

**a) Generate an AR(1) and ARMA(1,1) process. Do not use predefined functions. Estimate both the processes**

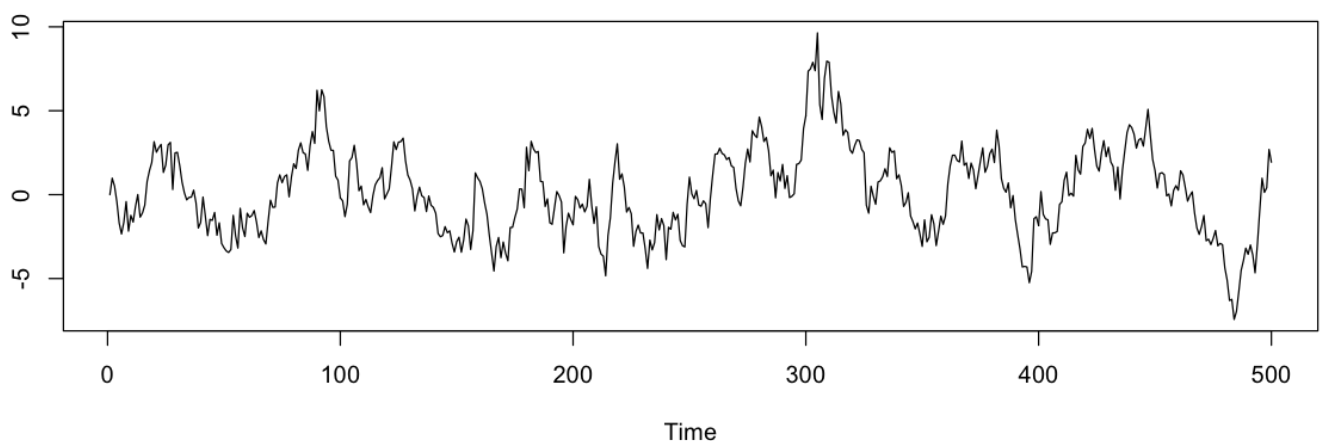
```
if (!require(forecast)) install.packages("forecast")
if (!require(forecast)) install.packages("uroot")

library(stats)
library(repr) -
library(tseries)
library(readr)
library(forecast)
library(uroot)

options(repr.plot.width = 10, repr.plot.height = 4)

File "<ipython-input-1-e605420c576c>", line 1
    if (!require(forecast)) install.packages("forecast")
        ^
SyntaxError: invalid syntax
```

```
#AR(1) process
set.seed(7257)
ability
l <- 500
e <- rnorm(l)
yt <- vector()
store values of yt for t=1,...,l
phil <- 0.9
nt phi 1
yt[1] <- 0
1
yt[2] <- phil * e[1]
2
for (i in 3 : l){
a for 2<t<l
    yt[i] <- phil * yt[i - 1] + e[i]
}
plot.ts(yt, ylab = NA)
```

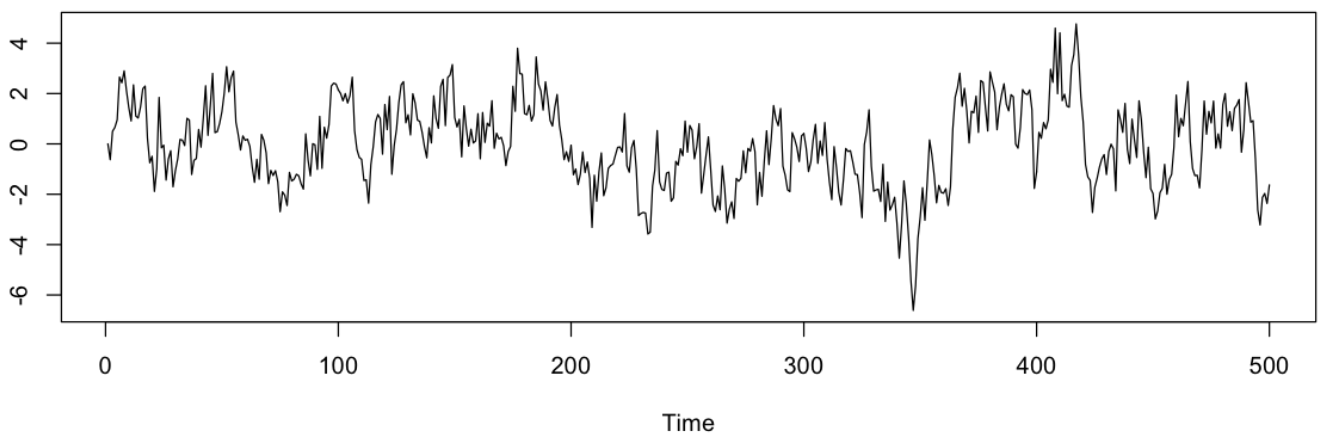


```
set.seed(8087) #setting seed for replic
```

```

ability
l <- 500                                     #number of observations
e <- rnorm(l)                                #white noise process
yt <- vector()                               #create blanc vector to
store values of yt for t=1,...,l
phi <- 0.9                                   #set value of coefficie
nt phi
theta <- 0.2                                 #set value of coefficie
nt theta
yt[1] <- 0                                   #set value of yt for t=
1
yt[2] <- phi * e[1]                           #set value of yt for t=
2
for (i in 3 : l){                             #loop to fill in yt dat
a for 2<t<l
    yt[i] <- phi * yt[i - 1] + e[i] - theta * e[i-1]
}
plot.ts(yt, ylab = NA)                       #plot the yt-s

```



**b) Choose one real time series and estimate the best linear model (AR, MA, ARMA, ARMA) that fits the time series.**

In [81]:

```

data <- read.csv("AAPL.csv")                 #load Apple stock data
opening <- data[,2]                           #assign the opening pri
ces
dopening <- diff(opening, lag = 1)            #take first differences
par(mfrow = c(1, 2))                         #make graphs show in pa
irs

plot.ts(opening, ylab = NA, main = 'opening', cex.main = 0.8) #plot the original openi
ng prices as time series
plot.ts(dopening, ylab = NA, main = 'dopening', cex.main = 0.8) #plot the first differen
ces of opening prices as time series

adf.test(opening)                             #confirm stacionarity wi
th a test
adf.test(dopening)                           #confirm stacionarity wi
th a test

```

Augmented Dickey-Fuller Test

```

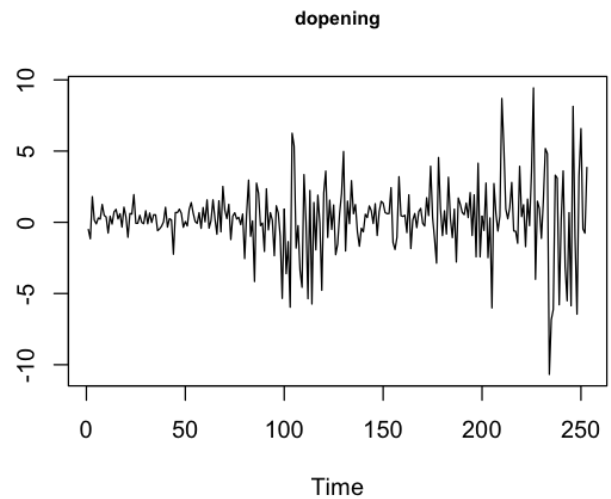
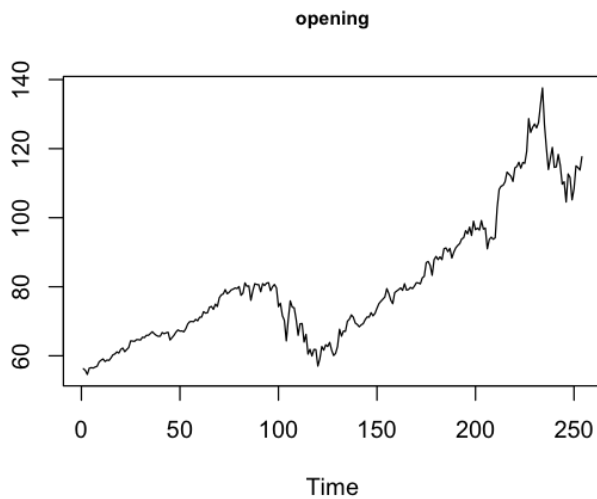
data: opening
Dickey-Fuller = -1.6281, Lag order = 6, p-value = 0.7324
alternative hypothesis: stationary

```

Warning message in adf.test(dopening):  
"p-value smaller than printed p-value"

Augmented Dickey-Fuller Test

```
data: dopening
Dickey-Fuller = -5.6958, Lag order = 6, p-value = 0.01
alternative hypothesis: stationary
```



In [82]:

```
kpss.test(opening)                                     #confirm stacionarity w
ith a test (double-checking because of suspicious rising trend of variance)
kpss.test(dopening)                                   #confirm stacionarity w
ith a test (double-checking because of suspicious rising trend of variance)
```

Warning message in `kpss.test(opening)`:  
"p-value smaller than printed p-value"

KPSS Test for Level Stationarity

```
data: opening
KPSS Level = 3.2184, Truncation lag parameter = 5, p-value = 0.01
```

Warning message in `kpss.test(dopening)`:  
"p-value greater than printed p-value"

KPSS Test for Level Stationarity

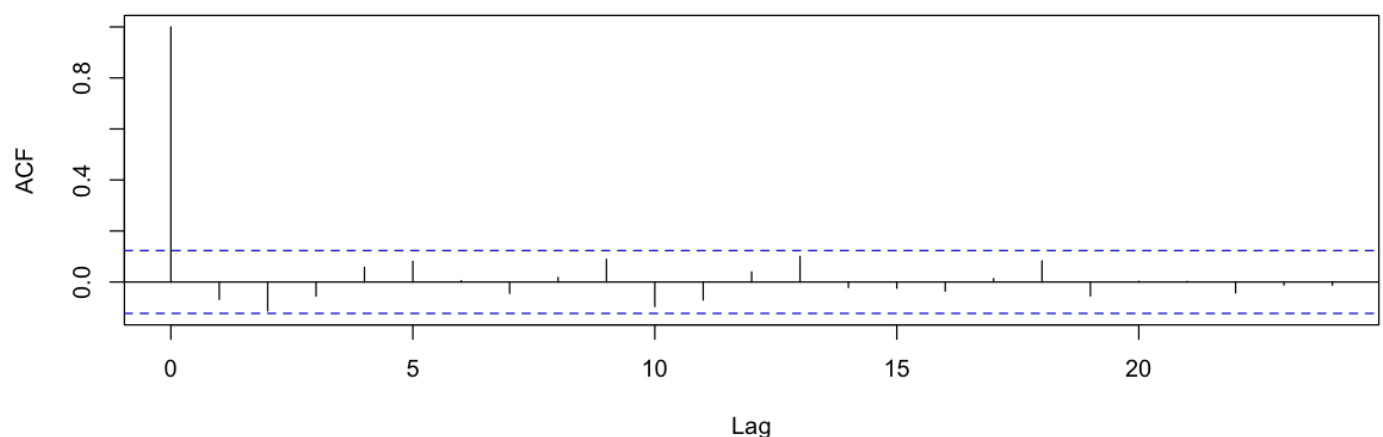
```
data: dopening
KPSS Level = 0.11993, Truncation lag parameter = 5, p-value = 0.1
```

### Plotting ACF and PACF to help with estimation of model.

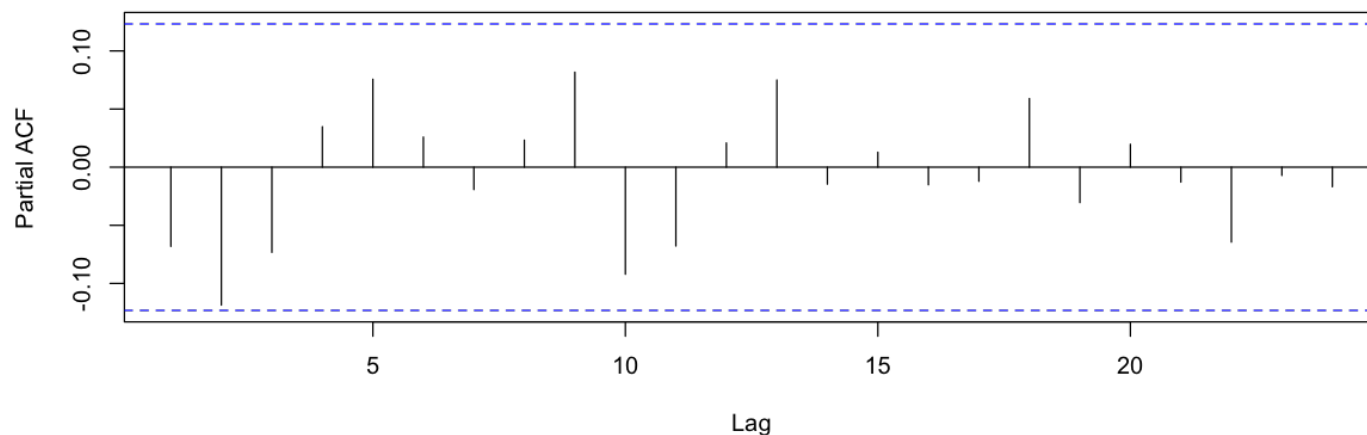
In [83]:

```
acf(dopening)
pacf(dopening)
```

**Series dopening**



## Series dopening



In [101]:

```
y_model <- Arima(dopening, order = c(1, 0, 0))
summary(y_model)
```

Series: dopening  
ARIMA(1,0,0) with non-zero mean

Coefficients:

	ar1	mean
	-0.0685	0.2419
s.e.	0.0629	0.1443

sigma<sup>2</sup> estimated as 6.059: log likelihood=-585.89  
AIC=1177.78 AICc=1177.87 BIC=1188.38

Training set error measures:

	ME	RMSE	MAE	MPE	MAPE	MASE
Training set	-0.0001913391	2.451791	1.58959	100.2983	124.2024	0.6403158

ACF1

Training set -0.008359758

In [100]:

```
y_model1 <- Arima(dopening, order = c(0, 0, 2))
summary(y_model1)
```

Series: dopening  
ARIMA(0,0,2) with non-zero mean

Coefficients:

	ma1	ma2	mean
	-0.0868	-0.1071	0.2410
s.e.	0.0621	0.0581	0.1235

sigma<sup>2</sup> estimated as 5.994: log likelihood=-584.03  
AIC=1176.06 AICc=1176.22 BIC=1190.19

Training set error measures:

	ME	RMSE	MAE	MPE	MAPE	MASE
Training set	-0.001148756	2.4337	1.575369	96.97446	126.3212	0.6345872

ACF1

Training set 0.002714232

In [99]:

```
y_model2 <- auto.arima(dopening)
summary(y_model2)
```

Series: dopening  
ARIMA(0,0,0) with non-zero mean

Coefficients:

```
      mean
0.2426
s.e. 0.1545
```

```
sigma^2 estimated as 6.064:  log likelihood=-586.48
AIC=1176.96   AICc=1177.01   BIC=1184.03
```

Training set error measures:

```
      ME      RMSE      MAE      MPE      MAPE      MASE
Training set 5.757756e-17 2.457552 1.611239 104.9005 127.7979 0.6490362
      ACF1
Training set -0.06813247
```

In [98]:

```
y_model3 <- auto.arima(dopening, approximation=FALSE, stepwise =FALSE )
summary(y_model3)
```

```
Series: dopening
ARIMA(0,0,2) with non-zero mean
```

Coefficients:

```
      ma1      ma2      mean
-0.0868 -0.1071 0.2410
s.e. 0.0621 0.0581 0.1235
```

```
sigma^2 estimated as 5.994:  log likelihood=-584.03
AIC=1176.06   AICc=1176.22   BIC=1190.19
```

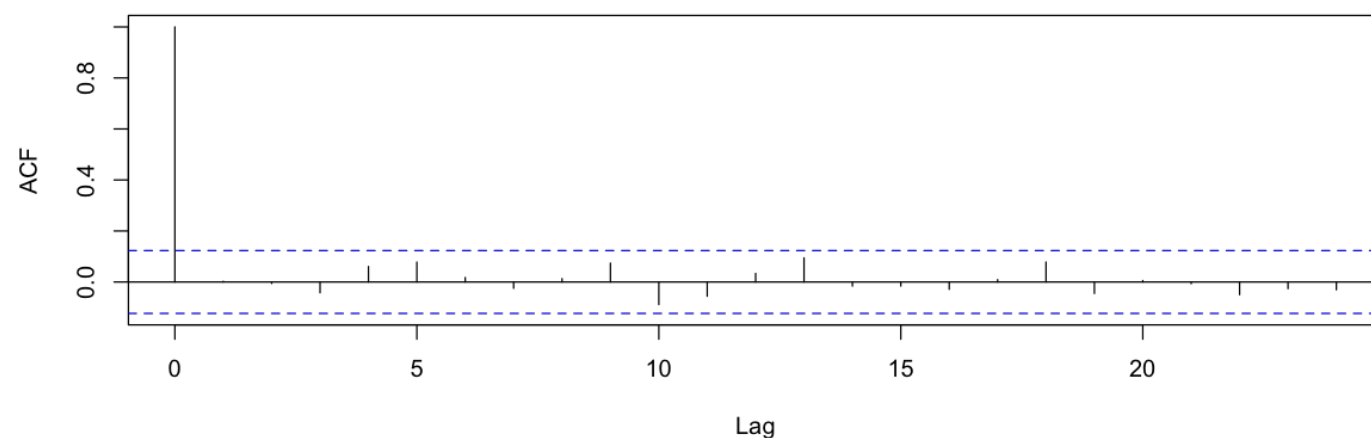
Training set error measures:

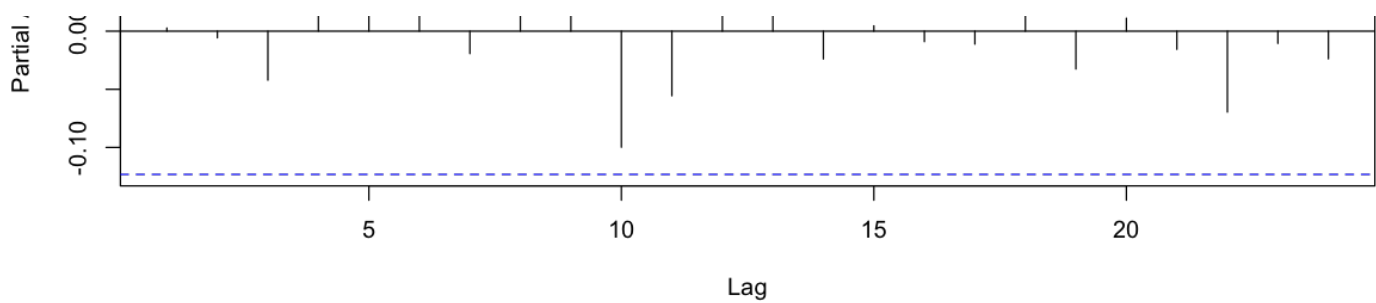
```
      ME      RMSE      MAE      MPE      MAPE      MASE
Training set -0.001148756 2.4337 1.575369 96.97446 126.3212 0.6345872
      ACF1
Training set 0.002714232
```

### Lowest AICc in y\_model3, ARIMA(0,0,2) with non-zero mean

In [116]:

```
acf(y_model3$residuals, main = NA) #plotting the residuals in ACF and
PACF to check whether the residuals show WN behavior
pacf(y_model3$residuals, main = NA)
```





***They do show WN behavior, using Ljung-Box test to check for lack of fit***

In [119]:

```
Box.test(y_model3$residuals, type = "Ljung-Box", lag = 4)
Box.test(y_model3$residuals, type = "Ljung-Box", lag = 8)
Box.test(y_model3$residuals, type = "Ljung-Box", lag = 12)
plot.ts(dopening, ylab = NA, main = 'fitted values')
lines(y_model3$fitted, col = 'red')
```

Box-Ljung test

```
data: y_model3$residuals
X-squared = 1.4265, df = 4, p-value = 0.8396
```

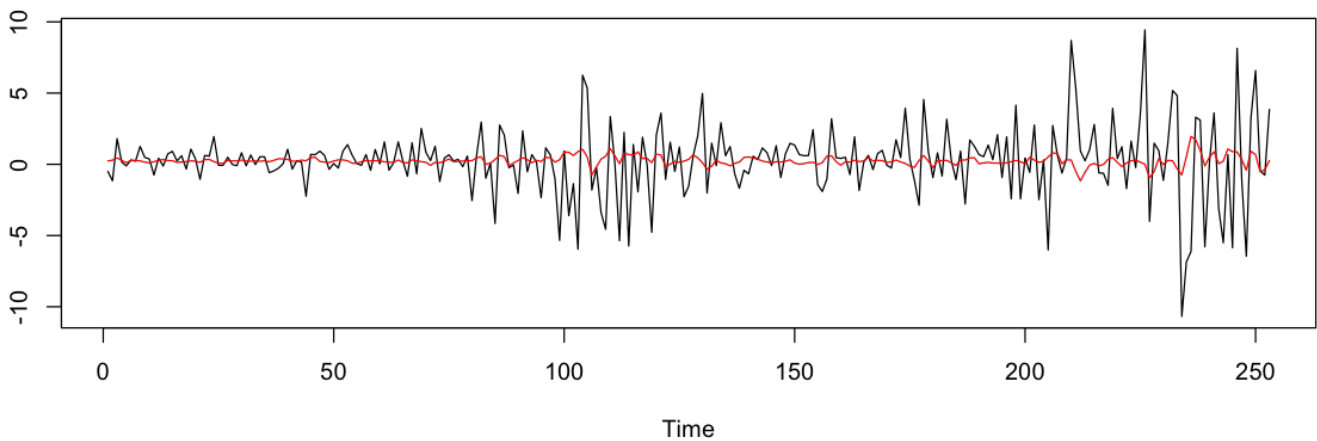
Box-Ljung test

```
data: y_model3$residuals
X-squared = 3.2962, df = 8, p-value = 0.9144
```

Box-Ljung test

```
data: y_model3$residuals
X-squared = 7.9595, df = 12, p-value = 0.7883
```

**fitted values**



***High p-values don't indicate lack of fit.***

In [ ]: