

# HW1

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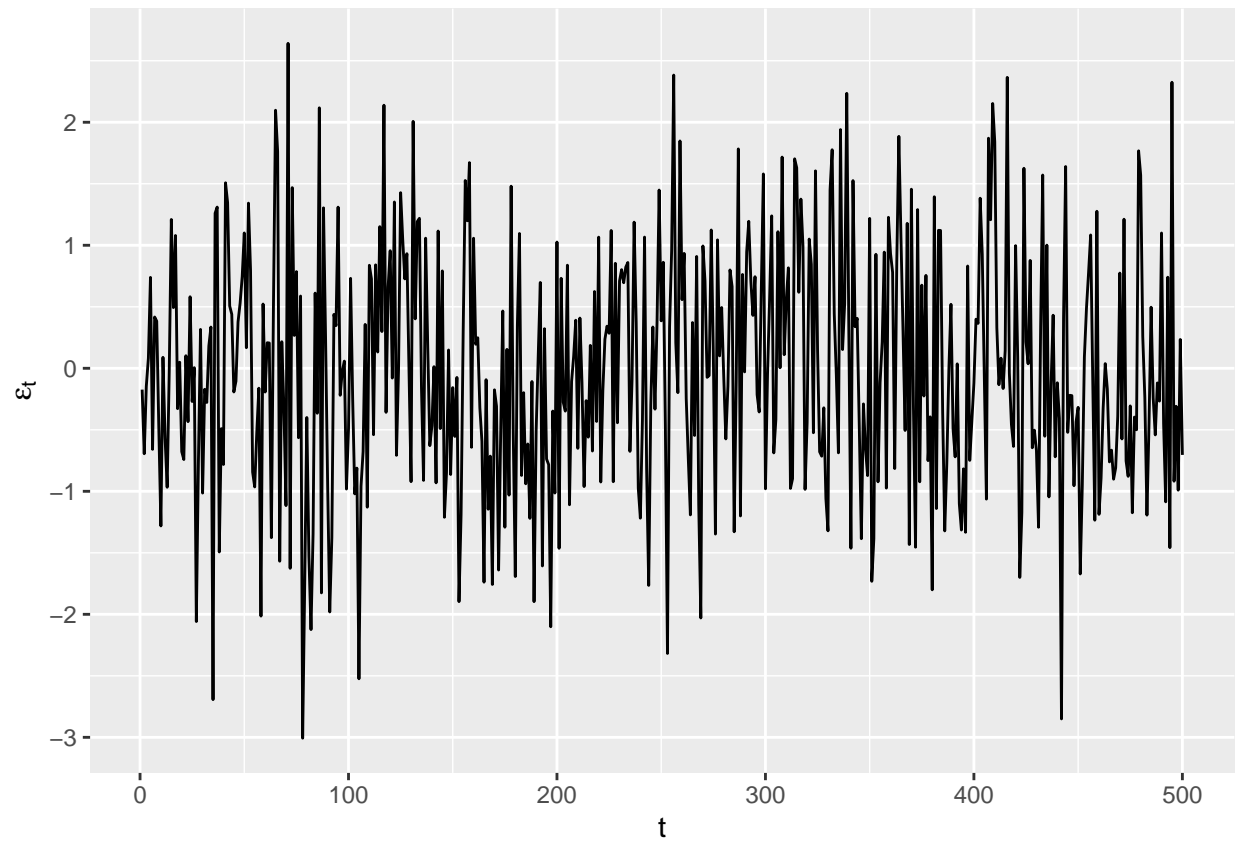
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## 1) Generate $\epsilon_t \sim N(0,1)$ ; IID samples, $1 \leq t \leq 500$

a)

$\epsilon_t$ (vs) $t$

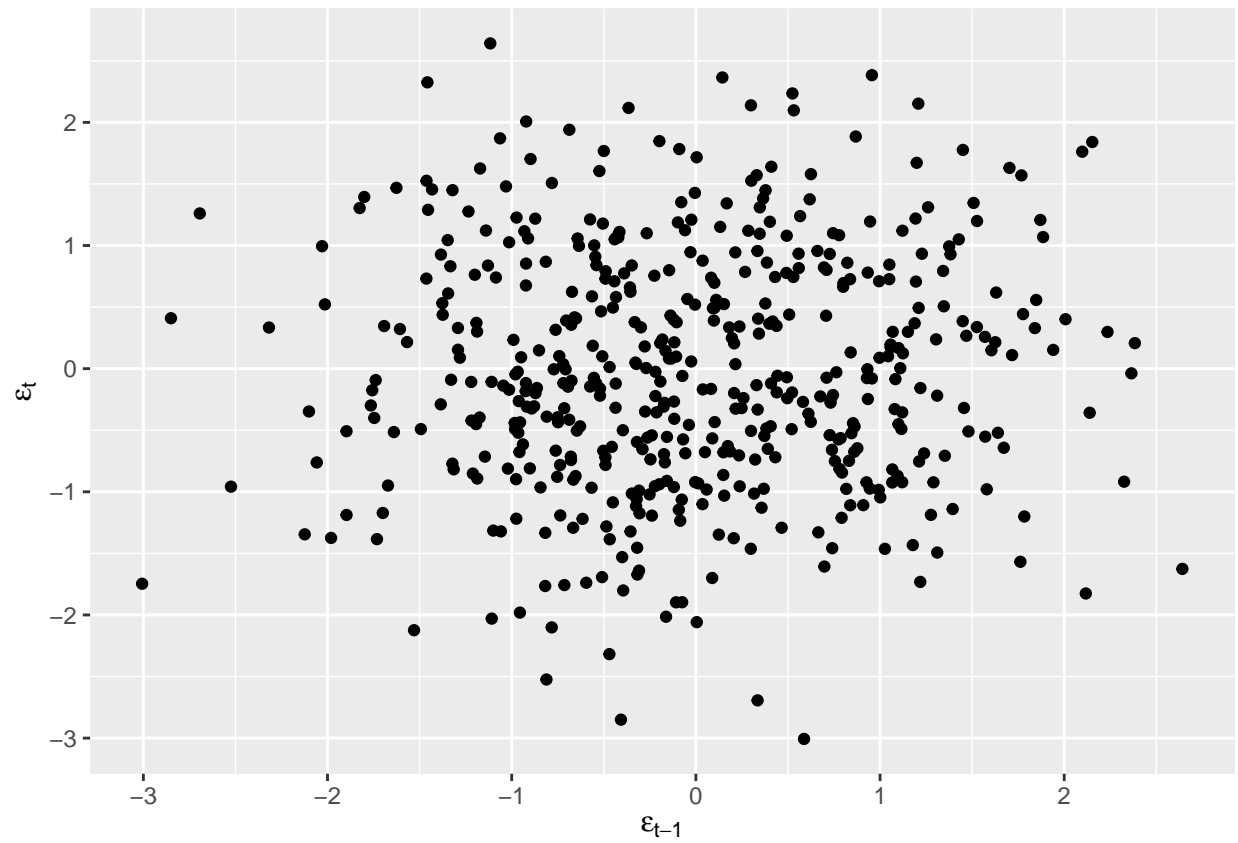
```
library(ggplot2)
x<-1:500
set.seed(6666)
y<-rnorm(500)
df<-data.frame(x=x,y=y)
p<-ggplot(df,aes(x=x,y=y))+
  geom_line()+
  xlab("t")+
  ylab(expression(epsilon[t]))
p
```



$\epsilon_t$  fluctuates around 0

$\epsilon_t$  (vs)  $\epsilon_{t-1}$

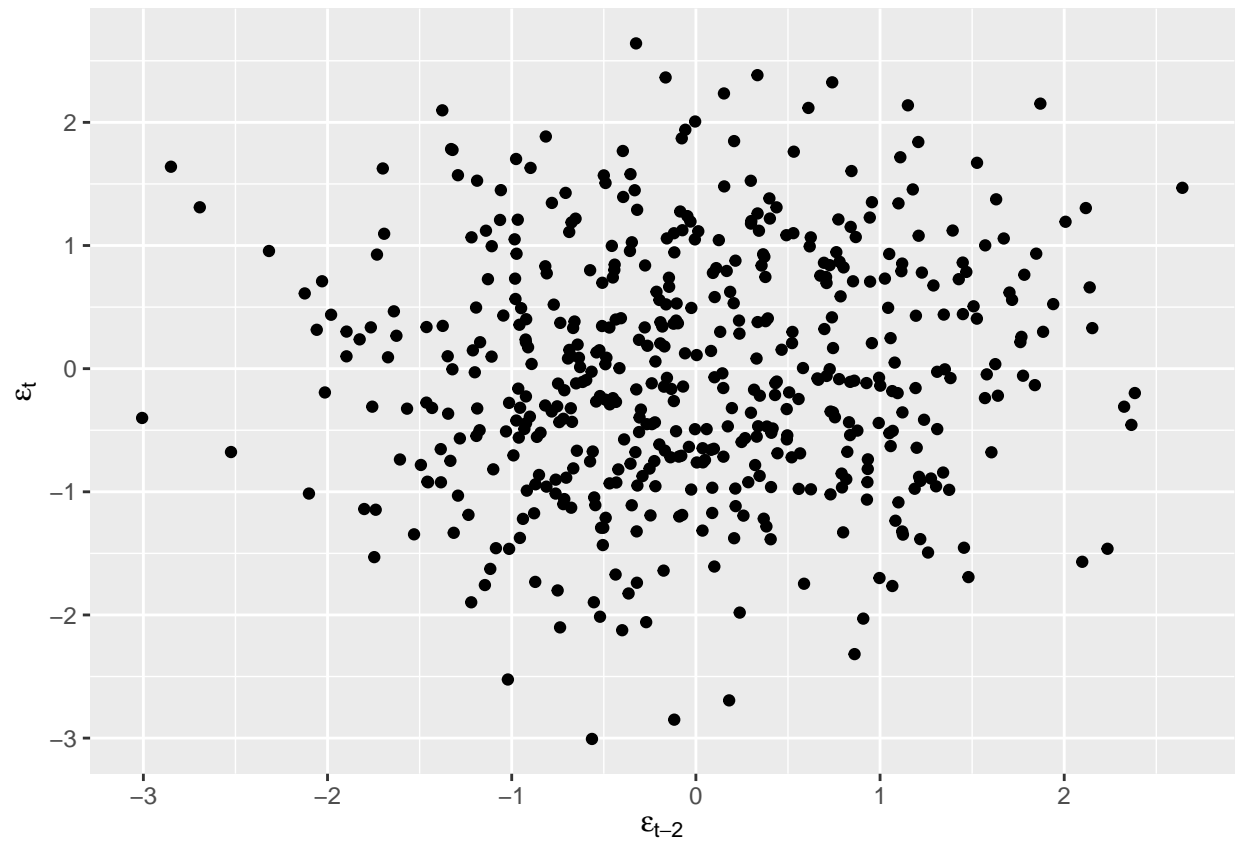
```
set.seed(6666)
y<-rnorm(501)
t<-501
df<-data.frame(x=y[1:c(t-1)],y=y[2:t])
p<-ggplot(df,aes(x=x,y=y))+
  geom_point()+
  xlab(expression(epsilon[t-1]))+
  ylab(expression(epsilon[t]))
p
```



it seems no correlation between  $\epsilon_t$  and  $\epsilon_{t-1}$

$\epsilon_t$  (vs)  $\epsilon_{t-2}$

```
set.seed(6666)
y<-rnorm(502)
t<-502
df<-data.frame(x=y[1:(t-2)],y=y[3:t])
p<-ggplot(df,aes(x=x,y=y))+
  geom_point()+
  xlab(expression(epsilon[t-2]))+
  ylab(expression(epsilon[t]))
p
```



it seems no correlation between  $\epsilon_t$  and  $\epsilon_{t-2}$

b)

mean

```
set.seed(6666)
y<-rnorm(500)
mean(y)
```

```
## [1] -0.02309015
```

variance

```
var(y)
```

```
## [1] 0.9683645
```

covariance  $\gamma_k$

```

set.seed(6666)
y<-rnorm(500)
getCov<-function(k){
  x1<-y[1:100]
  x2<-y[(k+1):(100+k)]
  cov(x1,x2)
}
k<-0:100
cov1<-sapply(k,getCov)
dfCov<-data.frame(k=k,cov=cov1)
head(dfCov)

```

```

##    k      cov
## 1 0  1.124203061
## 2 1  0.005641228
## 3 2  0.071936887
## 4 3 -0.011424680
## 5 4 -0.021561912
## 6 5 -0.008673083

```

$\rho_k$

```

p<-cov1/cov1[1]
dfP<-data.frame(k=k,p=p)
head(dfP)

```

```

##    k      p
## 1 0  1.000000000
## 2 1  0.005017980
## 3 2  0.063989229
## 4 3 -0.010162470
## 5 4 -0.019179730
## 6 5 -0.007714872

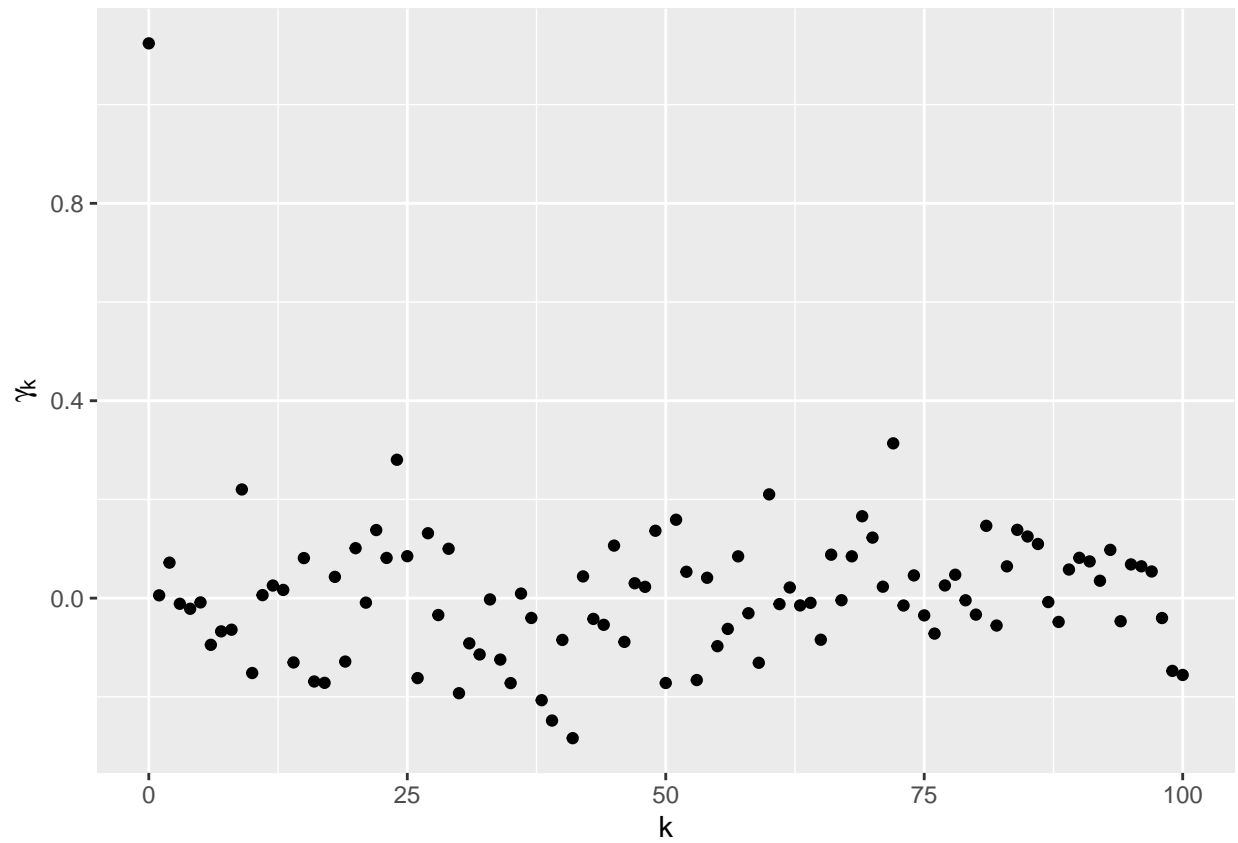
```

$\gamma_k$  (vs) k

```

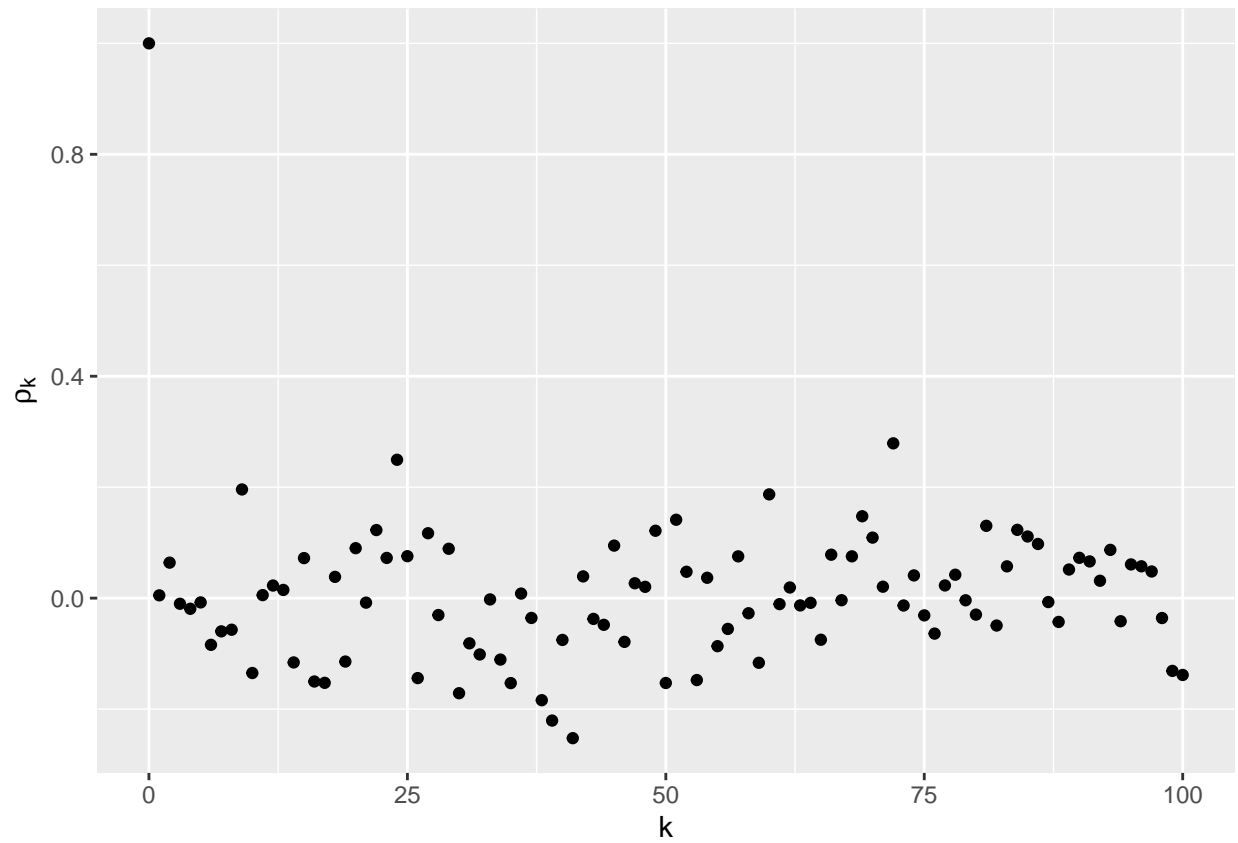
p<-ggplot(dfCov,aes(x=k,y=cov))+
  geom_point()+
  xlab(expression(k))+
  ylab(expression(gamma[k]))
p

```



$\rho_k$  (vs)  $k$

```
p<-ggplot(dfP,aes(x=k,y=p))+
  geom_point()+
  xlab(expression(k))+
  ylab(expression(rho[k]))
p
```



c)

**min**

```
set.seed(6666)
y<-rnorm(500)
min(y)
```

```
## [1] -3.006701
```

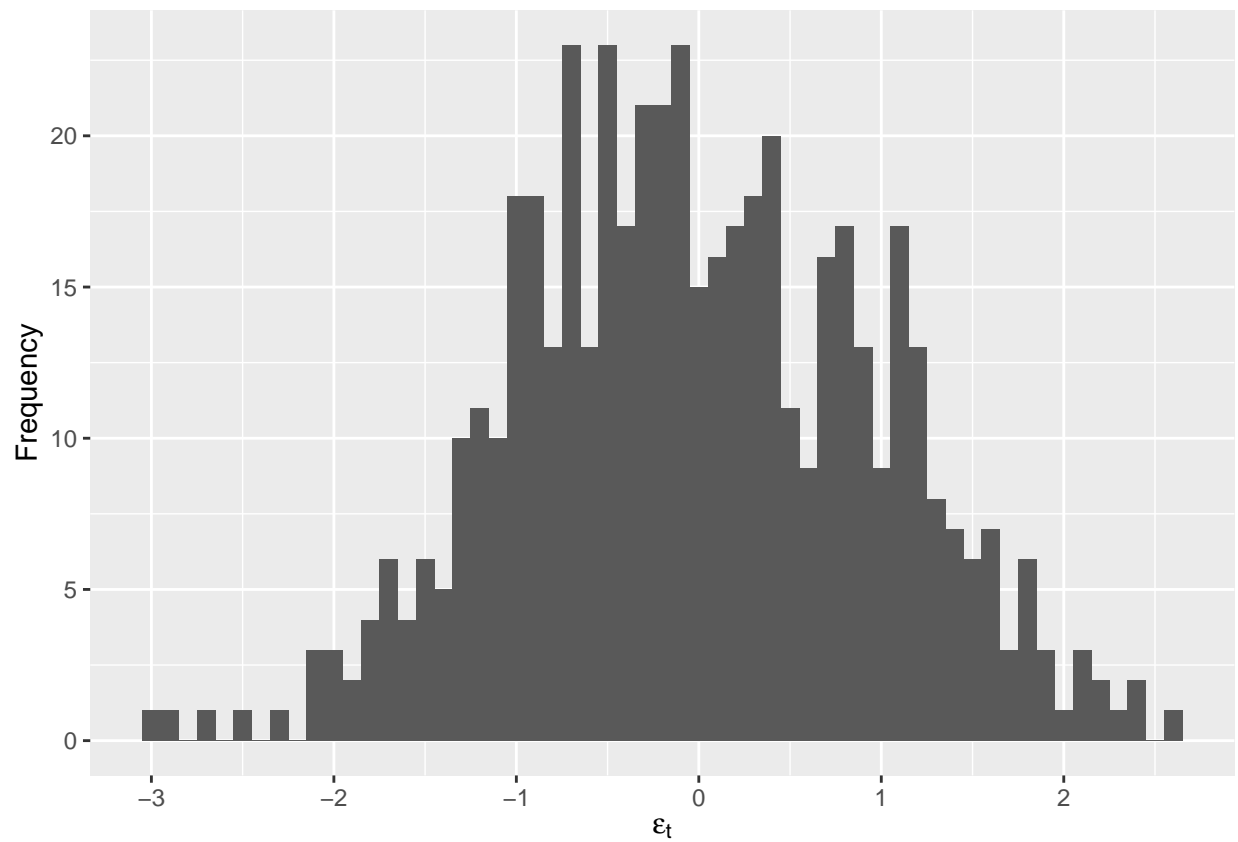
**max**

```
max(y)
```

```
## [1] 2.641487
```

**histogram**

```
qplot(y, binwidth=0.1, geom = "histogram", xlab=expression(epsilon[t]), ylab="Frequency")
```



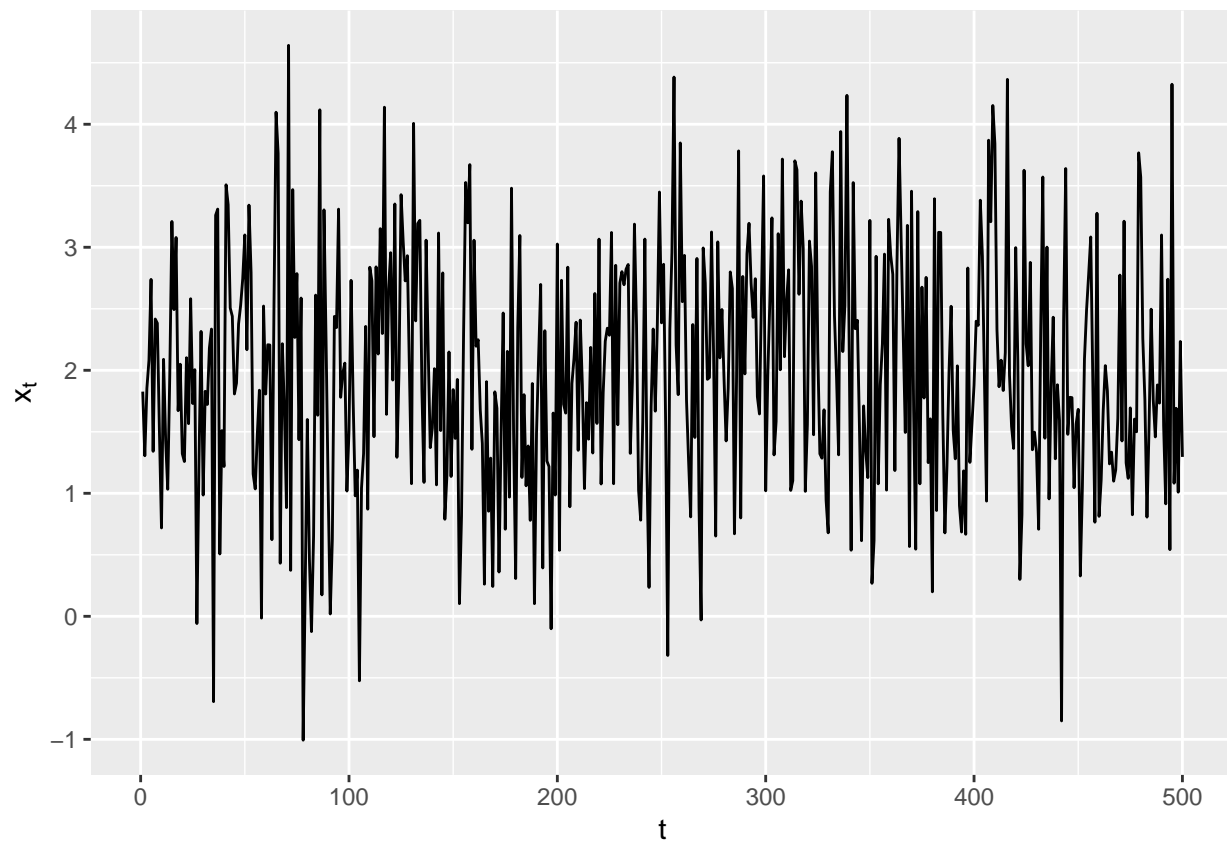
2) Repeat (Q1) on  $x_t$  when  $x_t$  is given by

a)  $x_t = 2.0 + \epsilon_t$ ,  $x_0 = 0$

$x_t$  (vs)  $t$

```
t<-1:500
set.seed(6666)
y<-rnorm(500)+2.0
df<-data.frame(x=t,y=y)
p<-ggplot(df,aes(x=x,y=y))+
  geom_line()+
  xlab("t")+
  ylab(expression(x[t]))
p
```

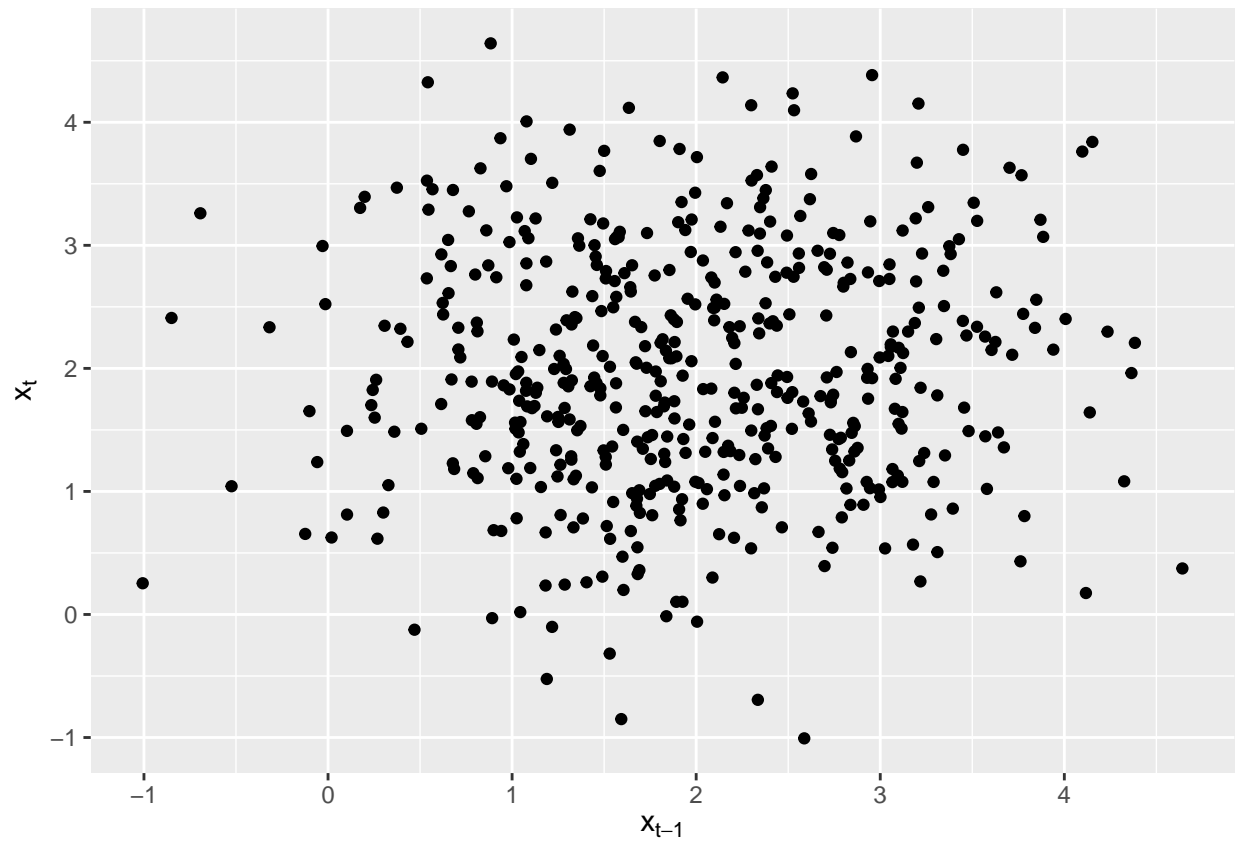




$x_t$  fluctuates around 2

$x_t$  (vs)  $x_{t-1}$

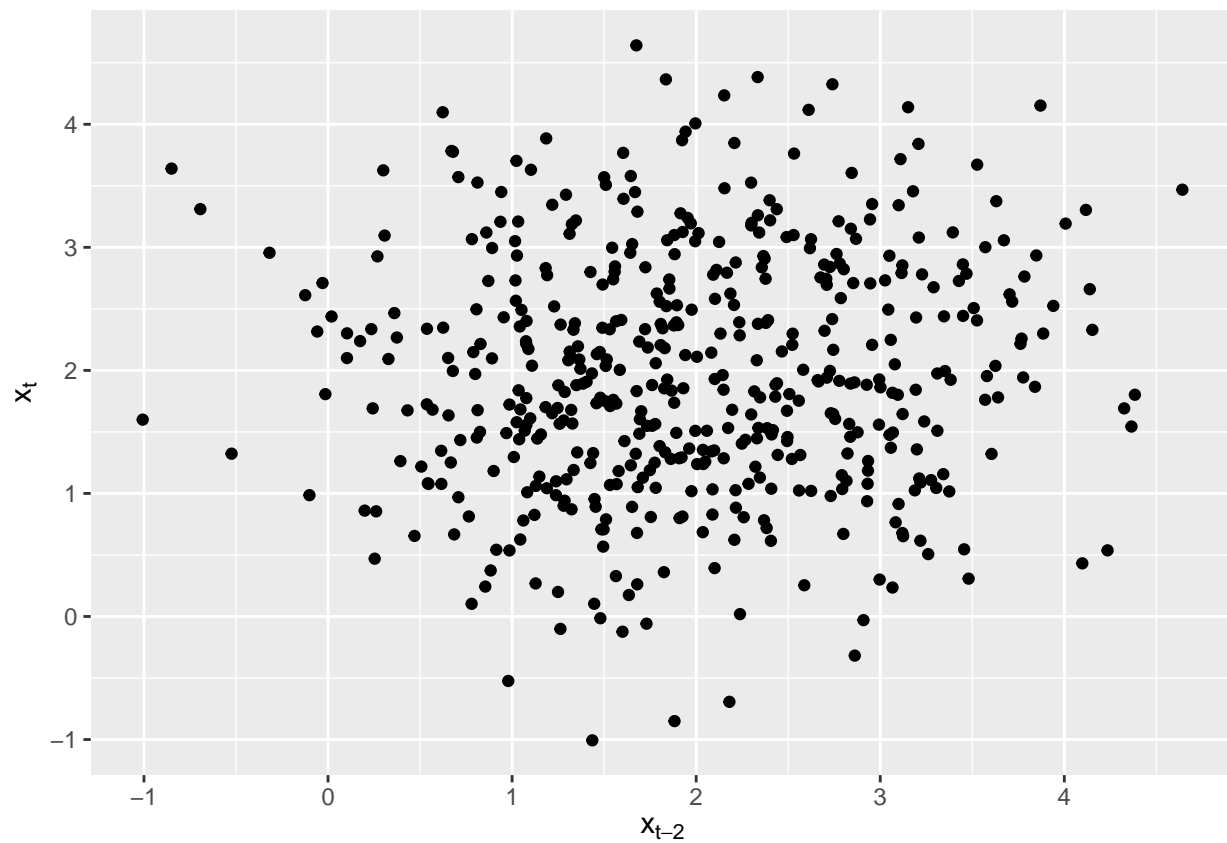
```
set.seed(6666)
y<-rnorm(501)+2.0
t<-501
df<-data.frame(x=y[1:c(t-1)],y=y[2:t])
p<-ggplot(df,aes(x=x,y=y))+
  geom_point()+
  xlab(expression(x[t-1]))+
  ylab(expression(x[t]))
p
```



it seems no correlation between  $x_t$  and  $x_{t-1}$

$x_t$  (vs)  $x_{t-2}$

```
set.seed(6666)
y<-rnorm(502)+2.0
t<-502
df<-data.frame(x=y[1:(t-2)],y=y[3:t])
p<-ggplot(df,aes(x=x,y=y))+
  geom_point()+
  xlab(expression(x[t-2]))+
  ylab(expression(x[t]))
p
```



it seems no correlation between  $x_t$  and  $x_{t-2}$

**mean**

```
set.seed(6666)
y<-rnorm(501)+2.0
mean(y)
```

```
## [1] 1.977736
```

**variance**

```
var(y)
```

```
## [1] 0.9667695
```

**covariance  $\gamma_k$**

```
set.seed(6666)
y<-rnorm(500)+2.0
```

```

getCov<-function(k){
  x1<-y[1:100]
  x2<-y[(k+1):(100+k)]
  cov(x1,x2)
}
k<-0:100
cov1<-sapply(k,getCov)
dfCov<-data.frame(k=k,cov=cov1)
head(dfCov)

```

```

##    k      cov
## 1 0  1.124203061
## 2 1  0.005641228
## 3 2  0.071936887
## 4 3 -0.011424680
## 5 4 -0.021561912
## 6 5 -0.008673083

```

$\rho_k$

```

p<-cov1/cov1[1]
dfP<-data.frame(k=k,p=p)
head(dfP)

```

```

##    k      p
## 1 0  1.000000000
## 2 1  0.005017980
## 3 2  0.063989229
## 4 3 -0.010162470
## 5 4 -0.019179730
## 6 5 -0.007714872

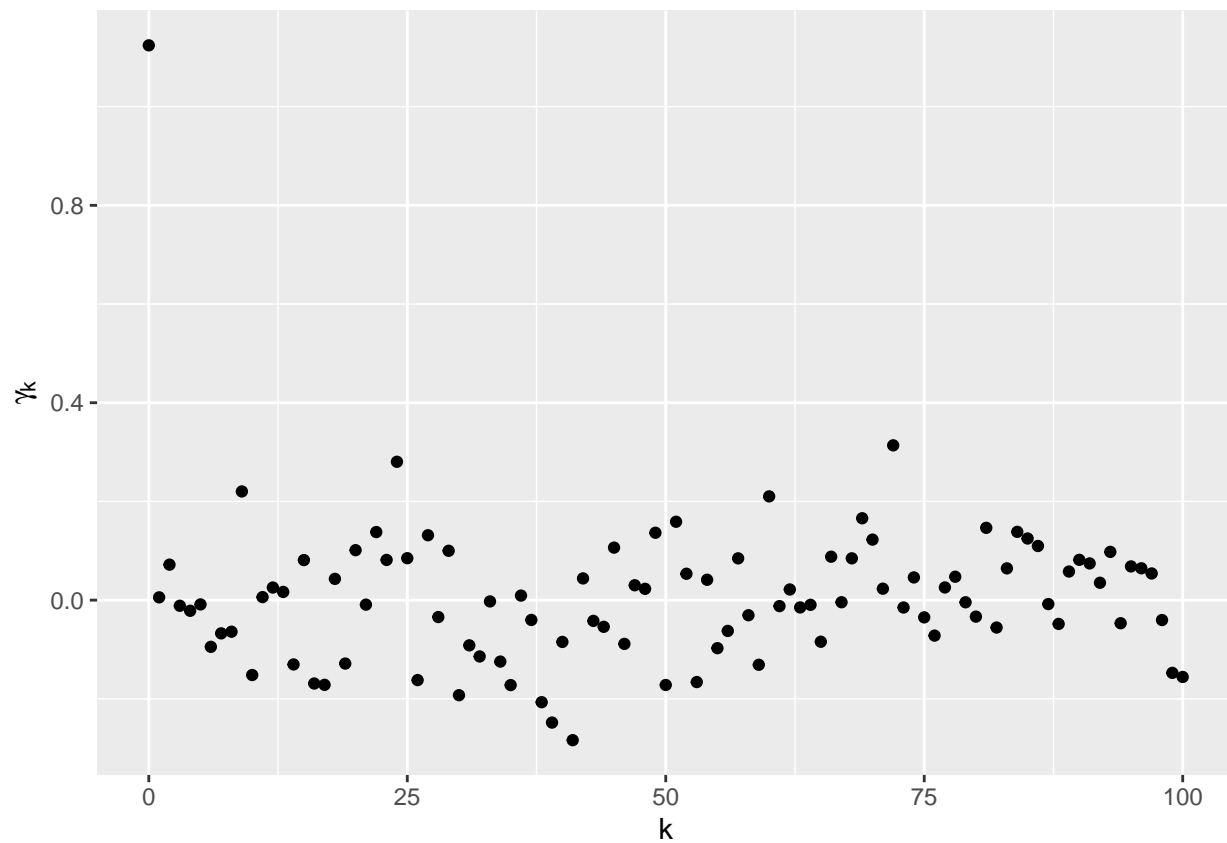
```

$\gamma_k$  (vs) k

```

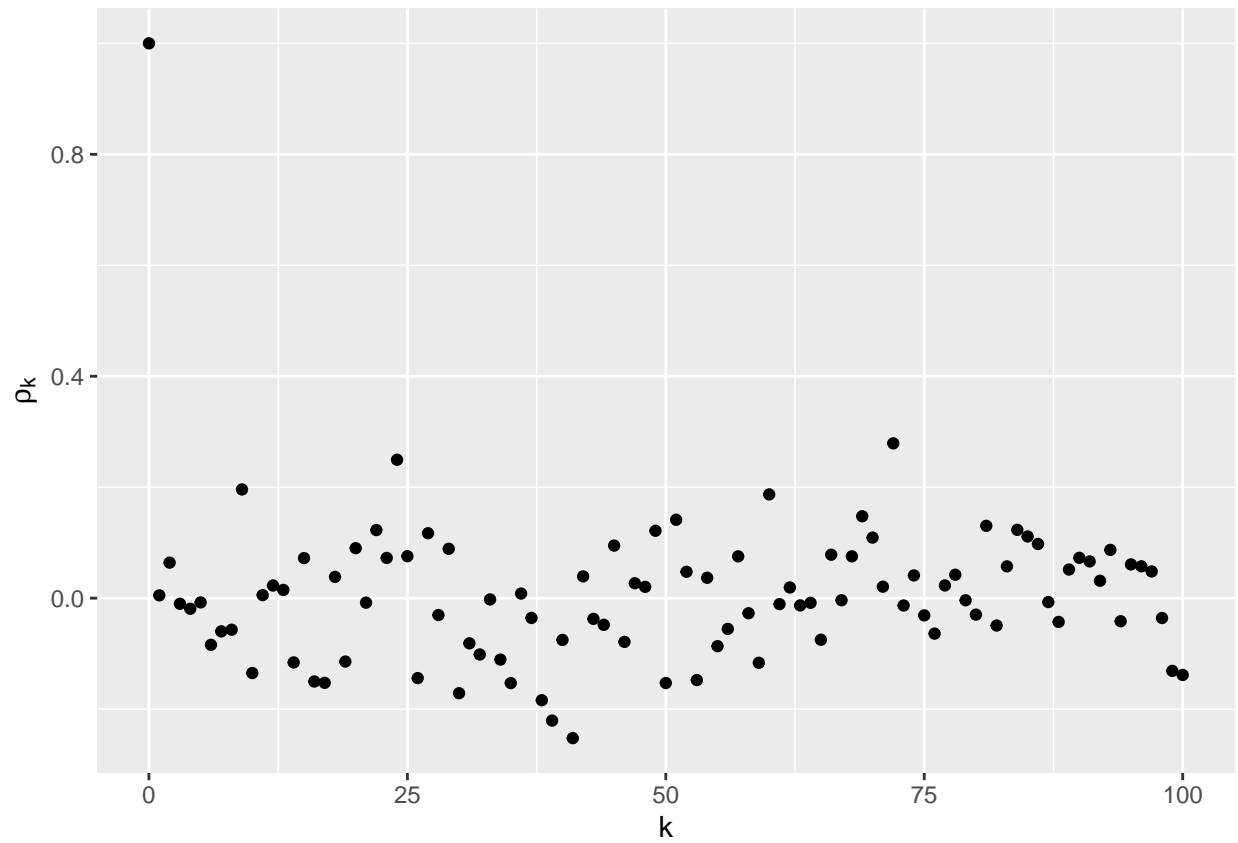
p<-ggplot(dfCov,aes(x=k,y=cov))+
  geom_point()+
  xlab(expression(k))+
  ylab(expression(gamma[k]))
p

```



$\rho_k$  (vs)  $k$

```
p<-ggplot(dfP,aes(x=k,y=p))+
  geom_point()+
  xlab(expression(k))+
  ylab(expression(rho[k]))
p
```



**min**

```
set.seed(6666)
y<-rnorm(500)+2.0
min(y)
```

```
## [1] -1.006701
```

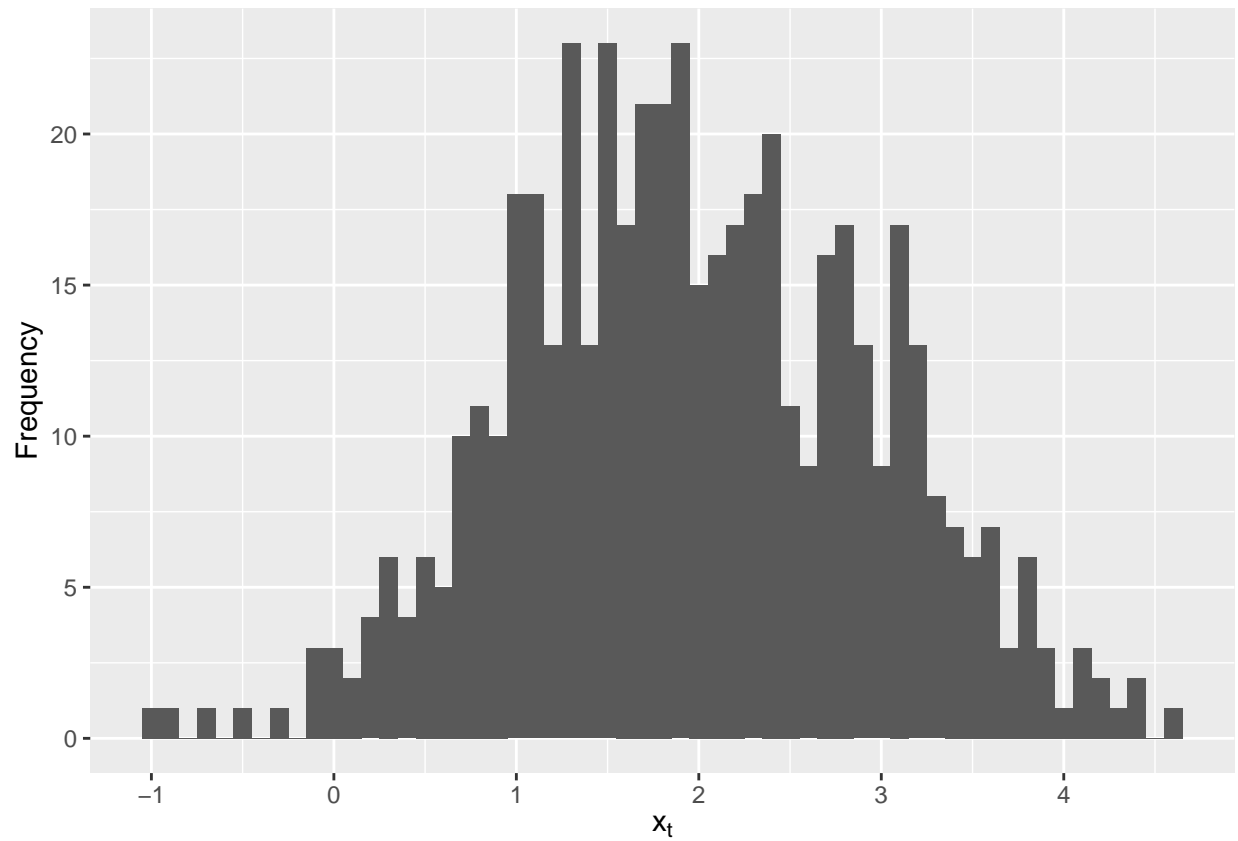
**max**

```
max(y)
```

```
## [1] 4.641487
```

**histogram**

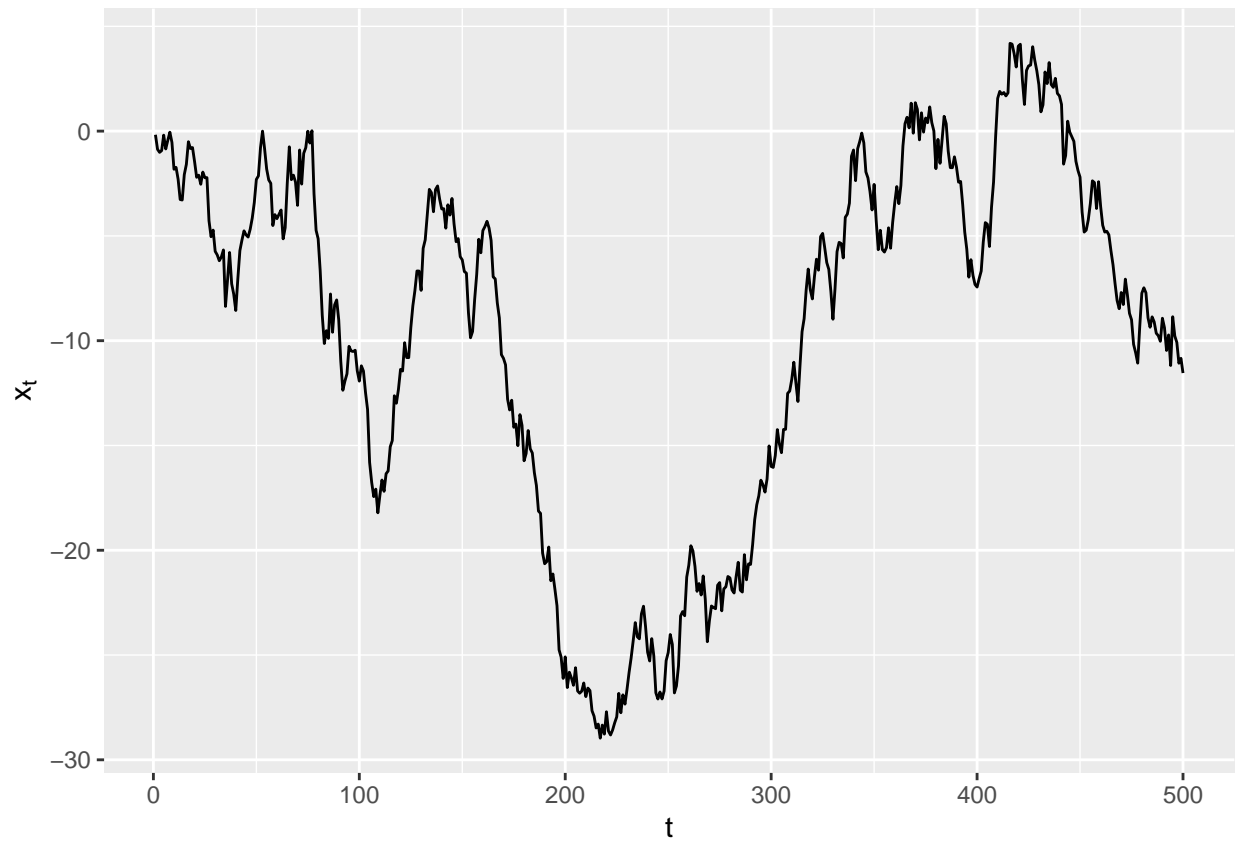
```
qplot(y, binwidth=0.1, geom = "histogram", xlab=expression(x[t]), ylab="Frequency")
```



b)  $x_t = x_{t-1} + \epsilon_t$ ,  $x_0 = 0$

$x_t$  (vs)  $t$

```
t<-1:500
set.seed(6666)
y<-rnorm(500)
xt<-function(t){
  if (t==0) return(0)
  else return(xt(t-1)+y[t])
}
y<-sapply(1:500,xt)
df<-data.frame(x=t,y=y)
p<-ggplot(df,aes(x=x,y=y))+
  geom_line()+
  xlab("t")+
  ylab(expression(x[t]))
p
```

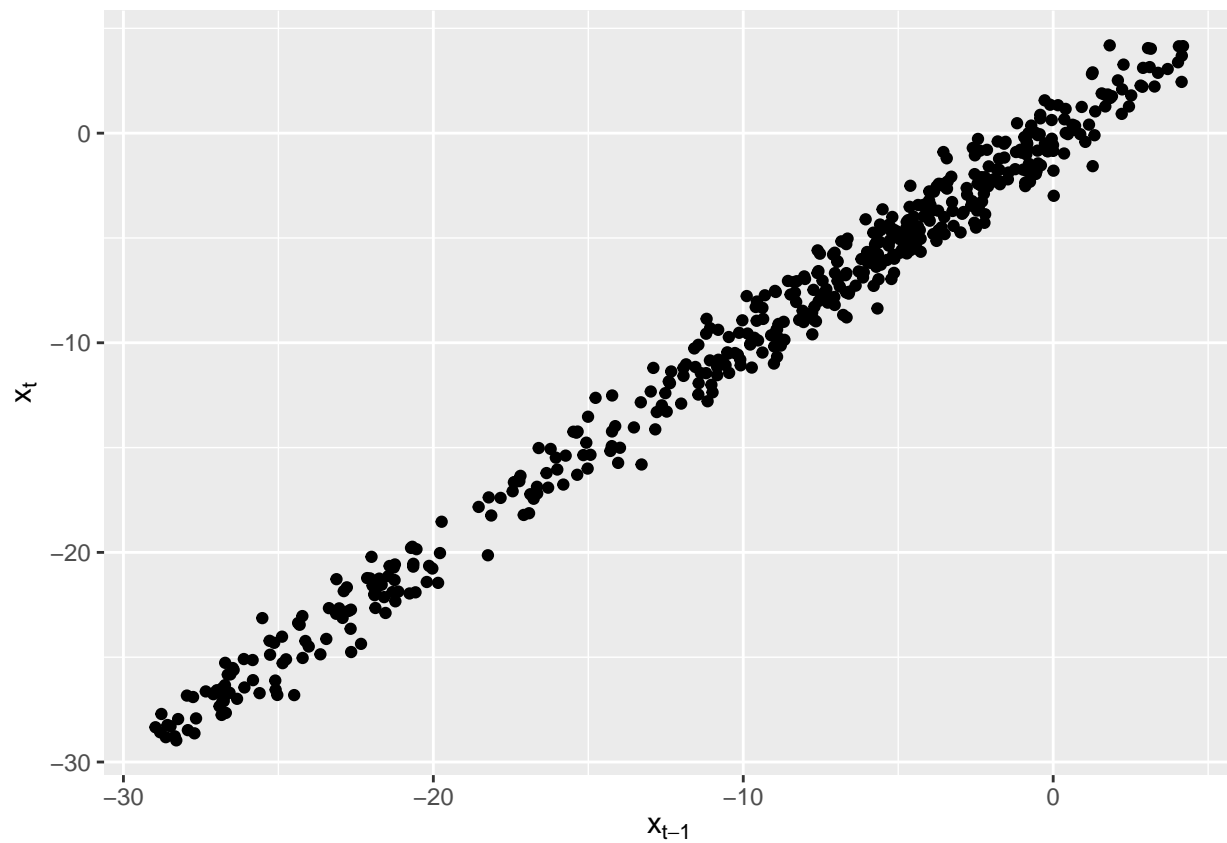


$x_t$  is unstable

$x_t$  (vs)  $x_{t-1}$

```
t<-501
set.seed(6666)
y<-rnorm(501)
xt<-function(t){
  if (t==0) return(0)
  else return(xt(t-1)+y[t])
}
y<-sapply(1:t,xt)
df<-data.frame(x=y[1:(t-1)],y=y[2:t])
p<-ggplot(df,aes(x=x,y=y))+
  geom_point()+
  xlab(expression(x[t-1]))+
  ylab(expression(x[t]))
p
```

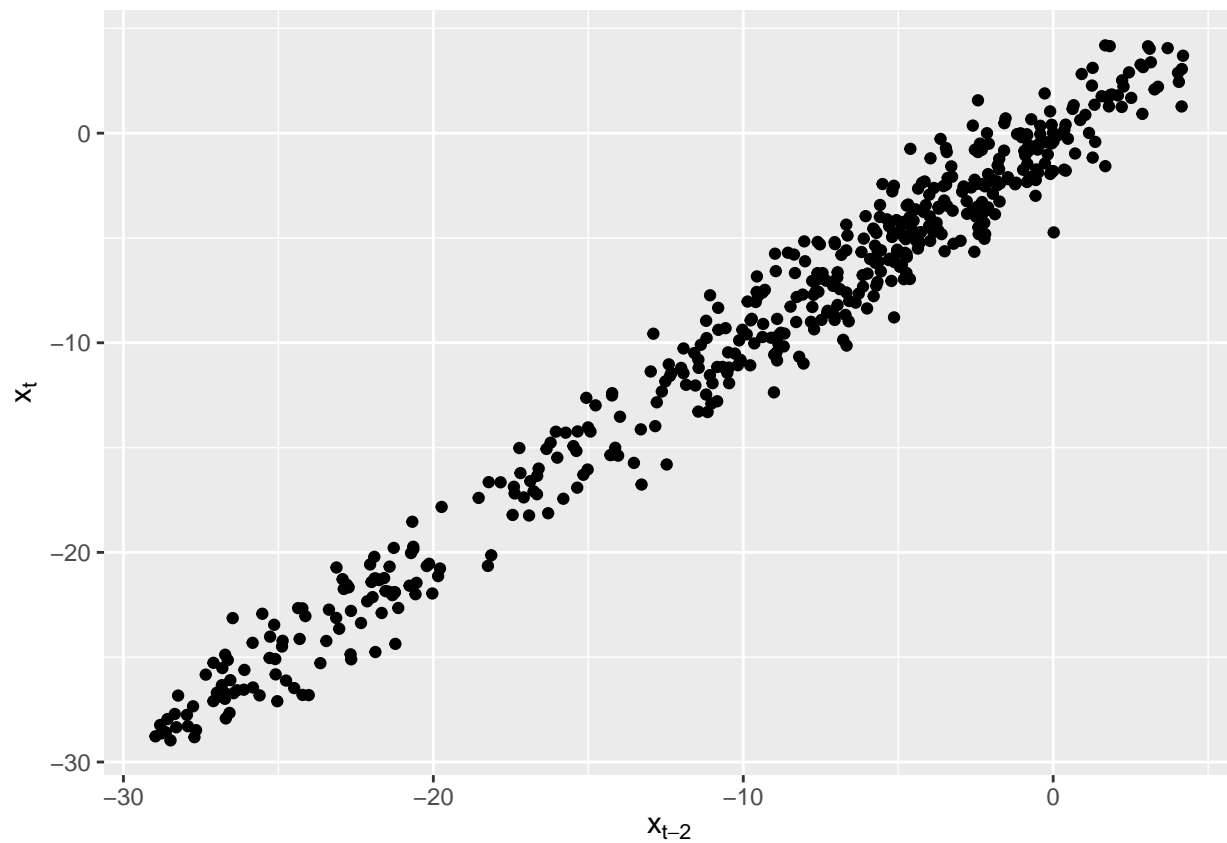




it seems strong correlation between  $x_t$  and  $x_{t-1}$

$x_t$  (vs)  $x_{t-2}$

```
t<-502
set.seed(6666)
y<-rnorm(502)
xt<-function(t){
  if (t==0) return(0)
  else return(xt(t-1)+y[t])
}
y<-sapply(1:t,xt)
df<-data.frame(x=y[1:(t-2)],y=y[3:t])
p<-ggplot(df,aes(x=x,y=y))+
  geom_point()+
  xlab(expression(x[t-2]))+
  ylab(expression(x[t]))
p
```



it seems strong correlation between  $x_t$  and  $x_{t-2}$

**mean**

```
set.seed(6666)
y<-rnorm(500)
xt<-function(t){
  if (t==0) return(0)
  else return(xt(t-1)+y[t])
}
y<-sapply(1:500,xt)
mean(y)
```

```
## [1] -9.604342
```

**variance**

```
var(y)
```

```
## [1] 79.92241
```

covariance  $\gamma_k$

```
set.seed(6666)
y<-rnorm(1000)
y<-cumsum(y)
getCov<-function(k){
  x1<-y[1:500]
  x2<-y[(k+1):(500+k)]
  cov(x1,x2)
}
k<-0:100
cov1<-sapply(k,getCov)
dfCov<-data.frame(k=k,cov=cov1)
head(dfCov)
```

```
##    k      cov
## 1 0 79.92241
## 2 1 79.35112
## 3 2 78.75464
## 4 3 78.09893
## 5 4 77.39016
## 6 5 76.61015
```

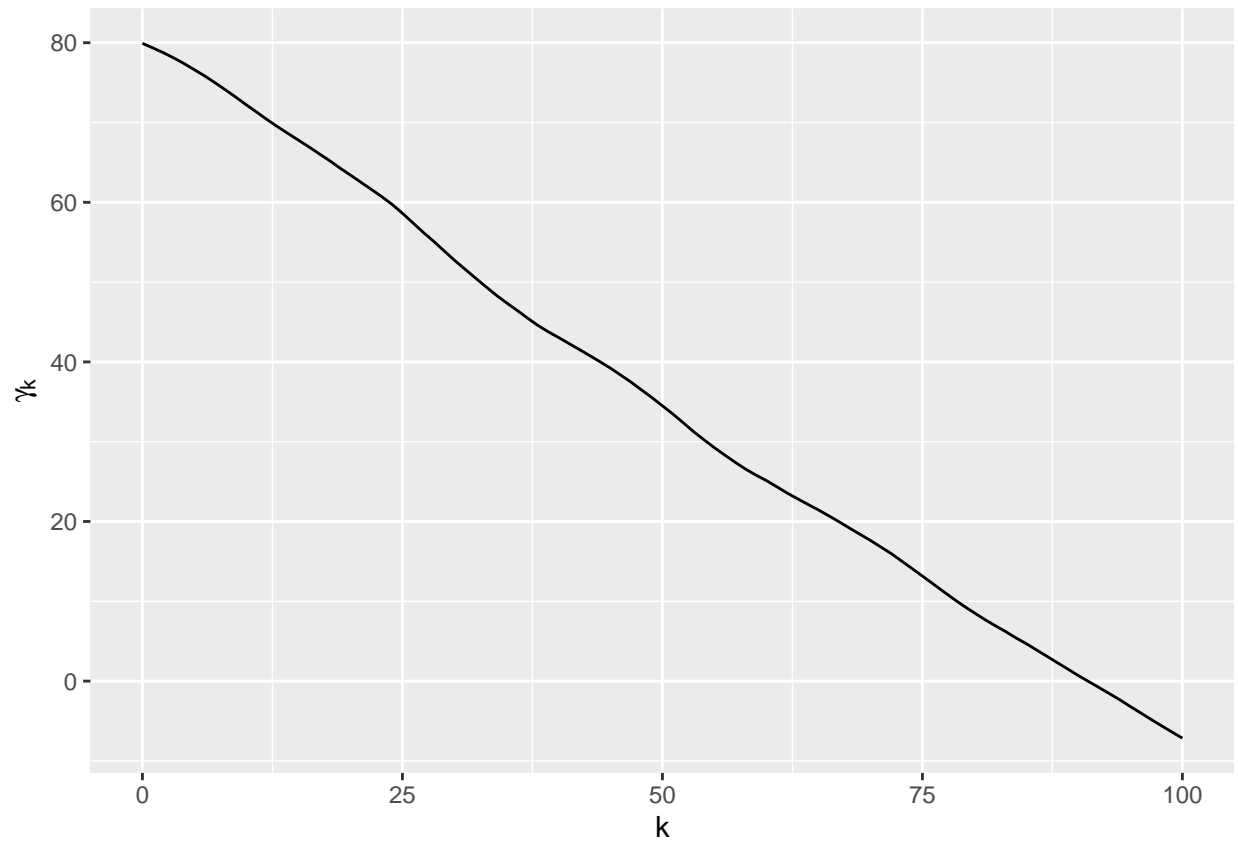
$\rho_k$

```
p<-cov1/cov1[1]
dfP<-data.frame(k=k,p=p)
head(dfP)
```

```
##    k      p
## 1 0 1.000000
## 2 1 0.9928520
## 3 2 0.9853887
## 4 3 0.9771844
## 5 4 0.9683162
## 6 5 0.9585566
```

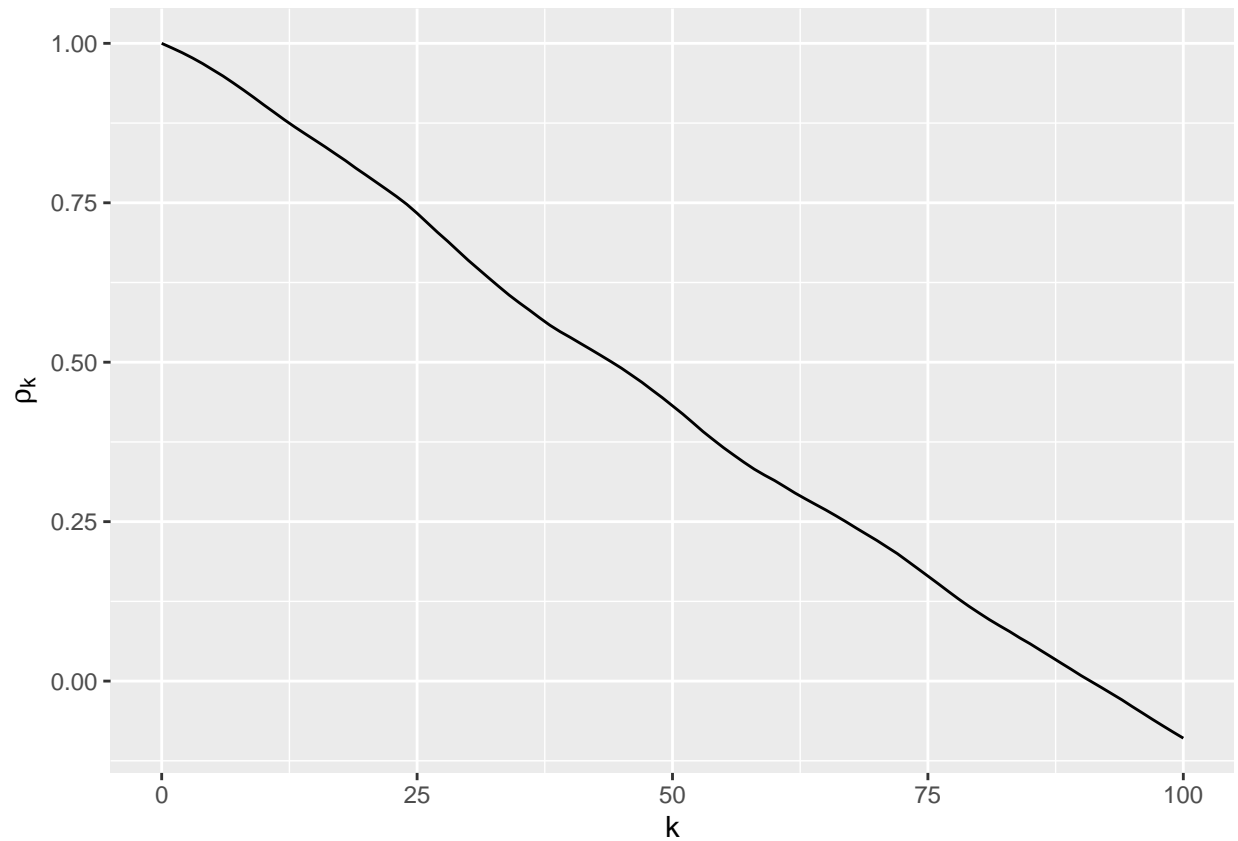
$\gamma_k$  (vs) k

```
p<-ggplot(dfCov,aes(x=k,y=cov))+
  geom_line()+
  xlab(expression(k))+
  ylab(expression(gamma[k]))
p
```



$\rho_k$  (vs)  $k$

```
p<-ggplot(dfP,aes(x=k,y=p))+  
  geom_line()+  
  xlab(expression(k))+  
  ylab(expression(rho[k]))  
p
```



**min**

```
set.seed(6666)
y<-rnorm(500)
y<-cumsum(y)
min(y)
```

```
## [1] -28.96659
```

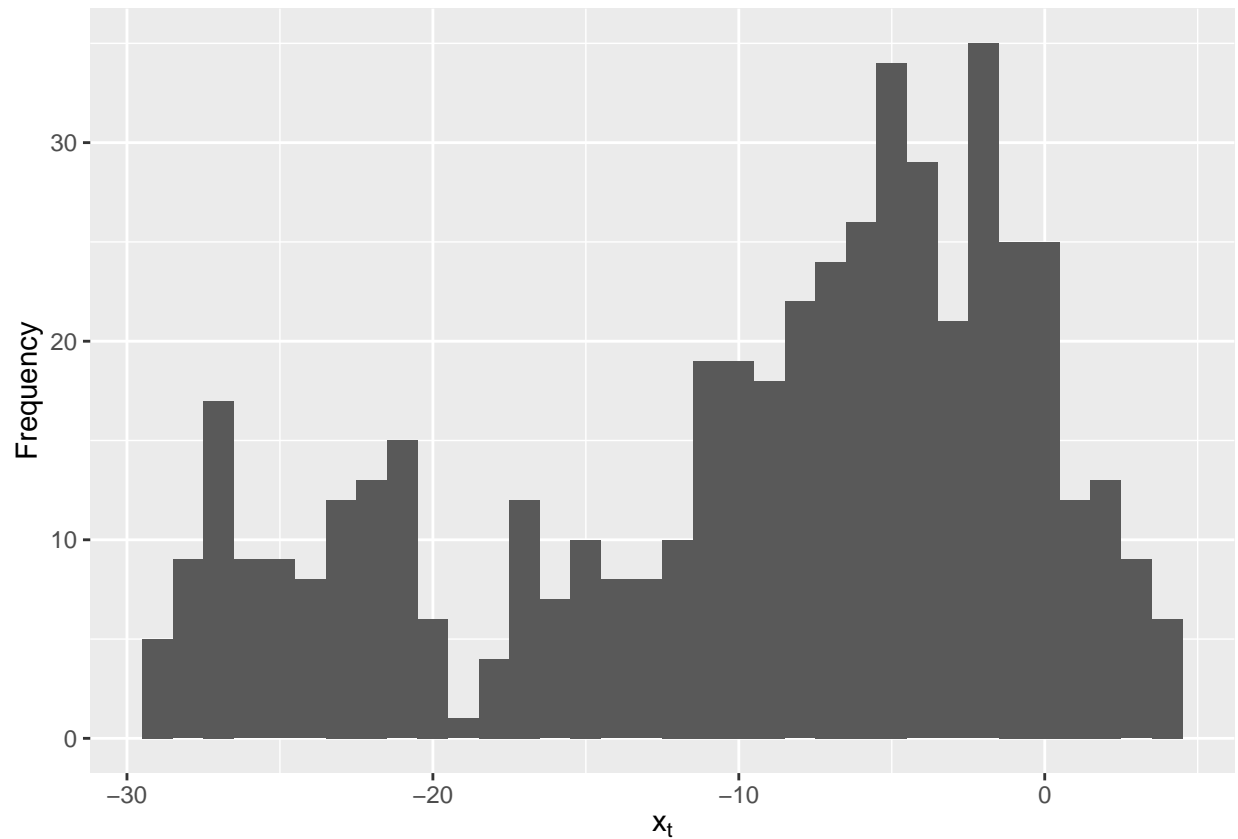
**max**

```
max(y)
```

```
## [1] 4.188588
```

**histogram**

```
qplot(y, binwidth=1, geom = "histogram", xlab=expression(x[t]), ylab="Frequency")
```



### 3) Verify covariance function $f(i, j)$ is non-negative definite

```
# define  $x_t \sim N(0, 1)$ 
set.seed(6666)
xt<-rnorm(500)
# each column of xt is  $x(i)$  or  $x(j)$ 
xt<-matrix(xt, ncol = 20)
# verify covariance function  $f(i, j)$  is non-negative definite
totalSum<-0
for (i in 1:20){
  for (j in 1:20){
    totalSum<-totalSum+(t(xt[,i])*cov(xt[,i], xt[,j]))%*%matrix(xt[,j])
  }
}
# TRUE
totalSum>0
```

```
##      [,1]
## [1,] TRUE
```

```
# define  $x_t \sim N(0, 1)$ 
set.seed(6666)
```

```

xt<-rnorm(500)
# define yt=y(t-1)+xt
yt<-cumsum(xt)
# each column of yt is y(i) or y(j)
yt<-matrix(yt,ncol = 20)
# verify covariance function f(i,j) is non-negative definite
totalSum<-0
for (i in 1:20){
  for (j in 1:20){
    totalSum<-totalSum+(t(yt[,i])*cov(yt[,i],yt[,j]))%%matrix(yt[,j])
  }
}
# TRUE
totalSum>0

```

```

##      [,1]
## [1,] TRUE

```