Big Data

# STAT7017 Final Project

*Rui Qiu*

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## 0. Setup

First, we load some required libraries for this project. Basically, they are libraries of `tidyverse` which are responsible for data frame pipelines and the rest are mainly focusing on some particular calculations. We will mention those functions later.

```
library(mvtnorm)
library(ggplot2)
library(ggfortify)
library(forecast)
library(readr)
library(dplyr)
library(reshape2)
library(heplots)
library(ks)
library(vars)
library(portes)

set.seed(7017)
```

## 1. Part 1 Testing Covariance Matrices

### 1.1 Q1 Reproduce Box's Test for Equality of Covariance Matrices

The followings are some customized helper functions in order to apply Box's M test and print out some intermediate values. We have also configured some arguments as flags so that it can be reused in the next few questions, but the output details might vary accordingly.

```
box.u <- function(n.vec,p,g) {
    u <- (sum(1/(n.vec-1))-1/sum(n.vec-1))*((2*p**2+3*p-1)/(6*(p+1)*(g-1)))
    return(u)
}

log.det <- function(S) {
    return(unlist(determinant(S,logarithm=T))[[1]])
}

box.M <- function(p,g,n.vec,S.list,print.log=F) {
    S.pooled <- matrix(rep(0,p**2),ncol=p,nrow=p)

    for (i in 1:g) {
        S.pooled <- S.pooled + (n.vec[i]-1)*S.list[[i]]/sum(n.vec-1)
    }

    # for this Q1 only
    if (print.log) {
        cat("log determinant of S.pooled:",log.det(S.pooled),"\n")
    }

    M <- sum(n.vec-1)*log.det(S.pooled)
    for (i in 1:g) {
        M <-  M - (n.vec[i]-1)*log.det(S.list[[i]])
    }
    return(M)
}

box.C <- function(u, M) {
    return((1-u)*M)
}

M.test <- function(p,g,n.vec,S.list,test=F,summary=F) {
    u <- box.u(n.vec,p,g)
    if (test) {
        M <- box.M(p,g,n.vec,S.list,print.log=T)
    } else {
        M <- box.M(p,g,n.vec,S.list)
    }
    C <- box.C(u,M)
    nu <- 0.5*p*(p+1)*(g-1)
    if (summary) {
        cat("u =",u,"\n",
        "M =",M,"\n",
        "C =",C,"\n",
        "chi-sq with", nu, "degrees of freedom is", qchisq(.05,nu), "\n",
        "reject null hypothesis:", C > qchisq(.05,nu), "\n")
    }
    return(c(C,qchisq(.05,nu)))
}
```

When all the helper functions are settled, we are safe to reproduce example 6.12 with the following Wisconsin Nursing Homes data. Here, as expected, we printed out an intermediate value in the middle process of calculation, which should be the cause of differences in final values. Further explanation can be found in the following paragraph

```
M.test(4,3,c(271,138,107),
       list(matrix(c(.291,0,0,0,-.001,.011,0,0,.002,0,.001,0,.010,.003,0,.01),
                   nrow=4,byrow=T),
            matrix(c(.561,0,0,0,.011,.025,0,0,.001,.004,.005,0,.037,.007,.002,.019),
                   nrow=4,byrow=T),
            matrix(c(.261,0,0,0,.030,.017,0,0,.003,-0.0,.004,0,.018,.006,.001,.013),
                   nrow=4,byrow=T)),
       test=T,summary=T)
```

```
## log determinant of S.pooled: -15.42671
## u = 0.01324946
##  M = 218.8517
##  C = 215.9521
##  chi-sq with 20 degrees of freedom is 10.85081
##  reject null hypothesis: TRUE

## [1] 215.95207  10.85081
```

Hence we reject the null hypothesis that $\Sigma_1 = \Sigma_2 = \Sigma_3$. We also notice that the reproduced valued of test statistic $C = 215.9521$ differs from the original value which is 285.5. To investigate this, we include an intermediate value, the logarithm of determinant of $\mathbf{S}_{\text{pooled}}$. Our reproduced value is $-15.42671$, while the textbook text has $-15.564$. The standalone computational error should be trivial, but $\ln|\mathbf{S}_{\text{pooled}}|$ is iterated and subtracted 3 times when calculating the value of $M$ (correspondingly, $C$). Therefore, the difference of our test statistic is quite "large", but of course, does not affect our conclusion anyways.

## 1.2 Q2 Trials on Classic Iris Data

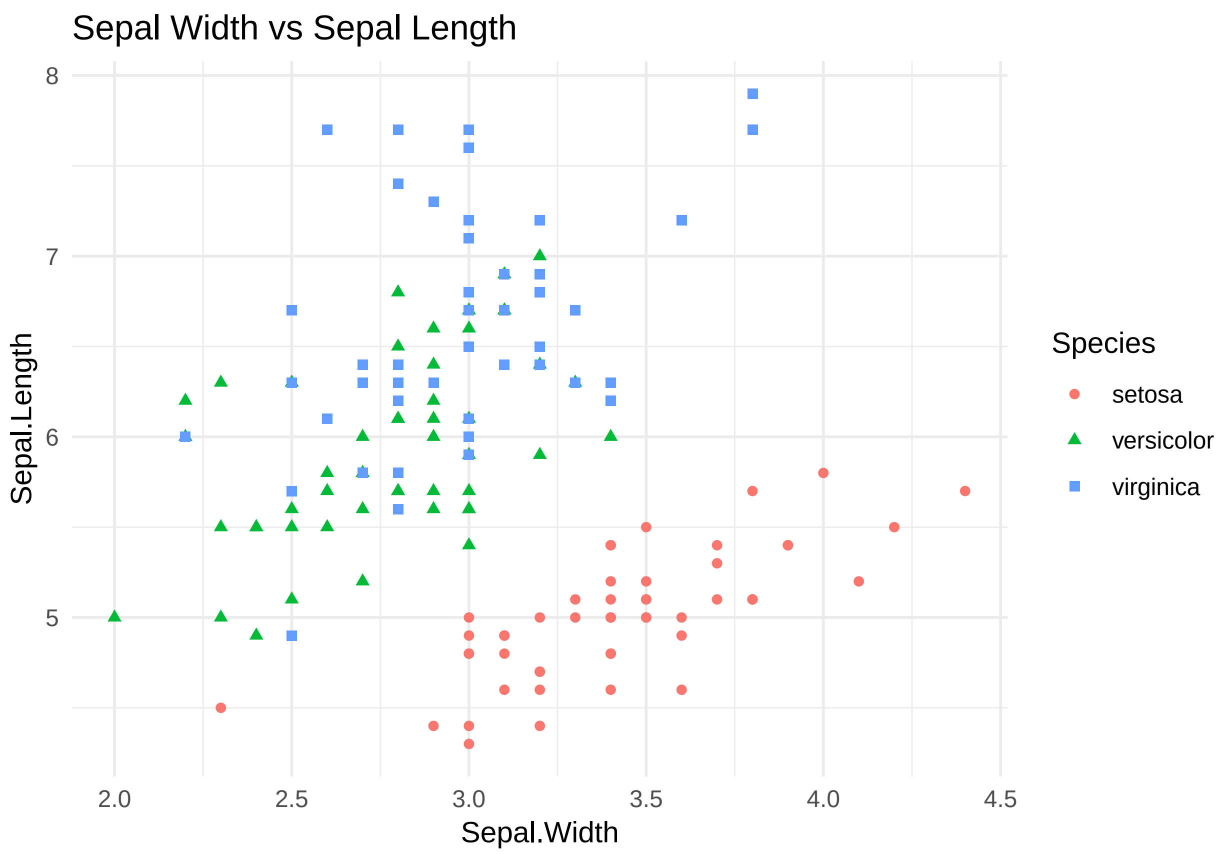
### 1.2.1 EDA Explanatory Data Analysis

For the famous Fisher's Iris data, we still would like to have some exploratory data analysis before starting our covariance homogeneity test. For simplicity, we just take a quick look at the two scatterplots.

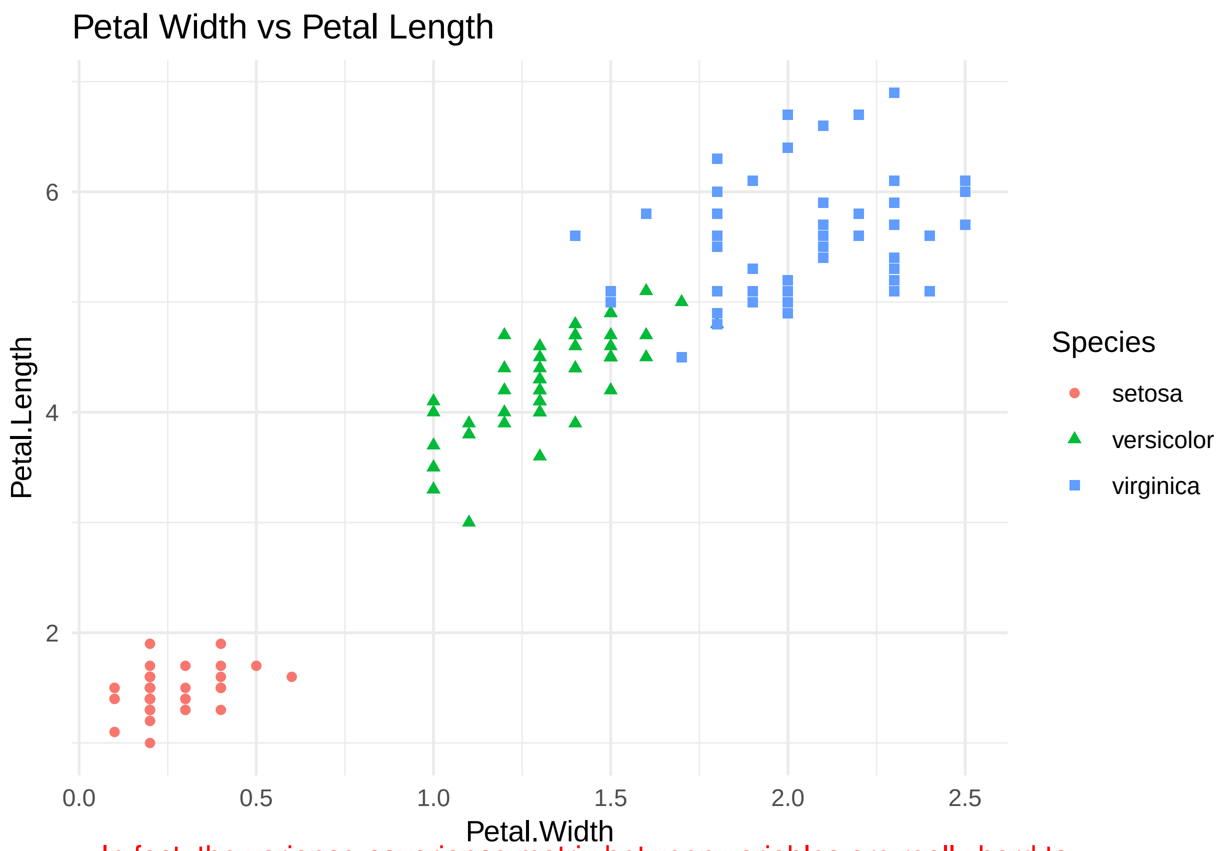
```
str(iris)
```

```
## 'data.frame':    150 obs. of  5 variables:
##  $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
##  $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
##  $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

```
ggplot(data=iris,aes(x=Sepal.Width, y=Sepal.Length)) +
    geom_point(aes(color=Species, shape=Species)) +
    ggtitle("Sepal Width vs Sepal Length") +
    theme_minimal()
```



```
ggplot(data=iris,aes(x=Petal.Width, y=Petal.Length)) +
    geom_point(aes(color=Species, shape=Species)) +
    ggtitle("Petal Width vs Petal Length") +
    theme_minimal()
```



In fact, the variance-covariance matrix between variables are really hard to evaluate graphically. So no direct conclusion can be generated at this point.

### 1.2.2 Method 1: Recycle Pre-defined Functions in Q1

The major reason that we implement Box's M Test with functional programming is the ability to recycle and reuse them! Here we only need to separate the data frame and treat them as inputs of the function `M.test()`.

```
versicolor <- iris %>%
    filter(Species=="versicolor") %>%
    dplyr::select(-"Species")
setosa <- iris %>%
    filter(Species=="setosa") %>%
    dplyr::select(-"Species")
virginica <- iris %>%
    filter(Species=="virginica") %>%
    dplyr::select(-"Species")
n1 <- nrow(versicolor)
n2 <- nrow(setosa)
n3 <- nrow(virginica)
n <- nrow(iris)

S1 <- cov(versicolor)
S2 <- cov(setosa)
S3 <- cov(virginica)
```

In this question, we are dealing with two null hypotheses. We do nothing but plug in the values respectively. as requested

Firstly, we test H_0: Sigma_1 = Sigma_2

```
M.test(4,2,c(n1,n2),list(S1,S2),summary=T)
```

```
## u = 0.04387755
##  M = 69.87649
##  C = 66.81048
##  chi-sq with 10 degrees of freedom is 3.940299
##  reject null hypothesis: TRUE
```

The result of this comparison is obvious, we reject H_0.

```
## [1] 66.810481  3.940299
```

Reject the null hypothesis. For the second part, we test H_0: S1=S2=S3.

```
M.test(4,3,c(n1,n2,n3),list(S1,S2,S3),summary=T)
```

```
## u = 0.03900227
##  M = 146.6632
##  C = 140.943
##  chi-sq with 20 degrees of freedom is 10.85081
##  reject null hypothesis: TRUE
```

```
## [1] 140.94305  10.85081
```

Again, reject the null hypothesis. we reject

### 1.2.3 Method 2: Use heplots Package

Alternatively, for this particular question, [insert link of package]

Or here, we could directly use `boxM()` function in Michael Friendly's `heplots` package, which is a package mainly focuses on visualizing hypothesis tests in multivariate linear models.

What we need to do here is to firstly eliminte `virginica` species and drop the level along our data pipeline, and do a hypothesis test for $\Sigma_1 = \Sigma_2$. After that, we would repeat for testing $\Sigma_1 = \Sigma_2 = \Sigma_3$.

The results are pretty neat:

```
~~#####################################################~~
~~# Use Michael Friendly's `heplots` package directly:#~~
~~#####################################################~~

iris2 <- iris %>%
    filter(Species!="virginica") %>%
    droplevels()
res2 <- boxM(iris2[, 1:4], iris2[, "Species"])
res2
```

```
##
##  Box's M-test for Homogeneity of Covariance Matrices
##
## data:  iris2[, 1:4]
## Chi-Sq (approx.) = 66.81, df = 10, p-value = 1.823e-10
```

```
summary(res2)
```

```
## Summary for Box's M-test of Equality of Covariance Matrices
##
## Chi-Sq:   66.81048
## df:   10
## p-value: 1.823e-10
##
## log of Covariance determinants:
##     setosa versicolor     pooled
##  -13.06736  -10.87433  -11.25782
##
## Eigenvalues:
##        setosa  versicolor     pooled
## 1 0.236455690 0.487873944 0.32938906
## 2 0.036918732 0.072384096 0.07721833
## 3 0.026796399 0.054776085 0.05032393
## 4 0.009033261 0.009790365 0.01008296
```

```
##
## Statistics based on eigenvalues:
##                 setosa   versicolor       pooled
## product   2.113088e-06 1.893828e-05 1.290601e-05
## sum       3.092041e-01 6.248245e-01 4.670143e-01
## precision 5.576122e-03 7.338788e-03 7.405502e-03
## max       2.364557e-01 4.878739e-01 3.293891e-01
```

```r
res3 <- boxM(iris[, 1:4], iris[, "Species"])
res3
```

```
##
##  Box's M-test for Homogeneity of Covariance Matrices
##
## data:  iris[, 1:4]
## Chi-Sq (approx.) = 140.94, df = 20, p-value < 2.2e-16
```

```r
summary(res3)
```

```
## Summary for Box's M-test of Equality of Covariance Matrices
##
## Chi-Sq:   140.943
## df:   20
## p-value: < 2.2e-16
##
## log of Covariance determinants:
##     setosa versicolor  virginica     pooled
## -13.067360 -10.874325  -8.927058  -9.958539
##
## Eigenvalues:
##        setosa  versicolor  virginica     pooled
## 1 0.236455690 0.487873944 0.69525484 0.44356592
## 2 0.036918732 0.072384096 0.10655123 0.08618331
## 3 0.026796399 0.054776085 0.05229543 0.05535235
## 4 0.009033261 0.009790365 0.03426585 0.02236372
##
## Statistics based on eigenvalues:
##                 setosa   versicolor    virginica       pooled
## product   2.113088e-06 1.893828e-05 0.0001327479 4.732183e-05
## sum       3.092041e-01 6.248245e-01 0.8883673469 6.074653e-01
## precision 5.576122e-03 7.338788e-03 0.0169121236 1.304819e-02
## max       2.364557e-01 4.878739e-01 0.6952548382 4.435659e-01
```

The results are identical to our "home-brewed" version.

there is nothing extra we need to emphasize, the results are …

## 1.3 Q3 what could go wrong with box's chisel approximation?

In this problem, we fix the parameter $g$ to be 2 and $p$ changes from 5 to 20 as requested. Since the problem itself does not mention how $n_l$'s behave, we also fix them to be $n_1 = n_2 = 25 > 20$. For each value of $p$, we iterate to resample data for $sim = 1000$ times.

In addition, my personal preference for monitoring complex for-loops is to add a timer keeping track of how long it takes. This will be repeated several times in the next few questions.

```
sim <- 1000
fixed.g <- 2
p.vec <- c(5:15)
n1 <- 25
n2 <- 25

table <- data.frame()

timer <- Sys.time()
for (iter in 1:length(p.vec)) {
    p <- p.vec[iter]

    for (s in 1:sim) {
        X1 <- matrix(rnorm(p*n1),n1,p)
        X2 <- matrix(rnorm(p*n2,mean=0,sd=1),n2,p)
        X2.prime <- matrix(rnorm(p*n2,mean=0,sd=1.5),n2,p)
        S1 <- cov(X1)
        S2 <- cov(X2)
        S2.prime <- cov(X2.prime)

        table <- rbind(table,c(p,M.test(p,fixed.g,c(n1,n2),list(S1,S2)),1))
        table <- rbind(table,c(p,M.test(p,fixed.g,c(n1,n2),list(S1,S2.prime)),2))
    }
}

Sys.time()-timer
```

```
## Time difference of 19.42585 secs
```

```
names(table) <- c("p","TS","chisq","type")

large.summary <- data.frame()
for (pv in p.vec) {
    nu <- 0.5*pv*(pv+1)*(fixed.g-1)

    table.size <- table %>%
        filter(p==pv,type==1)
    table.power <- table %>%
        filter(p==pv,type==2)

    pv.size <- mean(table.size$TS>qchisq(.05,nu,lower.tail=F))
    pv.power <- mean(table.power$TS>qchisq(.05,nu,lower.tail=F))
    large.summary <- rbind(large.summary, c(n1, n2, pv, fixed.g, pv.size, pv.power))
}
names(large.summary) <- c("n1","n2","p","g","size", "power")
```

Here we take a look at the table.

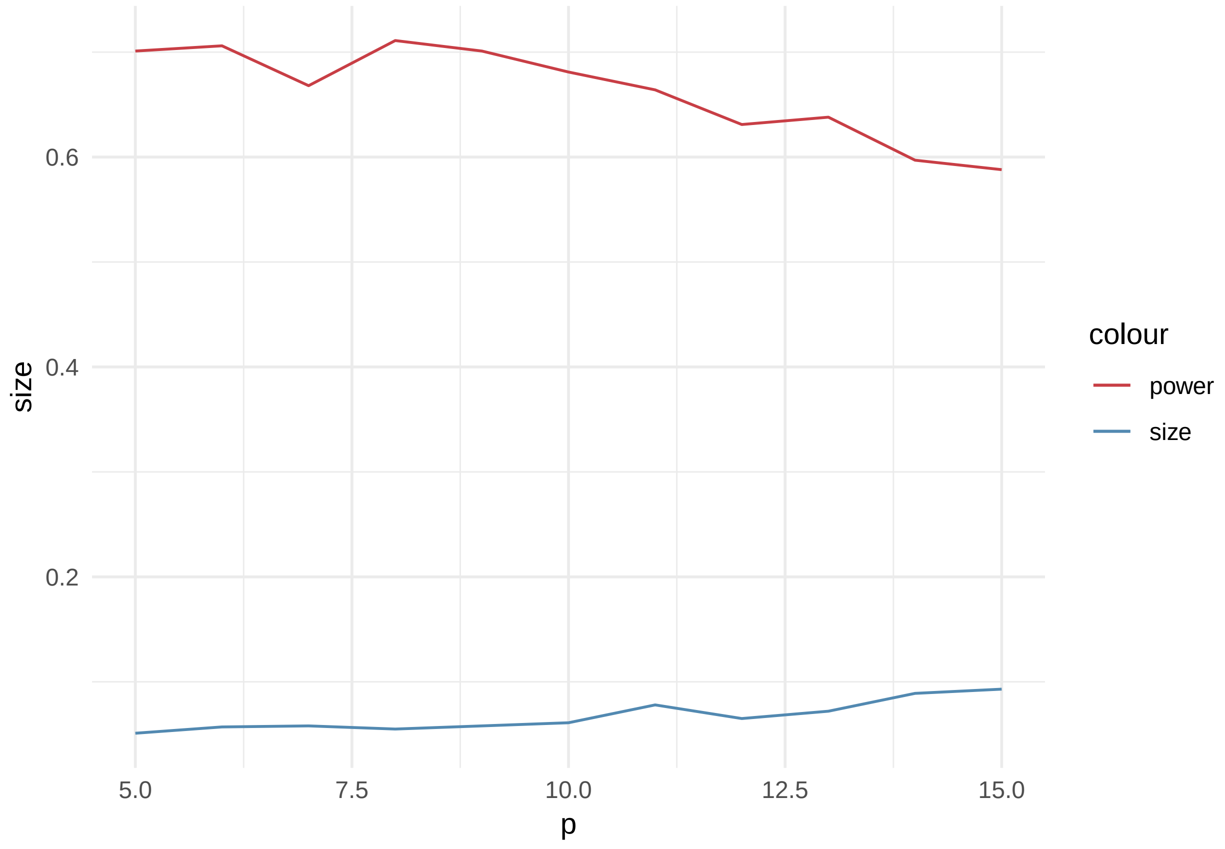
```
large.summary
```

```
##    n1 n2  p g  size power
## 1  25 25  5 2 0.051 0.701
## 2  25 25  6 2 0.057 0.706
## 3  25 25  7 2 0.058 0.668
## 4  25 25  8 2 0.055 0.711
## 5  25 25  9 2 0.058 0.701
## 6  25 25 10 2 0.061 0.681
## 7  25 25 11 2 0.078 0.664
## 8  25 25 12 2 0.065 0.631
## 9  25 25 13 2 0.072 0.638
## 10 25 25 14 2 0.089 0.597
## 11 25 25 15 2 0.093 0.588
```

Better with a visualization of the line plot.

To understand the performance of simulations, it is better to visualize the size and power changes as a line plot.

```
ggplot(large.summary, aes(x=p)) +
    geom_line(aes(y=size,color="size")) +
    geom_line(aes(y=power,color="power")) +
    scale_colour_manual(values=c("#C83E45", "#5289B1")) +
    theme_minimal()
```



One thing noticable is that, since we have set $n_1 = n_2 = 20$ which are definitely not large enough to be called “infinitely large”, our number of parameters $p$ soon catache s up with $n_1$ and $n_2$.

But how badly this performs? The power has a weak start with a value around 0.7 and gradually decreases to a more unpleasant range. On the other hand, the size is generally stable but not always significant ($< .05$). Overall, we would suggest that the Box’s $\chi^2$ approximation performs poorly when $p > 5$ while holding $g$ fixed below 5.

## Q4

### 1.4 Testing Covariance Matrices WITHOUT adjustment

Besides the required dimension p = 5, 10, 50, 100, 300, we add an additional 375 for comparison.

```r
n <- 500
p.vec <- c(5, 10, 50, 100, 300, 375)
N <- n - 1
sim <- 1000

table <- data.frame()

timer <- Sys.time()

for (i in 1:length(p.vec)) {
    p <- p.vec[i]
    mu <- rep(0, p)
    Sigma <- diag(p)
    Sigma2 <- diag(.05,p)
    Sigma2[1,1] <- 1

    for (s in 1:sim) {
        X <- rmvnorm(n, mu, Sigma)
        S <- cov(X)

        rho <- 1-(2*p**2+3*p-1)/(6*(n-1)*(p+1))
        ts <- -2*rho*(0.5*p*N + (0.5*N) *
                          (unlist(determinant(S,logarithm=T))[[1]]-sum(diag(S))))

        X2 <- rmvnorm(n, mu, Sigma2)
        S2 <- cov(X2)
        ts2 <- -2*rho*(0.5*p*N + (0.5*N) *
                           (unlist(determinant(S2,logarithm=T))[[1]]-sum(diag(S2))))

        table <- rbind(table,c(p,ts,1))
        table <- rbind(table,c(p,ts2,2))
    }
}

Sys.time()-timer
```

```
## Time difference of 12.51302 mins
```

```r
names(table) <- c("p","ts","type")

large.summary <- data.frame()
for (pv in p.vec) {
    table.size <- table %>%
        filter(p==pv,type==1)
    table.power <- table %>%
        filter(p==pv,type==2)

    f <- 0.5*pv*(pv+1)
    gamma2 <- pv*(2*pv**4+6*pv**3+pv**2-12*pv-13)/(288*(pv+1))
    rho <- 1-(2*pv**2+3*pv-1)/(6*(n-1)*(pv+1))

    pv.size <- mean(table.size$ts>(
        qchisq(.95,f)+gamma2/rho**2/N**2*(qchisq(.95,f+4)-qchisq(.95,f))))
    pv.power <- mean(table.power$ts>(
        qchisq(.95,f)+gamma2/rho**2/N**2*(qchisq(.95,f+4)-qchisq(.95,f))))
    large.summary <- rbind(large.summary, c(pv, pv.size, pv.power))
}
names(large.summary) <- c("p", "size", "power")
```

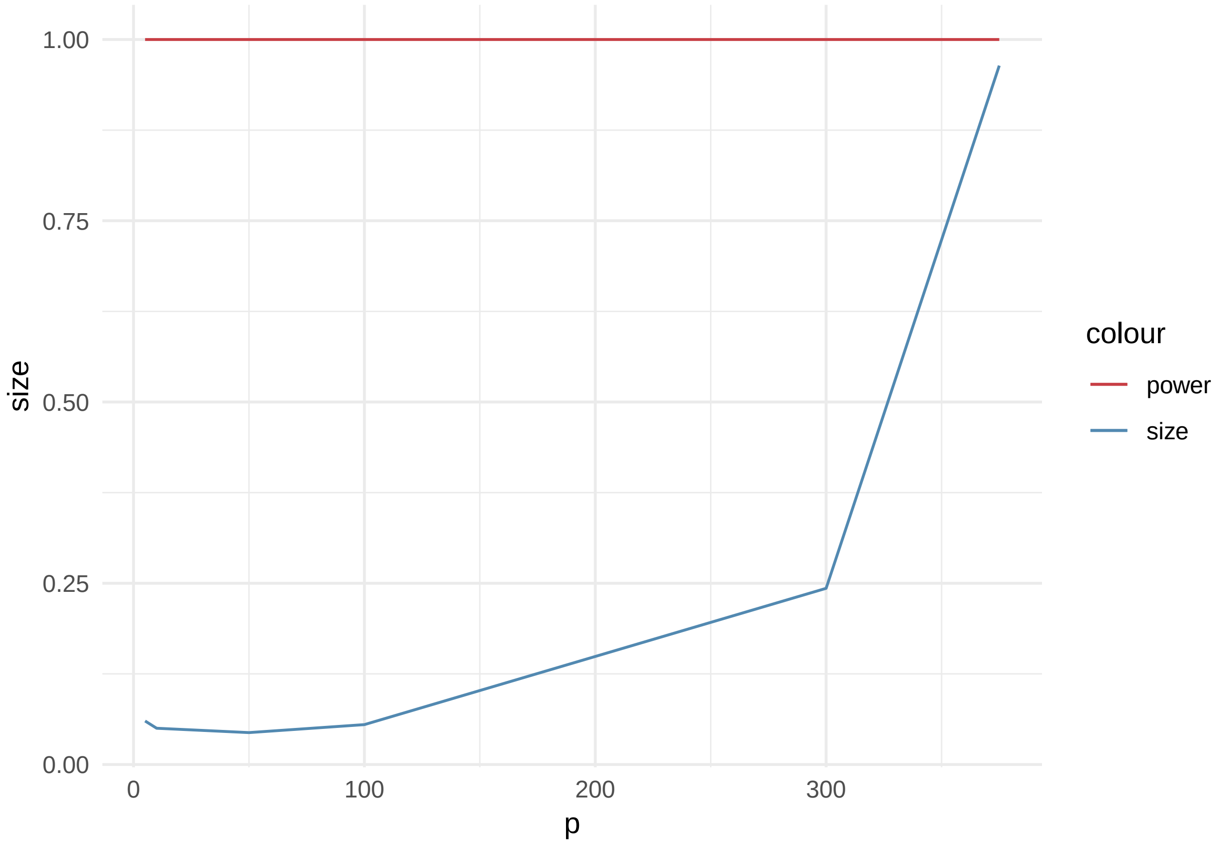
Summary:

```
large.summary
```

```
##     p  size power
## 1   5 0.060     1
## 2  10 0.050     1
## 3  50 0.044     1
## 4 100 0.055     1
## 5 300 0.243     1
## 6 375 0.964     1
```

Viz:

```
ggplot(large.summary, aes(x=p)) +
    geom_line(aes(y=size,color="size")) +
    geom_line(aes(y=power,color="power")) +
    scale_colour_manual(values=c("#C83E45", "#5289B1")) +
    theme_minimal()
```



The power is good. And the size is good at the beginning, but when $n$ gets really large, size tends to 1.

Note that our sample size is 500 which is not a small number, so when dimension $p$ gets large, modern RMT indicates that the likelihood ratio statistic drifts to infinity almost surely. Therefore, the classicial $\chi^2$ approximation may lead us to many false rejections of $H_0$ in case of high-dimensional data. (TODO: add footnotes)

add Bai Jiang Yao Zheng 2009

## 1.5 Q5 A Proof

TODO:

**Proof:**

$$\begin{aligned}
T_1 &= \text{tr}\mathbb{S} - \log|\mathbb{S}| - p \\
&= p \cdot F^{\mathbb{S}}(f) \\
&= p \cdot \int (x - \log x - 1) dF^{y_N}(x) \\
&= p \cdot \int f(x) d(F^{\mathbb{S}}(x) - F^{y_N}(x)) + p \cdot F^{y_N}(f)
\end{aligned}$$

Since $N = n-1, y_N = p/N$:

$$\begin{aligned}
F^{y_N}(f) &= 1 - \frac{y_N - 1}{y_N} \log(1 - y_N) \\
&\doteq 1 - \frac{y-1}{y} \log(1-y) \\
&= 1 + \frac{1-y}{y} \log(y-1) \\
&= d_1(y)
\end{aligned}$$

By Theorem in lecture notes,

$$T_1 - p \cdot F^{y_N}(f) \doteq T_1 - p \cdot d_1(y_N)$$

should weakly converges to a Gaussian vector with the mean

$$\mu_1 = -\frac{1}{2} \log(1-y),$$

and variance

$$\sigma_1^2 = -2\log(1-y) - 2y.$$

Testing Covariance Matrices WITH adjustment

## 1.6 Q6

This question is a refined version of Q4, an improvement has been made based on Q5 theoretically.

Note that we include a case with $p = 375$ for consistency as well.

```
n <- 500
p.vec <- c(5, 10, 50, 100, 300, 375)
N <- n - 1
sim <- 1000

table <- data.frame()

timer <- Sys.time()

for (i in 1:length(p.vec)) {
    p <- p.vec[i]
    mu <- rep(0, p)
    Sigma <- diag(p)
    Sigma2 <- diag(.05,p)
    Sigma2[1,1] <- 1

    for (s in 1:sim) {
        y <- p/n
        YN <- p/N
        d1 <- 1+(1-YN)/YN*log(1-YN)

        X <- rmvnorm(n, mu, Sigma)
        S <- cov(X)
        T1 <- sum(diag(S))-unlist(determinant(S,logarithm=T))[[1]]-p

        ts <- T1-p*d1

        X2 <- rmvnorm(n, mu, Sigma2)
        S2 <- cov(X2)
        T1.2 <- sum(diag(S2))-unlist(determinant(S2,logarithm=T))[[1]]-p

        ts.2 <- T1.2-p*d1

        table <- rbind(table,c(p,ts,1))
        table <- rbind(table,c(p,ts.2,2))
    }
}

Sys.time()-timer
```

```
## Time difference of 12.62086 mins
```

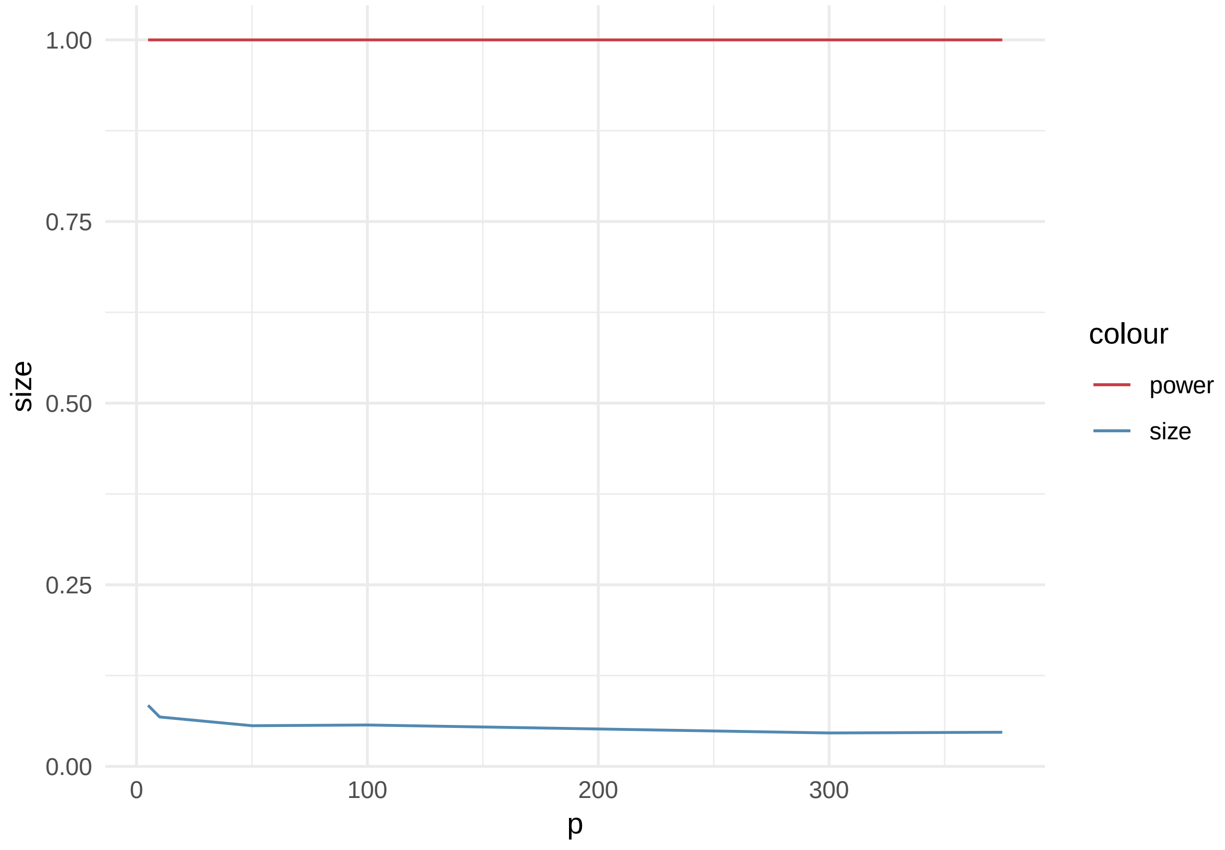
```
names(table) <- c("p","ts","type")

large.summary <- data.frame()

for (pv in p.vec) {
    y <- pv/n
    mu1 <- -0.5*log(1-y)
    sigma1 <- sqrt(-2*log(1-y)-2*y)

    table.size <- table %>%
        filter(p==pv,type==1)
    table.power <- table %>%
        filter(p==pv,type==2)
    pv.size <- mean(table.size$ts>qnorm(.95,mu1,sigma1))
    pv.power <- mean(table.power$ts>qnorm(.95,mu1,sigma1))
    large.summary <- rbind(large.summary, c(pv, pv.size, pv.power))
}
names(large.summary) <- c("p", "size", "power")
```

Check out the table again:

```
large.summary
```

```
##     p  size power
## 1   5 0.084     1
## 2  10 0.068     1
## 3  50 0.056     1
## 4 100 0.057     1
## 5 300 0.046     1
## 6 375 0.047     1
```

```
ggplot(large.summary, aes(x=p)) +
    geom_line(aes(y=size,color="size")) +
    geom_line(aes(y=power,color="power")) +
    scale_colour_manual(values=c("#C83E45", "#5289B1")) +
    theme_minimal()
```



This time, the size converges to 0.05 as expected, which in comparison, is of course an improvement from Q4.

# 2. Part 2 Multivariate Time Series

## 2.1 Q7 MTS Basics

### 2.1.1 7.(a)(b)(c)(d) MTS Generation and Visualization

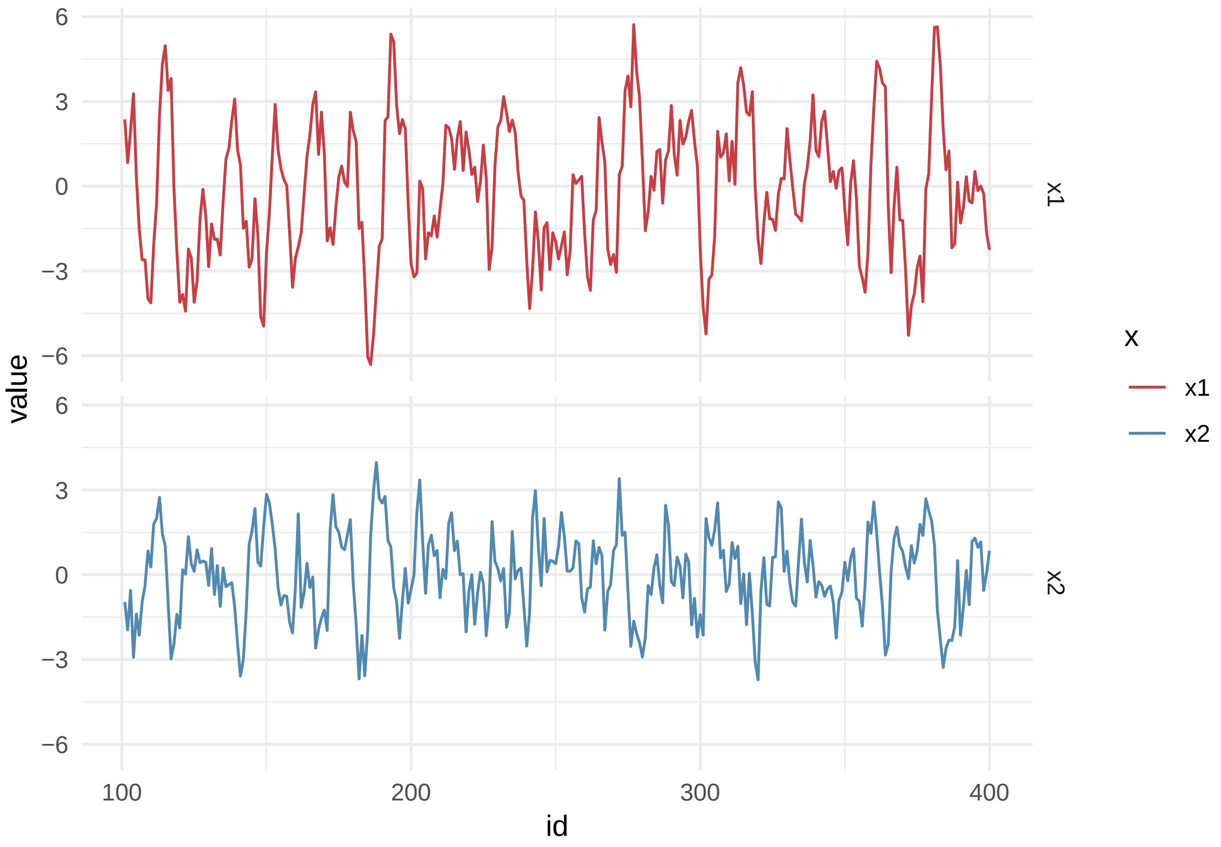
For this question, my multivariate first order VAR/VMA model generating function might seem a little bit complex due to the introduction of multiple “flag” arguments. To be specific,

- `viz` controls if a time series plot is needed in the output.
- `lag` controls the upper limit of $\tau$.
- `add.S0` controls if a lag-0 autocovariance matrix is added to the “correlation matrix list”, since it is also required for the portmanteau test.
- `burnin` is the number of discarded observations. By default, we include the first 100 observations as burn-ins. For example, if the required observation number is 300, we generate 300+100 such observations and discard the first 100 accordingly.
- `type` is set to be `lag` by default for part (a), (b), (c) and (d). In this case, we are storing observations into the data frame `df`. But if it is set to be `qm`, i.e. when we conduct a portmanteau test, we are operating on residuals of observations, so that the data frame `df` will be assigned with residuals instead.

```r
mts.gen.1 <- function(matrix.A, matrix.Sig, obs, method, viz=T, lag=0,
                      add.S0=F, burnin=100, type="lag") {
    df <- data.frame()
    if (method=="var") {
        epsilons <- rmvnorm((obs+burnin), c(0,0), matrix.Sig)
        Xt <- c(0,0)
        for (t in 1:(obs+burnin)) {
            Xt <- matrix.A%*%Xt + epsilons[t,]
            df <- rbind(df, c(Xt))
        }
        df <- df[(1+burnin):(obs+burnin),]
    } else if (method=="vma" || method=="ma") {
        epsilons <- rmvnorm(obs+burnin+1,c(0,0),matrix.Sig)
        for (t in 1:(obs+burnin)) {
            Xt <- epsilons[t+1,] + matrix.A%*%epsilons[t,]
            df <- rbind(df, c(Xt))
        }
        df <- df[(1+burnin):(obs+burnin),]
    }
    names(df) <- c("x1","x2")
    df$id <- (1+burnin):(obs+burnin)
    df2 <- melt(df, id.var = "id", variable.name = "x")
    if (viz) {
        print(ggplot(df2,aes(x=id,y=value)) +
                  geom_line(aes(color=x)) +
                  facet_grid(x ~ .) +
                  scale_colour_manual(values=c("#C83E45", "#5289B1")) +
                  theme_minimal())
    }
    if (lag>0) {
        if (type=="qm") {
            # if we conduct a portmanteau test on residuals,
            # reassign the residual df to current variable df
            mod <- VAR(df,p=1,lag.max=20)
            df <- as.data.frame(cbind(mod$varresult$x1$residuals,mod$varresult$x2$residuals))
            names(df) <- c("x1","x2")
        }
        rho.tau <- list()
        X.bar <- c(mean(df$x1), mean(df$x2))
        S0 <- cov(df[,1:2])
        D <- diag(1/sqrt(diag(S0)))

        # also record lag-0 autocovariance matrix, need to be used when doing portmanteau test
        if (add.S0) {
            rho.tau[[lag+1]] <- cov2cor(S0)  # the same as D %*% S0 %*% D
        }

        for (tau in 1:lag) {
            Stau <- 0
            for (t in (tau+1):nrow(df)) {
                Stau <- Stau + (c(df$x1[t], df$x2[t]) - X.bar) %*%
                    t(c(df$x1[t-tau],df$x2[t-tau]) - X.bar)
            }
            Stau <- Stau / (nrow(df)-1)
            rho.tau[[tau]] <- D %*% Stau %*% D
        }
        return(rho.tau)
    }
}

## (a) & (b) & (c) & (d)
A <- matrix(c(0.8,0.4,-0.3,0.6),byrow = T,ncol=2)
Sigma <- matrix(c(2,0.5,0.5,1),byrow = T,ncol=2)
```

Part (a) and (b) with time series visualization and its lag-5 correlation matrices.

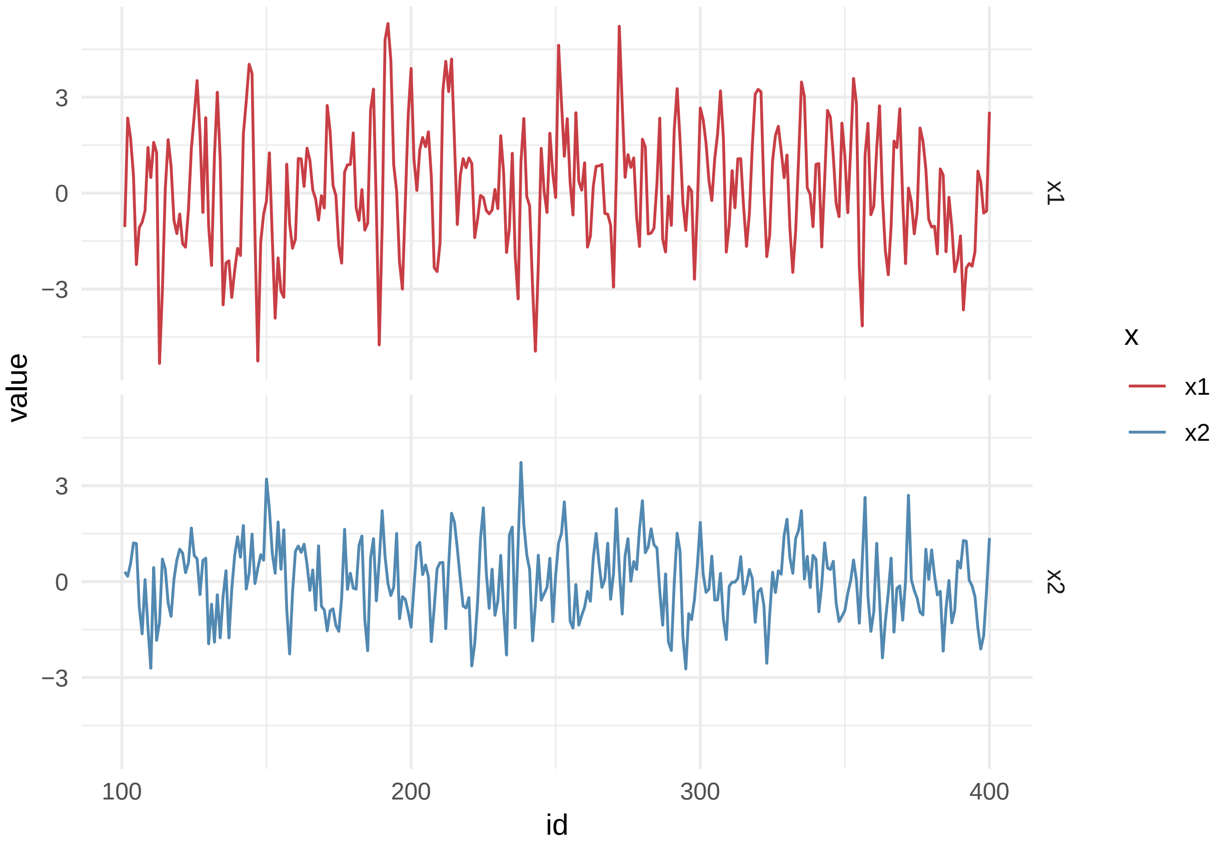
```
mts.gen.1(A, Sigma, 300, "var", viz=T, lag=5, add.S0=F, burnin=100, type="lag")
```



```
## [[1]]
##            [,1]      [,2]
## [1,]  0.7859249 0.1526886
## [2,] -0.4931342 0.6202365
##
## [[2]]
##            [,1]      [,2]
## [1,]  0.5184852 0.2744502
## [2,] -0.6265335 0.3241870
##
## [[3]]
##            [,1]      [,2]
## [1,]  0.2670795 0.3394800
## [2,] -0.6097292 0.1038583
##
## [[4]]
##             [,1]        [,2]
## [1,]  0.02212521  0.34494099
## [2,] -0.51048627 -0.06452215
##
## [[5]]
##            [,1]       [,2]
## [1,] -0.1600059  0.2918388
## [2,] -0.3385234 -0.2013264
```

Part (c) and (d) with time series visualization and its lag-2 correlation matrices.

```
mts.gen.1(A, Sigma, 300, "vma", viz=T, lag=2, add.S0=F, burnin=100, type="lag")
```



```
## [[1]]
##            [,1]      [,2]
## [1,]  0.4739894 0.2453092
## [2,] -0.2099934 0.3844573
##
## [[2]]
##             [,1]        [,2]
## [1,] -0.07149522 -0.09460774
## [2,] -0.04072408  0.01342928
```

### 2.1.2 7.(e) Q7(e) Replication

add reference link.

In this question, all parameters are set to be the values used in the paper (TODO)

```
A <- matrix(c(-.2, .3, -.6, 1.1), byrow = T, ncol=2)
B <- matrix(c(.4, .1, -1, .5), byrow = T, ncol=2)
C <- matrix(c(-1.5, 1.2, -.9, .5), byrow = T, ncol=2)
k <- 2 # 2 by 2 matrices
m <- 20
n <- 200
sim <- 1000

alpha.vec <- c(.25, -.25, .5, -.5, .75, -.75)

Delta.matrix <- function(alpha.value) {
    return(matrix(c(1, alpha.value, alpha.value, 1), byrow = T, ncol=2))
}

# kronecker(), vec()

inside.Qm <- function(rhol,rho0) {
    temp <- t(vec(t(rhol))) %*% kronecker(solve(rho0), solve(rho0)) %*% vec(t(rhol))
    return(unlist(temp)[[1]])
}

summary.table <- data.frame()

timer <- Sys.time()

for (i in 1:sim) {
    for (alpha in alpha.vec) {
        delta.matrix <- Delta.matrix(alpha)
        rho1 <- mts.gen.1(A, delta.matrix, n, "var", viz=F, lag=m, add.S0=T, type="qm")
        rho2 <- mts.gen.1(B, delta.matrix, n, "var", viz=F, lag=m, add.S0=T, type="qm")
        rho3 <- mts.gen.1(C, delta.matrix, n, "var", viz=F, lag=m, add.S0=T, type="qm")
        QA <- 0
        QB <- 0
        QC <- 0
        for (j in 1:m) {
            QA <- QA + inside.Qm(rho1[[j]], rho1[[m+1]])
            QB <- QB + inside.Qm(rho2[[j]], rho2[[m+1]])
            QC <- QC + inside.Qm(rho3[[j]], rho3[[m+1]])
        }
        QA <- n * QA
        QAs <- QA + k**2*m*(m+1)/(2*n)
        QB <- n * QB
        QBs <- QB + k**2*m*(m+1)/(2*n)
        QC <- n * QC
        QCs <- QC + k**2*m*(m+1)/(2*n)
        summary.table <- rbind(summary.table,
```

```r
                                c(alpha, QA, QAs, QB, QBs, QC, QCs))
    }
}
Sys.time() - timer
```

```
## Time difference of 35.70703 mins
```

```r
names(summary.table) <- c("alpha", "QA", "QAs", "QB", "QBs", "QC", "QCs")

critical <- qchisq(.05,76,lower.tail = F)  # k^2(m-p-q) = 4 * (20 - 1 - 0) = 76

summary.table %>%
    mutate(QA = QA>critical,
           QAs = QAs>critical,
           QB = QB>critical,
           QBs = QBs>critical,
           QC = QC>critical,
           QCs = QCs>critical) %>%
    group_by(alpha) %>%
    summarize(
        A.Q20 = sum(QA),
        A.Q20.star = sum(QAs),
        B.Q20 = sum(QB),
        B.Q20.star = sum(QBs),
        C.Q20 = sum(QC),
        C.Q20.star = sum(QCs)
    )
```

```
## # A tibble: 6 x 7
##   alpha A.Q20 A.Q20.star B.Q20 B.Q20.star C.Q20 C.Q20.star
##   <dbl> <int>      <int> <int>      <int> <int>      <int>
## 1 -0.75    30         47    23         41    29         49
## 2 -0.5     26         59    30         54    28         58
## 3 -0.25    26         45    26         54    28         49
## 4  0.25    28         58    19         41    27         49
## 5  0.5     31         52    21         42    33         55
## 6  0.75    23         53    23         46    32         60
```

NOTE 1: The original table in paper (TODO: 1981) might have a serious typo, where "per cent" should actually be "count". Consider a test with typo 1 error about 50%. Since the simulation run has a valeu of 1000 instead of 100, I guess this in fact is the "count", which also explains why $Q_m^*$ is better in the perspective of "closer to 0.05".

NOTE 2: The difference between our simulation and the original table might originate from the fact that we discard 100 observations in the implented function as burnin, while the paper didn't specifies their approach or their particular parameter.

Note 3: 30 minutes runtime, still have space for optimization.

### 2.1.3 7.(f) Q7(f) An Experiment on Federal Debts Data.

The two authors of package `portes` are… also… function oo good.

```r
debt <- read.table("q-fdebt.txt",header = T) %>%
    dplyr::select(hbfin, hbfrbn, hbpun) %>%
    mutate(hbfin = log(hbfin), hbfrbn = log(hbfrbn), hbpun = log(hbpun))
debt <- as.matrix(debt)
DiffData <- matrix(numeric(ncol(debt) * (nrow(debt)-1)), ncol = ncol(debt))
for (i in 1:ncol(debt)) DiffData[, i] <- diff(debt[, i], lag = 1)
Fit <- ar.ols(DiffData, aic=F, order.max = 1)

# theoretical
LiMcLeod(Fit, lags=1:10)
```

transformation, just taking the difference

insert there are two versions, theoretical with… or monte carlo simulation with portes

```
##   lags  statistic df      p-value
##      1   7.161042  0 0.000000e+00
##      2  18.339335  9 3.143462e-02
##      3  36.555260 18 5.985399e-03
##      4 111.935815 27 2.609801e-12
##      5 137.487311 36 8.859580e-14
##      6 144.074991 45 2.663314e-12
##      7 153.214982 54 1.954914e-11
##      8 201.506096 63 2.220446e-16
##      9 213.347314 72 6.661338e-16
##     10 220.915081 81 6.550316e-15
```

```
# Monte Carlo version
portest(Fit, lags=1:10, test="LiMcLeod", ncores=4)
```

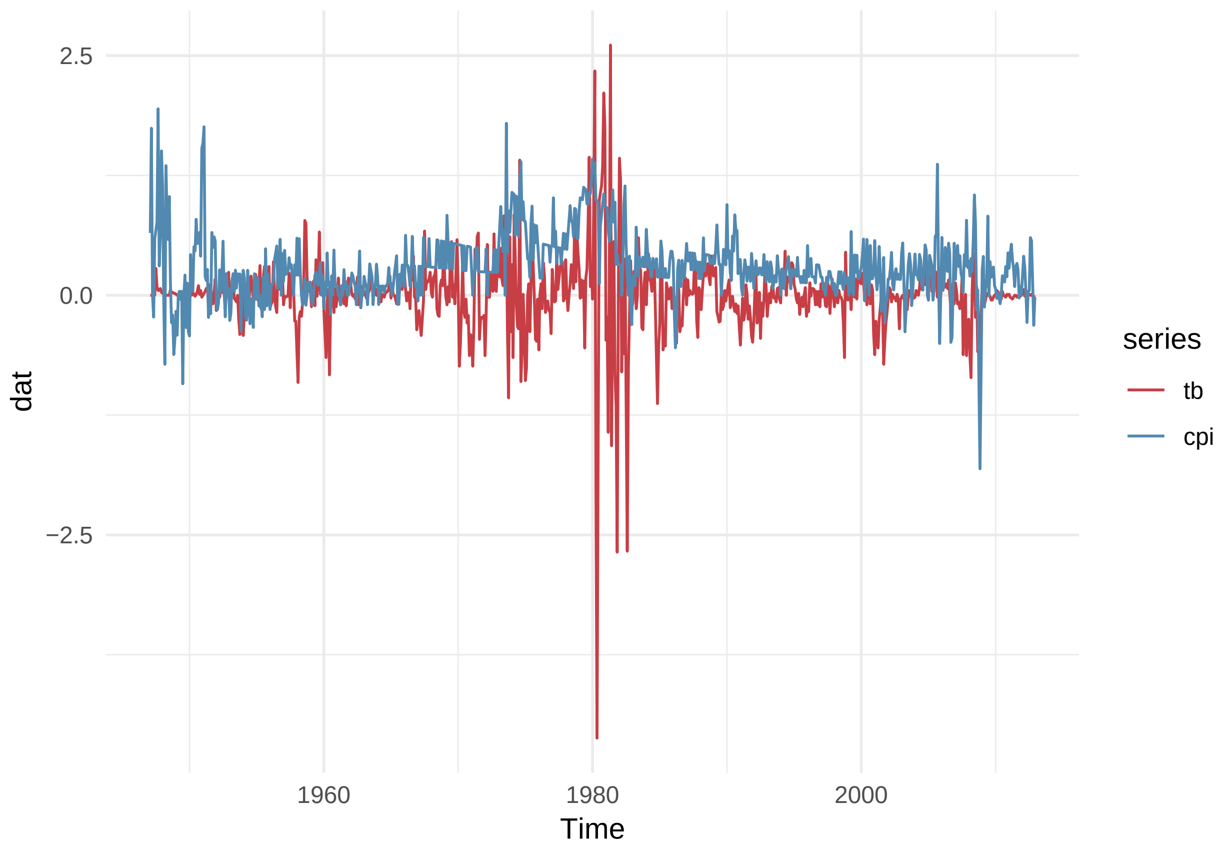
```
##   lags  statistic     p-value
##      1   7.161042 0.003996004
##      2  18.339335 0.038961039
##      3  36.555260 0.003996004
##      4 111.935815 0.000999001
##      5 137.487311 0.000999001
##      6 144.074991 0.000999001
##      7 153.214982 0.000999001
##      8 201.506096 0.000999001
##      9 213.347314 0.000999001
##     10 220.915081 0.000999001
```

2.2 **Q8** VAR model order selection on CPI data

aka plotting CPI data

2.2.1 **(a)** unlike Q7 part f, here we take more complex transformation on CPI index, so that the CPI rate is ======

```
dat <- read.table("m-cpitb3m.txt",header = T) %>%
    dplyr::select(tb=tb3m, cpi=cpiaucsl) %>%
    mutate(cpi=100*log(cpi))

dat <- diff(ts(dat,frequency = 12,start = c(1947,1)))

autoplot(dat) +
    scale_colour_manual(values=c("#C83E45", "#5289B1")) +
    theme_minimal()
```



2.2.2 **(b)** The selection algorithm inconsistency in notation

modified the VARorder function in MTS library. Actually I simplified it by removing the order selection criteria like AIC, BIC, only keeping the Barlet test statistic and calculated p-value. And implement my own version of m selection.

```
# library(MTS)
# MTS::VARorder(dat,maxp=10)


VARorder2 <- function (x, P = 10) {
    x1 <- as.matrix(x)
    T <- nrow(x1)
    k <- ncol(x1)
    if (P < 1) {P = 1}
    obs = T - P
    y = x1[(P + 1):T, , drop = FALSE]
    ist = P + 1
    xmtx = cbind(rep(1, obs), x1[P:(T - 1), ])
    if (P > 1) {
        for (i in 2:P) {
            xmtx = cbind(xmtx, x1[(ist - i):(T - i), ])
        }
    }
    chidet = rep(0, (P + 1))
    s = cov(y) * (obs - 1)/obs
    chidet[1] = log(det(s))
    y = as.matrix(y)
    for (l in 1:P) {
        idm = k * l + 1
        xm = xmtx[, 1:idm]
        xm = as.matrix(xm)
        xpx <- crossprod(xm, xm)
        xpy <- crossprod(xm, y)
        beta <- solve(xpx, xpy)
        yhat <- xm %*% beta
        resi <- y - yhat
        sse <- crossprod(resi, resi)/obs
        d1 = log(det(sse))
        chidet[l + 1] = d1
    }
    Mstat = rep(0, P)
    pv = rep(0, P)
    for (j in 1:P) {
        Mstat[j] = (T - P - k * j - 1.5) * (chidet[j] - chidet[j + 1])
        pv[j] = 1 - pchisq(Mstat[j], k ** 2)
    }

    output = cbind(c(0:P), c(0, Mstat), c(0, pv))
    colnames(output) <- c("l", "M(l)", "p-value")

    # which m? i.e. starting from this l=m, the p-value of following models
    # should all be greater than 0.05

    m.output <- 1
    for (m in 1:nrow(output)) {
        if (all(output[m:nrow(output),3] >= 0.05)) {
            m.output <- m
            break()
        }
    }
    print(round(output, 3))
    cat("Select VAR (", m.output-1, ")")
}
```

insert here

```
VARorder2(dat, 50)
```

For this part of the question, we only set P=50

```
##        l    M(l) p-value
## [1,]   0   0.000   0.000
## [2,]   1 441.733   0.000
## [3,]   2  66.496   0.000
## [4,]   3   9.399   0.052
## [5,]   4  25.067   0.000
## [6,]   5  19.022   0.001
## [7,]   6  55.022   0.000
## [8,]   7  19.353   0.001
##  [9,]  8  21.604   0.000
## [10,]  9  23.523   0.000
## [11,] 10  15.876   0.003
## [12,] 11   5.698   0.223
## [13,] 12  23.276   0.000
## [14,] 13  13.020   0.011
## [15,] 14   8.099   0.088
## [16,] 15  19.250   0.001
## [17,] 16  13.831   0.008
## [18,] 17   5.467   0.243
## [19,] 18   2.474   0.649
## [20,] 19  13.430   0.009
## [21,] 20  11.943   0.018
## [22,] 21   2.940   0.568
## [23,] 22   1.783   0.776
## [24,] 23   3.090   0.543
## [25,] 24  12.153   0.016
## [26,] 25   8.388   0.078
## [27,] 26   4.946   0.293
## [28,] 27   1.894   0.755
## [29,] 28   1.726   0.786
## [30,] 29   8.431   0.077
## [31,] 30   0.724   0.948
## [32,] 31  10.173   0.038
## [33,] 32   1.822   0.768
## [34,] 33   0.308   0.989
## [35,] 34   0.291   0.990
## [36,] 35   5.653   0.227
## [37,] 36   2.444   0.655
## [38,] 37   0.444   0.979
## [39,] 38   0.866   0.929
## [40,] 39   6.145   0.189
## [41,] 40   6.934   0.139
## [42,] 41   0.881   0.927
## [43,] 42   0.892   0.926
## [44,] 43   4.728   0.316
## [45,] 44   0.774   0.942
## [46,] 45   8.692   0.069
## [47,] 46   2.158   0.707
## [48,] 47   2.106   0.716
## [49,] 48   3.445   0.486
## [50,] 49   3.054   0.549
## [51,] 50   2.979   0.561
## Select VAR ( 32 )
```

didn't run the algorithm with a bunch of different P as a simulation.

I totally understand the result model selection highly depends on the P you select. But seriously, for small P, say we have P around 10, the selected $m$ is pretty much close to P. But if P becomes large enough, m would tend to a stable value.

the curse of dimensionality

**(c)**

THE INTUITION OF THIS PART OF THE QUESTION IS

```r
library(tsDyn)
increase.dim <- function(data, p) {
    dat.p <- dat
    # dim 3 to p
    for (dim.p in 3:p) {
        dat.p <- cbind(dat.p, sample(dat[,sample(1:2, 1, prob=c(0.5,0.5))],
                                     nrow(dat), replace=T))
    }
    dim(dat.p)
    mod <- lineVar(dat.p, lag=1)
    new.mod <- VAR.boot(mod, "resample")
    VARorder2(new.mod, P=20)
}

increase.dim(dat, 10)
```

```
##        l    M(l) p-value
##   [1,]  0   0.000   0.000
##   [2,]  1 608.674   0.000
##   [3,]  2  89.173   0.773
##   [4,]  3  98.026   0.537
##   [5,]  4  80.760   0.921
##   [6,]  5  78.809   0.942
##   [7,]  6  93.331   0.668
##   [8,]  7  89.448   0.766
##   [9,]  8 110.501   0.222
##  [10,]  9 109.152   0.250
##  [11,] 10  89.639   0.762
##  [12,] 11 105.577   0.332
##  [13,] 12  89.135   0.773
##  [14,] 13 124.502   0.049
##  [15,] 14 124.377   0.050
##  [16,] 15 109.658   0.239
##  [17,] 16 101.651   0.435
##  [18,] 17  92.212   0.698
##  [19,] 18  89.250   0.771
##  [20,] 19 114.667   0.150
##  [21,] 20  86.146   0.837
## Select VAR ( 15 )
```

```
increase.dim(dat, 20)
```

```
##        l     M(l) p-value
##   [1,]  0    0.000   0.000
##   [2,]  1 1149.768   0.000
##   [3,]  2  414.855   0.294
##   [4,]  3  371.294   0.845
##   [5,]  4  436.758   0.099
##   [6,]  5  399.094   0.503
##   [7,]  6  398.796   0.508
##   [8,]  7  377.260   0.787
##   [9,]  8  422.052   0.215
##  [10,]  9  412.137   0.327
##  [11,] 10  377.474   0.785
##  [12,] 11  393.017   0.589
##  [13,] 12  390.518   0.623
##  [14,] 13  406.624   0.399
##  [15,] 14  448.810   0.046
##  [16,] 15  443.344   0.066
##  [17,] 16  389.596   0.636
##  [18,] 17  425.331   0.184
##  [19,] 18  433.851   0.117
##  [20,] 19  385.575   0.689
##  [21,] 20  385.094   0.695
## Select VAR ( 15 )
```

```
increase.dim(dat, 30)
```

```
##         l     M(l) p-value
##  [1,]  0    0.000   0.000
##  [2,]  1 2117.922   0.000
##  [3,]  2  888.507   0.601
##  [4,]  3  993.378   0.016
##  [5,]  4  818.134   0.976
##  [6,]  5  872.855   0.736
##  [7,]  6  881.030   0.668
##  [8,]  7  944.988   0.145
##  [9,]  8  813.550   0.982
## [10,]  9 1053.468   0.000
## [11,] 10  948.118   0.129
## [12,] 11  963.036   0.071
## [13,] 12  914.459   0.361
## [14,] 13  986.043   0.024
## [15,] 14  957.778   0.089
## [16,] 15  965.372   0.064
## [17,] 16  878.385   0.691
## [18,] 17  895.413   0.537
## [19,] 18  911.608   0.387
## [20,] 19  951.776   0.112
## [21,] 20  976.452   0.038
## Select VAR ( 0 )
```

```
increase.dim(dat, 40)  # computationally singular
```

```
## Error in solve.default(xpx, xpy): system is computationally singular: reciprocal condition number = 2.206
```

```
increase.dim(dat, 50)  # computationally singular
```

```
## Error in solve.default(xpx, xpy): system is computationally singular: reciprocal condition number = 1.531
```

Curse of dimensionality

reference

2.3

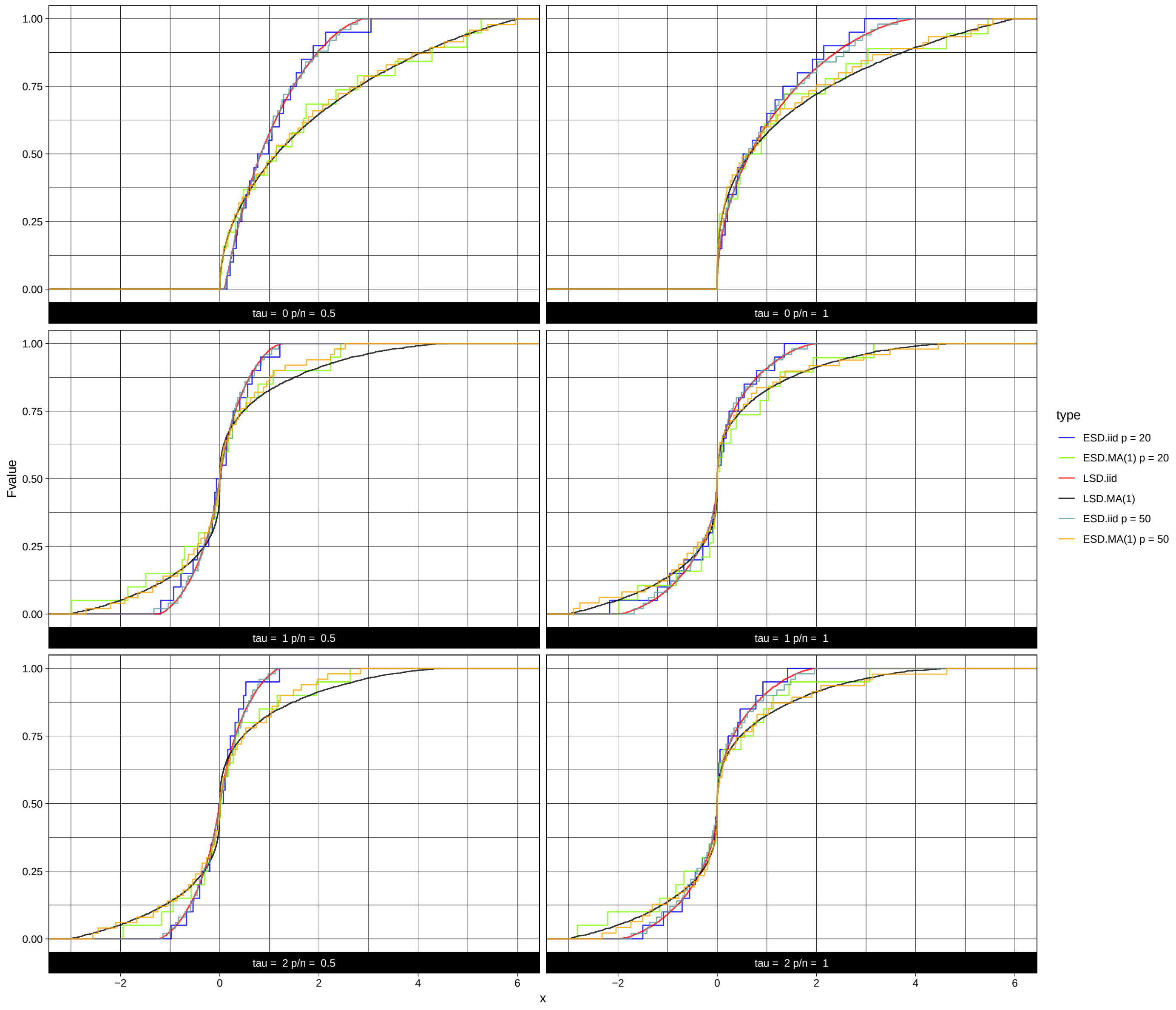
### Q9

how we separate data?

- plot 1
  - $p = 20, n = 40, \tau = 0$
  - $p = 50, n = 100, \tau = 0$
- plot 2
  - $p = 20, n = 20, \tau = 0$
  - $p = 50, n = 50, \tau = 0$
- plot 3
  - $p = 20, n = 40, \tau = 1$
  - $p = 50, n = 100, \tau = 1$
- plot 4
  - $p = 20, n = 20, \tau = 1$
  - $p = 50, n = 50, \tau = 1$
- plot 5
  - $p = 20, n = 40, \tau = 2$
  - $p = 50, n = 100, \tau = 2$
- plot 6
  - $p = 20, n = 20, \tau = 2$
  - $p = 50, n = 50, \tau = 2$

```r
ps <- c(20,50)
ratios <- c(.5, 1)
taus <- c(0,1,2)

lag.sample.acf <- function(n, tau, X) {
    if (tau==0) {
        return(cov(X))
    } else {
        Ctau <- 0
        for (t in 1:(n-tau)) {
            Ctau <- Ctau + X[t,] %*% t(X[t+tau,]) + X[t+tau,] %*% t(X[t,])
        }
        Ctau <- Ctau/(2*n)
        return(Ctau)
    }
}

df <- data.frame()
for (ratio in ratios) {
    for (tau in taus){
        for (p in ps) {
            n <- p / ratio

            # draw the ESDs for iid
            Z <- rmvnorm(n,mean=rep(0,p),sigma=diag(p))
            S <- lag.sample.acf(n, tau, Z)
            ev <- eigen(S)$values

            F_ <- function(x) {
                total <- 0.
                for (i in 1:p) {
                    if (ev[i] <= x){
                        total <- total + 1
                    }
                }
                return(total/p)
            }
            empirical.cdf <- Vectorize(F_)

            df <- rbind(df, data.frame(p=rep(p,n),
                                       ratio=rep(ratio,n),
                                       tau=rep(tau, n),
                                       x=ev,
                                       Fvalue=empirical.cdf(ev),
                                       type=rep(paste("ESD.iid p =",p),n)))

            # draw the ESDs for MA(1)
            A1 <- diag(ncol(Z))
            Z.copy <- Z
            Z.copy <- cbind(rep(1,ncol(Z.copy)), Z.copy[,1:(ncol(Z.copy)-1)])
            X <- Z+Z.copy
            ev2 <- eigen(lag.sample.acf(n, tau, X))$values
            df <- rbind(df, data.frame(p=rep(p,n),
                                       ratio=rep(ratio,n),
                                       tau=rep(tau, n),
                                       x=ev2,
                                       Fvalue=empirical.cdf(ev2),
                                       type=rep(paste("ESD.MA(1) p =",p),n)))

            # draw the LSD for iid
            pp <- 500
            nn <- pp / ratio
            Zn <- rmvnorm(nn,mean=rep(0,pp),sigma=diag(pp))
            Sn <- lag.sample.acf(nn,tau,Zn)
            evn <- eigen(Sn)$values

            df <- rbind(df, data.frame(p=rep(pp,length(evn)),
                                       ratio=rep(ratio,length(evn)),
                                       tau=rep(tau,length(evn)),
                                       x=evn,
                                       Fvalue=empirical.cdf(evn),
                                       type=rep("LSD.iid",length(evn))))

            # draw the LSD for MA(1)
            A1n <- diag(ncol(Zn))
            Zn.copy <- Zn
            Zn.copy <- cbind(rep(1,ncol(Zn.copy)), Zn.copy[,1:(ncol(Zn.copy)-1)])
            Xn <- Zn+Zn.copy
            ev2n <- eigen(lag.sample.acf(length(evn), tau, Xn))$values
            df <- rbind(df, data.frame(p=rep(pp,length(ev2n)),
                                       ratio=rep(ratio,length(ev2n)),
                                       tau=rep(tau, length(ev2n)),
                                       x=ev2n,
                                       Fvalue=empirical.cdf(ev2n),
                                       type=rep("LSD.MA(1)",length(ev2n))))
        }
    }
}
```

```r
# plotting

df$para <- paste("tau = ", df$tau, "p/n = ", df$ratio)
ggplot(df, aes(x=x, y=Fvalue, color=type)) +
    stat_ecdf(geom = "step", size=.5, alpha=.8) +
    facet_wrap(para ~ ., nrow=3, strip.position = "bottom") +
    scale_x_continuous(limits = c(-3,6)) +
    scale_y_continuous(limits = c(0,1)) +
    scale_color_manual(values=c("LSD.iid" = "red",
                                "LSD.MA(1)" = "black",
                                "ESD.iid p = 20" = "blue",
                                "ESD.MA(1) p = 20" = "chartreuse",
                                "ESD.iid p = 50" = "cadetblue",
                                "ESD.MA(1) p = 50" = "orange")) +
    theme_linedraw()
```



We are pretty sure that we had some mistakes in the MA(1) model since they look different comparing with the ones in the paper (TODO:Li) but the three of iid models are pretty much the same.

3.

## References

- Visualizing Tests for Equality of Covariance Matrices, Michael Friendly and Matthew Siga. https://arxiv.org/pdf/1805.05756.pdf
- https://stats.stackexchange.com/questions/40868/experiment-or-simulation-to-undestand-type-i-and-type-ii-errors/40874#40874
- TODO: and many more with decent format of citations

1. all covariance matrix use `cov()` for better accuracy
2. all log(det()) use `determinant()` with argument `log=TRUE`
3. for type 1 error and power calculation, use statistic vs critical value instead p-value vs significance.

portmanteau test

https://faculty.chicagobooth.edu/ruey.tsay/teaching/mts/sp2009/lec1-09.pdf https://faculty.chicagobooth.edu/ruey.tsay/teaching/mts/sp2009/lec2-09.pdf

- https://rdrr.io/cran/MTS/man/VARorder.html