HW01_zilinw3

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Question 1 (Multivariate Normal Distribution)

(a).

Generate a set of n=2000 observations from the bivariate Normal Distribution $N(\mu, \Sigma)$, where $\mu = (1, 2)^{\mathrm{T}}$ and

$$\Sigma = \begin{pmatrix} 1 & 0.5 \\ 0.5 & 1 \end{pmatrix}$$

Use random seed 1. Report the sample covariance matrix of the generated data and compare it with the true covariance matrix Σ.

Answer:

This can be done using the `mvrnorm` function in the `MASS` package:

```r
library(MASS)
set.seed(1)
Sigma <- matrix(c(1,0.5,0.5,1),2,2)
mu <- c(1, 2)

# Generate 2000 observations
n <- 2000
X <- mvrnorm(n = n, mu, Sigma)

# Display the first 5 observations
head(X, 5)
```

```
##            [,1]     [,2]
## [1,]  0.9005499 1.014400
## [2,]  2.1201672 1.197912
## [3,] -0.5335260 2.086175
## [4,]  2.1219187 3.641189
## [5,]  1.3132871 2.257437
```

```r
# Compute the sample covariance matrix
sample_cov <- cov(X)
print(sample_cov)
```

```
##           [,1]      [,2]
## [1,] 1.0443799 0.5392157
## [2,] 0.5392157 1.1045078
```

```r
# Compare sample covariance with true covariance matrix
print(Sigma)
```

```
##      [,1] [,2]
## [1,]  1.0  0.5
## [2,]  0.5  1.0
```

The sample covariance matrix of the generated data is

$$\begin{pmatrix} 1.044 & 0.539 \\ 0.539 & 1.105 \end{pmatrix}$$

Compared to the true covariance matrix, the sample covariance matrix's individual numbers are a little bit bigger, but not by much. They are very similar and close to each other.

(b).

Instead of using the mvrnorm function from the MASS package, use an alternative way to complete question (a). First generate n standard normal random variables, and then transform them to the desired distribution.

Use random seed 1. Report the sample covariance matrix of the generated data and compare it with the true covariance matrix Σ.

Answer:

The mathematical formula of this approach is:

$X = \mu + AZ$,

where Z is an $n \times p$ matrix of standard normal random variables, and A is the Cholesky decomposition of Σ, i.e., A satisfies $AA^T = \Sigma$.

Then implement this approach in R:

```r
set.seed(1)

# Generate standard normal variables
Z <- matrix(rnorm(n * 2), nrow = n)

# Compute Cholesky decomposition of Sigma
A <- chol(Sigma)

# Transform standard normal variables
data_manual <- t(A %*% t(Z)) + matrix(rep(mu, n), ncol = 2, byrow = TRUE)

# Display the first 5 observations
head(data_manual, 5)
```

```
##             [,1]      [,2]
## [1,] -0.0695286 1.2325719
## [2,]  0.2225159 0.3352784
## [3,]  0.9742218 3.4027020
## [4,]  2.8549158 2.4497009
## [5,]  1.3015828 1.9516325
```

```r
# Compute the sample covariance matrix
sample_cov_manual <- cov(data_manual)
print(sample_cov_manual)
```

```
##           [,1]      [,2]
## [1,] 1.3781020 0.4935851
## [2,] 0.4935851 0.8028422
```

```r
# Compare sample covariance with true covariance matrix
print(Sigma)
```

```
##      [,1] [,2]
## [1,]  1.0  0.5
## [2,]  0.5  1.0
```

The sample covariance matrix of the generated data is

$$\begin{pmatrix} 1.378 & 0.494 \\ 0.494 & 0.803 \end{pmatrix}$$

Compared to the true covariance matrix, the covariance for (1,1) is larger, and the rest of the covariances are smaller. All in all, the difference is relatively large.

(c).

Write an R function called mymvnorm that takes the following arguments: n, mu, sigma. Use the logic in part b) to generate the data.

Report the sample covariance matrix of the generated data and compare it with the true covariance matrix Σ.

Answer:

```r
mymvnorm <- function(n, mu, sigma) {
  # Generate standard normal variables
  Z <- matrix(rnorm(n * length(mu)), nrow = n)

  # Compute Cholesky decomposition of sigma
  A <- chol(sigma)

  # Transform standard normal variables
  data <- t(A %*% t(Z)) + matrix(rep(mu, n), ncol = length(mu), byrow = TRUE)
```

```r
  return(data)
}

# Test the function
set.seed(1)
mu <- c(1, 2)
sigma <- matrix(c(1, 0.5, 0.5, 1), nrow = 2)
n <- 2000

# Generate the data
data_function <- mymvnorm(n, mu, sigma)

# Display the first 5 observations
head(data_function, 5)
```

```
##             [,1]      [,2]
## [1,] -0.0695286 1.2325719
## [2,]  0.2225159 0.3352784
## [3,]  0.9742218 3.4027020
## [4,]  2.8549158 2.4497009
## [5,]  1.3015828 1.9516325
```

```r
# Compute the sample covariance matrix
sample_cov_function <- cov(data_function)
print(sample_cov_function)
```

```
##           [,1]      [,2]
## [1,] 1.3781020 0.4935851
## [2,] 0.4935851 0.8028422
```

```r
# Compare sample covariance with true covariance matrix
print(sigma)
```

```
##      [,1] [,2]
## [1,]  1.0  0.5
## [2,]  0.5  1.0
```

The answer in this question is identical to the one in part b). The sample covariance matrix of the generated data is

$$\begin{pmatrix} 1.378 & 0.494 \\ 0.494 & 0.803 \end{pmatrix}$$

Compared to the true covariance matrix, the covariance for (1,1) is larger, and the rest of the covariance are smaller. All in all, the difference is relatively large.

(d).

I used ChatGPT. For the prompt, I just copied the question and asked ChatGPT to answer them. The tool suggested a corrected answer to the question. Only when part (b) asked to use Latex to write the mathematical formula and it didn't use Latex, so I wrote it in Latex myself.

Question 2 (Data Manipulation Plots)

Write a function that calculates the price gap between any two given dates.

(a).

Calculate a 90-day moving average of the closing price of AAPL and plot it on the same graph. Do this in two ways: 1) there is a built-in function called SMA in the quantmod package; 2) write a function to calculate the moving average.

Answer:

The first approach uses the SMA function from the quantmod package to compute the moving average.

```r
# install.packages("quantmod")
library(quantmod)
```

```
## Warning:   'quantmod' R 4.3.3
```

```
##      xts
```

```
## Warning:   'xts' R 4.3.3
```

```
##      zoo
```

```
## Warning:   'zoo' R 4.3.3
```

```
##
##    'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
##      TTR
```

```
## Warning:   'TTR' R 4.3.3
```

```
## Registered S3 method overwritten by 'quantmod':
##   method            from
##   as.zoo.data.frame zoo
```

```r
getSymbols("AAPL")
```

```
## [1] "AAPL"
```

```r
# Calculate the 90-day simple moving average using quantmod's built-in function
AAPL$SMA90 <- SMA(Cl(AAPL), n = 90)

# Plot the original closing prices
plot(AAPL$AAPL.Close, pch = 19)
```

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```


```r
# Add the 90-day moving average to the plot
lines(AAPL$SMA90, col = "red", lwd = 3)
```

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## 'mbcsToSbcs'  '1  03  2007'  <e6>  dot

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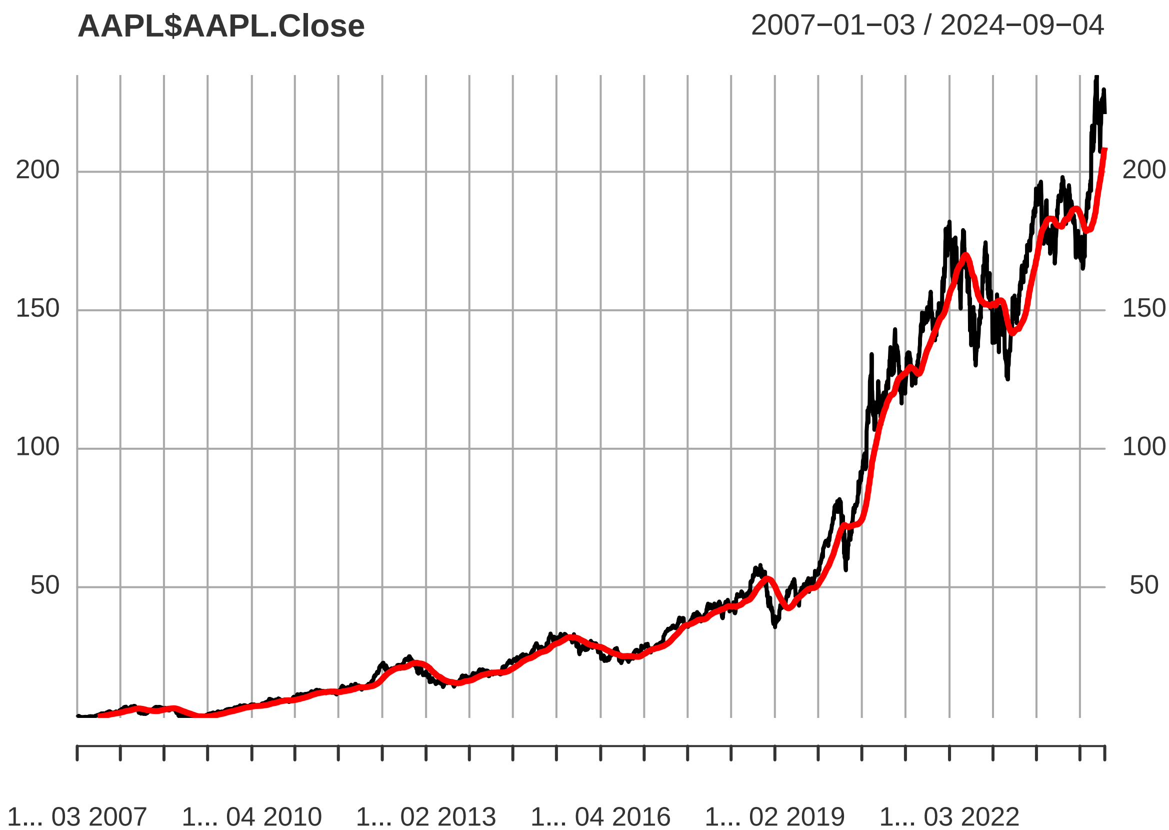

The second approach writes a custom function to calculate the moving average.

```r
# Define the custom moving average function
my_moving_average <- function(x, window) {
  n <- length(x)                  # Length of the input data
  ma <- rep(NA, n)                # Initialize an output vector of NAs (same length as the input)

  for (i in window:n) {
    # Calculate the average of the previous 'window' days
    ma[i] <- mean(x[(i - window + 1):i], na.rm = TRUE)
  }

  return(ma)
}

# Apply the custom function to calculate the 90-day moving average
AAPL$CustomMA90 <- my_moving_average(Cl(AAPL), 90)

# Plot the closing prices of AAPL
plot(AAPL$AAPL.Close, main = "AAPL Closing Price with 90-Day Moving Average (Custom)", pch = 19)
```

```
## Warning in axis(1, at = xcoords[axt], labels = labels, las = theme$las, :
## 'mbcsToSbcs'  '1  03 2007'  <e6>  dot
```

```
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## Warning in axis(1, at = xcoords[axt], labels = labels, las = theme$las, :
## 'mbcsToSbcs' '9 04 2024' <88> dot
```


```
# Add the custom 90-day moving average to the plot
lines(AAPL$CustomMA90, col = "red", lwd = 2)
```

```
## Warning in axis(1, at = xcoords[axt], labels = labels, las = theme$las, :
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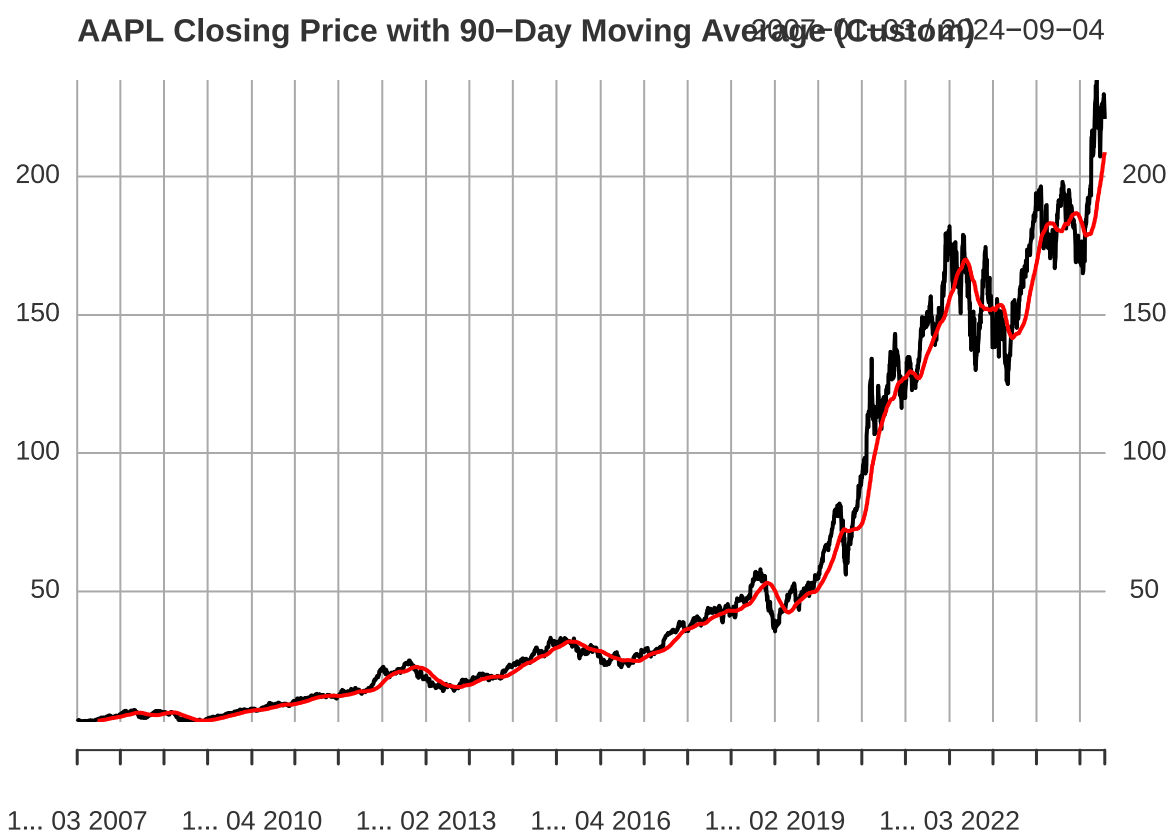

(b).

Differences: The my_average() function calculates a centered moving average, whereas SMA() calculates a lagging moving average. The SMA() result is delayed by the window size (90 days) because it only considers past data. The my_average() is centered, meaning it uses both past and future data. This creates a smoother curve because it averages around the current data point rather than just looking at the past. Also, the custom function uses a for loop, which is less efficient than the vectorized operations in SMA().

I don't think your line is a good choice when it is used for predicting future prices. Because it uses future data points to calculate the centered moving average. In real trading scenarios, we don't have access to future prices, so this method isn't practical for actual trading or forecasting. Also, we can't use future data to predict future prices.

For practical purposes, I would prefer the built-in SMA function because it's efficient, simple to use, and reliable for most time series analysis. The SMA function is highly optimized for time series operations, making it faster for large data sets. This method is highly efficient. Also, we don't need to write any extra code to handle the moving average logic and it's easy to implement. What's more, it is part of a well-maintained library, meaning it's less prone to bugs or edge case failures.

Question 3 (Read/write Data)

(a).

Install the devtools package and run the find the code to install the ElemStatLearn package.

Answer:

```r
# install.packages("devtools")
library(devtools)
```

```
## Warning:   'devtools' R 4.3.3
```

```
##      usethis
```

```
## Warning:   'usethis' R 4.3.3
```

```r
install_github("cran/ElemStatLearn")
```

```
## Skipping install of 'ElemStatLearn' from a github remote, the SHA1 (253e5401) has not changed since l
##   Use `force = TRUE` to force installation
```

(b).

Load the ElemStatLearn package and obtain the ozone data. Save this data into a .csv file, and then read the data back from that file into R. Print out the first 5 observations.

Answer:

```r
library(ElemStatLearn)
data(ozone)
head(ozone, 5)
```

```
##   ozone radiation temperature wind
## 1    41       190          67  7.4
## 2    36       118          72  8.0
## 3    12       149          74 12.6
## 4    18       313          62 11.5
## 5    23       299          65  8.6
```

```r
write.csv(ozone, "ozone_data.csv", row.names = FALSE)
ozone_data_back <- read.csv("ozone_data.csv")
head(ozone_data_back, 5)
```

```
##   ozone radiation temperature wind
## 1    41       190          67  7.4
## 2    36       118          72  8.0
## 3    12       149          74 12.6
## 4    18       313          62 11.5
## 5    23       299          65  8.6
```