5160 - Homework 4

Mostafa

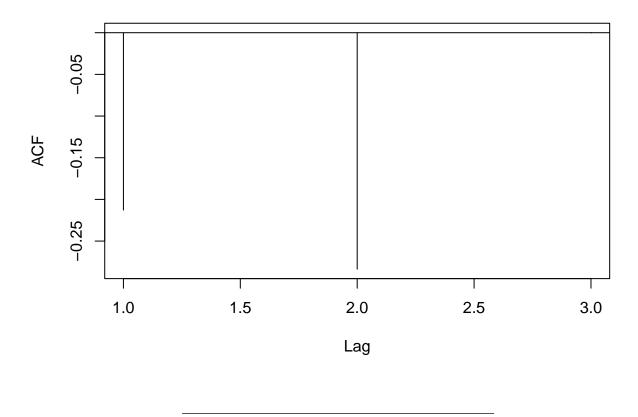
2/27/2021

```
# To clean the environment
rm(list = ls())
library (TSA) # Load the TSA package
## Warning: package 'TSA' was built under R version 4.3.1
## Attaching package: 'TSA'
## The following objects are masked from 'package:stats':
##
##
    acf, arima
## The following object is masked from 'package:utils':
##
##
    tar
1
1.(a)
k=0:1
k=1:-0.2127
k=2:-0.2836
k>2:0
1.(b)
ACF = ARMAacf(ma=c(-0.5,-0.4), lag.max=3)
ACF
##
## 1.0000000 -0.2127660 -0.2836879 0.0000000
```

1.(c)

```
ACF=ARMAacf(ma=c(-0.5,-0.4),lag.max=3)
plot(y=ACF[-1],x=1:3,xlab='Lag',ylab='ACF',main="Population ACF", type='h')
abline(h=0)
```

Population ACF



2

Hint for Problem 2 - Homework #4:

Please note that this problem only asks about population ACF, not sample ACF, because the problem does not even ask you to simulate time series. The ACF you obtained in a) and b) should be exactly the same. Neither 1 nor 2 says a sample size so both of them are about the **population** and the **ARMAacf()** function should be used. The **acf()** function is for the calculation of the **sample** autocorrelations. Hope it helps.

	Function
population samlpe	ARMAacf() acf()

2.(a)

```
phi = 0.6
phi^(0:8)

## [1] 1.00000000 0.600000000 0.360000000 0.21600000 0.12960000 0.07776000 0.04665600

## [8] 0.02799360 0.01679616

2.(b)

ACF=ARMAacf(ar=c(0.6),lag.max=8)
ACF

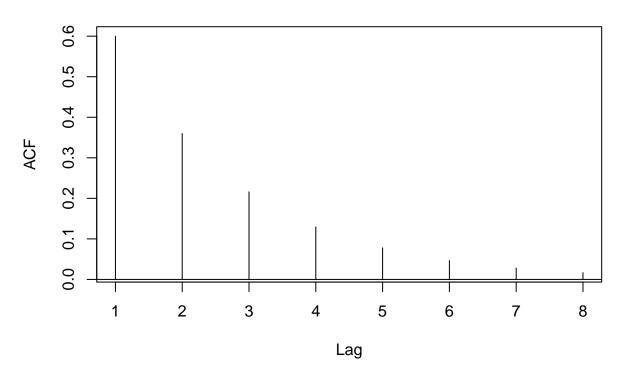
## 0 1 2 3 4 5 6
## 1.00000000 0.600000000 0.360000000 0.21600000 0.12960000 0.07776000 0.04665600

## 7 8
## 0.02799360 0.01679616

2.(c)

ACF=ARMAacf(ar=c(0.6),lag.max=8)
plot(y=ACF[-1],x=1:8,xlab='Lag',ylab='ACF',main="Population ACF",type='h')
abline(h=0)
```

Population ACF



3

```
RNGkind (sample.kind = "Rounding") # To make the result of set.seed() identical in different OSs

## Warning in RNGkind(sample.kind = "Rounding"): non-uniform 'Rounding' sampler

## used

set.seed(2)
ar.sim.1 <- arima.sim(list(order = c(1,0,0), ar = -0.6), n = 200)

RNGkind (sample.kind = "Rounding") # To make the result of set.seed() identical in different OSs

## Warning in RNGkind(sample.kind = "Rounding"): non-uniform 'Rounding' sampler

## used

set.seed(2)
ma.sim.2 <- arima.sim(list(order = c(0,0,2), ma = c(-0.8,+0.5)), n = 200)

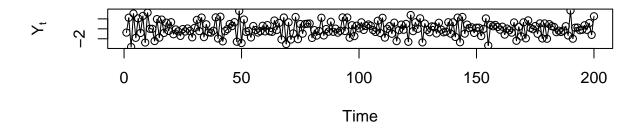
# Important! R's convention is to use positive thetas for MA models (so we have to negate)

# E.g., ma = 0.9 means theta = -0.9.
```

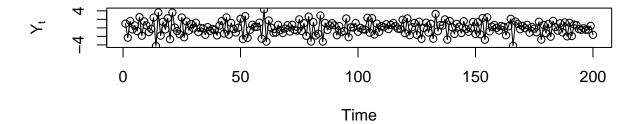
3.(a)

```
par(mfrow=c(2,1))
plot(ar.sim.1,ylab=expression(Y[t]),xlab="Time",type="o",main="AR(1) simulation, phi=-0.6")
plot(ma.sim.2,ylab=expression(Y[t]),xlab="Time",type="o",main="MA(2) simulation, theta1=+0.8, theta2=-0
```

AR(1) simulation, phi=-0.6



MA(2) simulation, theta1=+0.8, theta2=-0.5



3.(b)

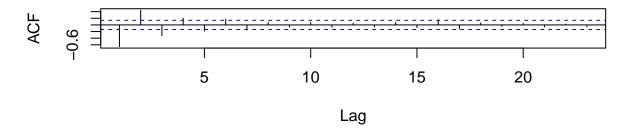
```
par(mfrow=c(2,1))

#plot(ar.sim.1,ylab=expression(Y[t]),xlab="Time",type="o",main="AR(1) simulation, phi=-0.6")

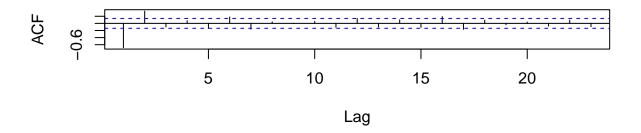
acf(ar.sim.1,main="Sample ACF AR(1), phi=-0.6")

#plot(ma.sim.2,ylab=expression(Y[t]),xlab="Time",type="o",main="MA(2) simulation, theta1=+0.8, theta2=-acf(ma.sim.2,main="Sample ACF MA(2), theta1=+0.8, theta2=-0.5")
```

Sample ACF AR(1), phi=-0.6



Sample ACF MA(2), theta1=+0.8, theta2=-0.5

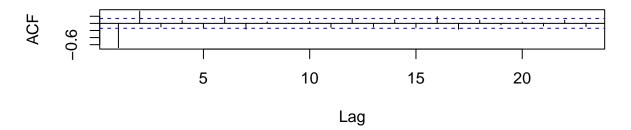


3.(c)

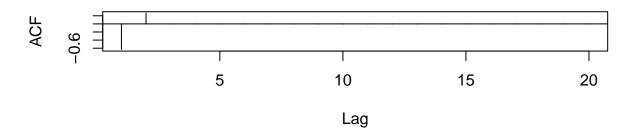
MA(2): There are two spikes on K=1,2 that are in agreement with the theory. To compare the population and sample I plot both in the same frame.

```
# MA(2)
par(mfrow=c(2,1))
acf(ma.sim.2,main="Sample ACF MA(2), theta1=+0.8, theta2=-0.5")
ACF=ARMAacf(ma=c(-0.8,+0.5),lag.max=20)
plot(y=ACF[-1],x=1:20,xlab='Lag',ylab='ACF',main="Population ACF MA(2), theta1=+0.8, theta2=-0.5", type
abline(h=0)
```

Sample ACF MA(2), theta1=+0.8, theta2=-0.5



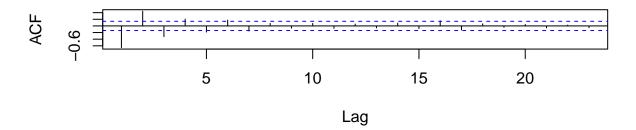
Population ACF MA(2), theta1=+0.8, theta2=-0.5



AR(2): Spikes decay quickly with an alternating pattern. To compare the population and sample, I plot both in the same frame.

```
# AR(1)
par(mfrow=c(2,1))
acf(ar.sim.1,main="Sample ACF AR(1), phi=-0.6")
ACF=ARMAacf(ar=c(-0.6),lag.max=20)
plot(y=ACF[-1],x=1:20,xlab='Lag',ylab='ACF',main="Population ACF AR(1), phi=-0.6",type='h')
abline(h=0)
```

Sample ACF AR(1), phi=-0.6



Population ACF AR(1), phi=-0.6

