 64 | 610 | 3.13 |
| 3 | 579 | 3.24 | 24 | 575 | 3.01 | **(45)** | 545 | 2.76 | 65 | 562 | 3.01 |
| **(4)** | 653 | 3.12 | 25 | 662 | 3.39 | 46 | 645 | 3.27 | 66 | 635 | 3.30 |
| 5 | 606 | 3.09 | 26 | 627 | 3.41 | **(47)** | 651 | 3.36 | 67 | 614 | 3.15 |
| **(6)** | 576 | 3.39 | 27 | 608 | 3.04 | 48 | 562 | 3.19 | 68 | 546 | 2.82 |
| 7 | 620 | 3.10 | 28 | 632 | 3.29 | 49 | 609 | 3.17 | 69 | 598 | 3.20 |
| 8 | 615 | 3.40 | 29 | 587 | 3.16 | **(50)** | 555 | 3.00 | **(70)** | 666 | 3.44 |
| 9 | 553 | 2.97 | 30 | 581 | 3.17 | 51 | 586 | 3.11 | 71 | 570 | 3.01 |
| 10 | 607 | 2.91 | **(31)** | 605 | 3.13 | **(52)** | 580 | 3.07 | 72 | 570 | 2.92 |
| 11 | 558 | 3.11 | 32 | 704 | 3.36 | **(53)** | 594 | 2.96 | 73 | 605 | 3.45 |
| 12 | 596 | 3.24 | 33 | 477 | 2.57 | 54 | 594 | 3.05 | 74 | 565 | 3.15 |
| **(13)** | 635 | 3.30 | 34 | 591 | 3.02 | 55 | 560 | 2.93 | 75 | 686 | 3.50 |
| 14 | 581 | 3.22 | **(35)** | 578 | 3.03 | 56 | 641 | 3.28 | 76 | 608 | 3.16 |
| **(15)** | 661 | 3.43 | **(36)** | 572 | 2.88 | 57 | 512 | 3.01 | 77 | 595 | 3.19 |
| 16 | 547 | 2.91 | 37 | 615 | 3.37 | 58 | 631 | 3.21 | 78 | 590 | 3.15 |
| 17 | 599 | 3.23 | 38 | 606 | 3.20 | 59 | 597 | 3.32 | **(79)** | 558 | 2.81 |
| 18 | 646 | 3.47 | 39 | 603 | 3.23 | 60 | 621 | 3.24 | 80 | 611 | 3.16 |
| 19 | 622 | 3.15 | 40 | 535 | 2.98 | 61 | 617 | 3.03 | 81 | 564 | 3.02 |
| 20 | 611 | 3.33 | 41 | 595 | 3.11 | 62 | 637 | 3.33 | **(82)** | 575 | 2.74 |
| 21 | 546 | 2.99 | 42 | 575 | 2.92 | | | | | | |

Sampled schools have bold-faced school numbers.

Code:

```
#HW3
#1#################################
library(ISR3)
x1 <- c(rep(1300,6),rep(1200,6), rep(1100,4))
x2 <- c(7.5, 9.0, 11.0, 13.5, 17.0,
      23.0, 5.3, 7.5, 11.0, 13.5,
```

```
      17.0, 23.0, 5.3, 7.5, 11.0,
      17.0)
x3 <- c(0.012, 0.012, 0.0115, 0.013, 0.0135,
      0.012, 0.040, 0.038, 0.032, 0.026,
      0.034, 0.041, 0.084, 0.098, 0.092,
      0.086)
y <- c(49.0, 50.2, 50.5, 48.5, 47.5,
     44.5, 28.0, 31.5, 34.5, 35.0,
     38.0, 38.5, 15.0, 17.0, 20.5,
     29.5)

x4 <- x1 * x1
x5 <- x2 * x2
x6 <- x3 * x3
x7 <- x1 * x2
x8 <- x1 * x3
x9 <- x2 * x3

X <- matrix(c(rep(1,16), x1, x2, x3, x4, x5, x6, x7, x8, x9), ncol =
10)

#Cholesky
A <- t(X) %*% X
L <- t(chol(A))
B <- solve(t(L), solve(L, t(X) %*% y))
round(B, 2)

#SWEEP
M <- matrix(rbind(cbind(A, t(X) %*% y), cbind(t(y) %*% X, t(y) %*%
y)), nrow = 11)
M2 <- SWP(M, 1:10)
M2

XX <- -M2[1:10,1:10]
round(sqrt(diag(XX * (M2[11,11]/6))) , 2)

g <- lm(y~x1+x2+x3+x4+x5+x6+x7+x8+x9)
summary(g)

#2################################
plot(lynx, type= 'l', main = 'Time series plot of Lynx')
ar.ols(lynx, order = 1)
ar.ols(lynx, order = 2)


#3################################
library(forecast)
mortality <- read.csv("StatisticalSimulation/malemortality.csv", h =
T)
x <- scale(log(mortality[mortality$year <= 99, -1]), scale = FALSE)
svd.x <- svd(x, 1, 1)
b <- svd.x$v
k <- svd.x$u * svd.x$d[1]
```

```
fit.k <- ar.ols(k, order = 1)
pred.k <- NULL
p.k <- k[19]
for(i in 1:5){
 p.k <- fit.k$x.intercept + fit.k$ar * p.k
 pred.k <- c(pred.k, p.k)
}
xnew.appr <- pred.k %*% t(b)
round(xnew.appr, 2)
xnew <- scale(log(mortality[mortality$year > 99, -1]), scale = FALSE)
sum((xnew - xnew.appr)^2)


pca.x <- princomp(x)

#4################################
#(a)
library(gtools)
DDT <- c(65, 98, 117, 122, 130)
egg <- c(0.52, 0.53, 0.49, 0.49, 0.37)
p <- permutations(5,5)
DDT2 <- matrix(DDT[t(p)], byrow = T ,ncol = 5)
length(which(DDT2 %*% sort(egg) <= sum(DDT * egg)))/nrow(DDT2)
cor.test(DDT, egg, method = "pearson")
cor.test(DDT, egg, method ="spearman")


x <- c(585, 1002, 472, 493, 408, 690, 291)
y <- c(0.1, 0.2, 0.5, 1, 1.5, 2, 3)
p2 <- permutations(7,7)
x2 <- matrix(x[t(p2)], byrow = T, ncol = 7)
length(which(x2 %*% sort(y) <= sum(x * y)))/nrow(x2)
cor.test(x, y, method="pearson")
cor.test(x, y, method="spearman")

#(b)
choln2u <- function(rho = 0.2){
 A <- matrix(c(1, rho, rho, 1), ncol=2)
 B <- t(chol(A))
 t1 <- NULL
 t2 <- NULL
 t3 <- NULL
 for (i in 1:100) {
  x1 <- rnorm(10)
  y1 <- rnorm(10)
  xy1 <- rbind(x1, y1)
  xy <- B %*% xy1
  xy.unif <- floor(10*pnorm(xy))
  z1 <- cor.test(xy.unif[1, ], xy.unif[2, ], method =
"pearson")$p.value
  z2 <- cor.test(xy.unif[1, ], xy.unif[2, ], method =
"spearman")$p.value
  t1 <- c(t1, z1)
```

```
    t2 <- c(t2, z2)
    t <- NULL
    z0 <- sum(x1*y1)
    for (j in 1:1000) {
      x0 <- sample(x1, 10, F)
      y0 <- sample(y1, 10, F)
      t <- c(t, sum(x0*y0))
    }
    z3 <- sum(t >= z0)/1000
    t3 <- c(t3, z3)
  }
  print(paste('pearson p<0.05 個數:', length(t1[t1<0.05])))
  print(paste('spearman p<0.05 個數:', length(t2[t2<0.05])))
  print(paste('permutation test p<0.05 個數:', length(t2[t2<0.05])))
}

choln2u(0.2)
choln2u(0.8)

#5#################################


#6#################################
library(bootstrap)
law
```