

Time-Series-Analysis

shang-chieh0830

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Chapter 1

About

This book is a concise lecture note about *Time Series Analysis*.

The content of this book is from the course Time Series Analysis taught by Chris Bilder. You can check his YouTube channel to get full(and correct) information about this course.

Again, I do **NOT** own the content of this book. I write this book only for studying. All credits belong to Chris Bilder.

If there is any copyright concerns, I will make this book private ASAP.

Chapter 2

Introduction to R

We will go over some of the basic R operations in this section.

If you have questions, you should check Chris Bilder's website for full information.

2.1 Basic Operation

```
2+2  
#> [1] 4
```

```
2^3  
#> [1] 8
```

```
# calculate the cdf of std. normal  
pnorm(1.96) # 1.96 is the quantile  
#> [1] 0.9750021
```

```
log(1)  
#> [1] 0
```

```
sin(pi/2)  
#> [1] 1
```

```
3/4  
#> [1] 0.75
```

```
save <- 2+2
save
#> [1] 4
```

```
objects()
#> [1] "save"
```

```
ls()
#> [1] "save"
```

```
# quit operaiton
# q()
```

2.2 Vectors

```
x <- c(1,2,3,4,5)
x
#> [1] 1 2 3 4 5
```

```
sd(x)
#> [1] 1.581139
```

```
mysd <- function(x){
  cat(" My data \n", x, "\n has std deviation",sqrt(var(x)))
}
```

```
mysd(x)
#> My data
#> 1 2 3 4 5
#> has std deviation 1.581139
```

```
pnorm(q=1.96, mean=1.96, sd=1)
#> [1] 0.5
```

The full syntax for `pnorm()` is `pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)`

```
pnorm(q=c(-1.96,1.96))
#> [1] 0.0249979 0.9750021
```



```

x <- c(3.68, -3.63, 0.80, 3.03, -9.86, -8.66,
      -2.38, 8.94, 0.52, 1.25)

y <- c(0.55, 1.65, 0.98, -0.07, -0.01, -0.31,
      -0.34, -1.38, -1.32, 0.53)

x+y
#> [1] 4.23 -1.98 1.78 2.96 -9.87 -8.97 -2.72 7.56 -0.80
#> [10] 1.78

x*y
#> [1] 2.0240 -5.9895 0.7840 -0.2121 0.0986 2.6846
#> [7] 0.8092 -12.3372 -0.6864 0.6625

mean(x)
#> [1] -0.631
x-mean(x)
#> [1] 4.311 -2.999 1.431 3.661 -9.229 -8.029 -1.749 9.571
#> [9] 1.151 1.881

x*2
#> [1] 7.36 -7.26 1.60 6.06 -19.72 -17.32 -4.76 17.88
#> [9] 1.04 2.50

```

The element(elt)-wise operation makes our life easier.

2.3 Files

Click [gpa.csv](#) to download the GPA csv file.

Click [gpa.txt](#) to download the GPA txt file.

```

getwd()
#> [1] "/Users/weishangjie/Desktop/Time-Series-Analysis"

gpatxt <- read.table("gpa.txt", header=TRUE, sep="")
gpacsv <- read.csv("gpa.csv")

gpacsv$HSGPA
#> [1] 3.04 2.35 2.70 2.55 2.83 4.32 3.39 2.32 2.69 2.83 2.39
#> [12] 3.65 2.85 3.83 2.22 1.98 2.88 4.00 2.28 2.88

```

```
gpacsv$CollegeGPA
#> [1] 3.10 2.30 3.00 2.45 2.50 3.70 3.40 2.60 2.80 3.60 2.00
#> [12] 2.90 3.30 3.20 2.80 2.40 2.60 3.80 2.20 2.60
```

```
gpacsv[1,1] # [row, col]
#> [1] 3.04
```

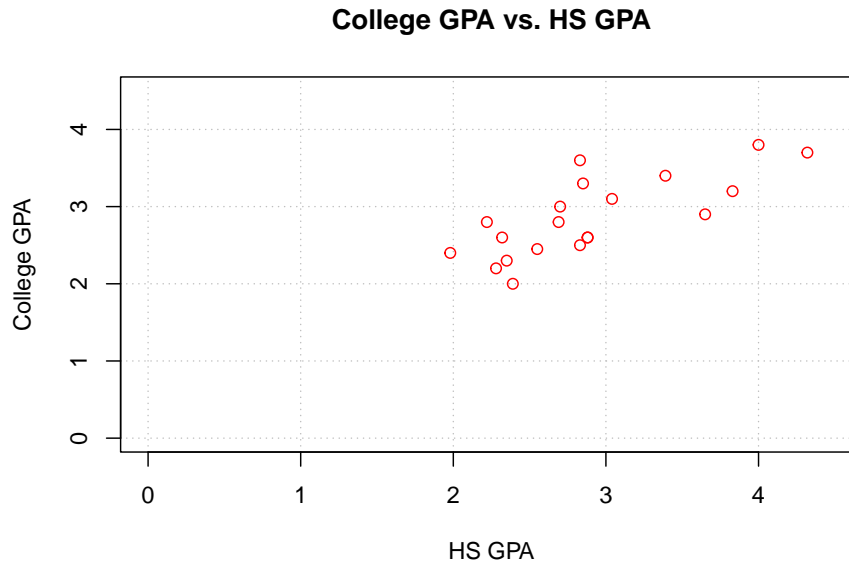
```
gpacsv[,1]
#> [1] 3.04 2.35 2.70 2.55 2.83 4.32 3.39 2.32 2.69 2.83 2.39
#> [12] 3.65 2.85 3.83 2.22 1.98 2.88 4.00 2.28 2.88
```

```
gpacsv[c(1,3,5),2]
#> [1] 3.1 3.0 2.5
```

```
gpacsv[, "HSGPA"]
#> [1] 3.04 2.35 2.70 2.55 2.83 4.32 3.39 2.32 2.69 2.83 2.39
#> [12] 3.65 2.85 3.83 2.22 1.98 2.88 4.00 2.28 2.88
```

```
summary(gpacsv)
#>      HSGPA      CollegeGPA
#> Min.   :1.980   Min.   :2.000
#> 1st Qu.:2.380   1st Qu.:2.487
#> Median :2.830   Median :2.800
#> Mean   :2.899   Mean   :2.862
#> 3rd Qu.:3.127   3rd Qu.:3.225
#> Max.   :4.320   Max.   :3.800
```

```
plot(x = gpacsv$HSGPA, y = gpacsv$CollegeGPA,
     xlab = "HS GPA", ylab = "College GPA",
     main = "College GPA vs. HS GPA",
     xlim = c(0,4.5), ylim = c(0,4.5), col = "red",
     pch = 1, cex = 1.0, panel.first = grid(col = "gray", lty
     = "dotted"))
```



The `plot()` function creates a two dimensional plot of data.

Here are descriptions of its arguments:

- `x` specifies what is plotted for the x-axis.
- `y` specifies what is plotted for the y-axis.
- `xlab` and `ylab` specify the x-axis and y-axis labels, respectively.
- `main` specifies the main title of the plot.
- `xlim` and `ylim` specify the x-axis and y-axis limits, respectively.
 - Notice the use of the `c()` function.
- `col` specifies the color of the plotting points.
 - Run the `colors()` function to see what possible colors can be used.
 - Also, you can see [Here](#) for the colors from `colors()`.
- `pch` specifies the plotting characters.
- `cex` specifies the height of the plotting characters. The value 1.0 is the default.
- `panel.first = grid()` specifies grid lines will be plotted.

- The line types can be specified as follows: 1=solid, 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash or as one of the character strings "blank", "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash". These line type specifications can be used in other functions.
- The `par()`(parameter) function's Help contains more information about the different plotting options!

2.4 Regression

Our is model is:

$$\text{CollegeGPA} = \beta_0 + \beta_1 \text{HSGPA} + \epsilon$$

```
mod.fit <- lm(formula= CollegeGPA~ HSGPA, data=gpacsv)
mod.fit
#>
#> Call:
#> lm(formula = CollegeGPA ~ HSGPA, data = gpacsv)
#>
#> Coefficients:
#> (Intercept)      HSGPA
#>      1.0869      0.6125
```

```
names(mod.fit)
#> [1] "coefficients" "residuals"      "effects"
#> [4] "rank"         "fitted.values"  "assign"
#> [7] "qr"           "df.residual"    "xlevels"
#> [10] "call"         "terms"          "model"
```

```
mod.fit$coefficients
#> (Intercept)      HSGPA
#>  1.0868795    0.6124941
```

```
round(mod.fit$residuals[1:5],2)
#>      1      2      3      4      5
#>  0.15 -0.23  0.26 -0.20 -0.32
```

```
library(tidyverse)
#> -- Attaching packages ----- tidyverse 1.3.2 --
#> v ggplot2 3.4.1      v purrr  1.0.1
#> v tibble  3.1.8      v dplyr  1.1.0
```

```

#> v tidyr 1.3.0 v stringr 1.5.0
#> v readr 2.1.4 v forcats 0.5.2
#> -- Conflicts ----- tidyverse_conflicts() --
#> x dplyr::filter() masks stats::filter()
#> x dplyr::lag() masks stats::lag()
save.fit <- data.frame(gpacsv, C.GPA.hat =
  round(mod.fit$fitted.values,2), residuals =
  round(mod.fit$residuals,2))

save.fit %>% head()
#> HSGPA CollegeGPA C.GPA.hat residuals
#> 1 3.04 3.10 2.95 0.15
#> 2 2.35 2.30 2.53 -0.23
#> 3 2.70 3.00 2.74 0.26
#> 4 2.55 2.45 2.65 -0.20
#> 5 2.83 2.50 2.82 -0.32
#> 6 4.32 3.70 3.73 -0.03

summary(mod.fit)
#>
#> Call:
#> lm(formula = CollegeGPA ~ HSGPA, data = gpacsv)
#>
#> Residuals:
#> Min 1Q Median 3Q Max
#> -0.55074 -0.25086 0.01633 0.24242 0.77976
#>
#> Coefficients:
#> Estimate Std. Error t value Pr(>|t|)
#> (Intercept) 1.0869 0.3666 2.965 0.008299 **
#> HSGPA 0.6125 0.1237 4.953 0.000103 ***
#> ---
#> Signif. codes:
#> 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Residual standard error: 0.3437 on 18 degrees of freedom
#> Multiple R-squared: 0.5768, Adjusted R-squared: 0.5533
#> F-statistic: 24.54 on 1 and 18 DF, p-value: 0.0001027

```

Hence, our estimated regression model is

$$\widehat{\text{collge.GPA}} = \hat{\beta}_0 + \hat{\beta}_1 \text{HS.GPA} = 1.0869 + 0.6125 \text{HS.GPA}$$

```

# Open a new graphics window
# device new
dev.new(width = 8, height = 6, pointsize = 10)

# 1 row and 2 columns of plots
par(mfrow = c(1,2))
# par= graphic parameter
# mfrow= make a frame by row

# Same scatter plot as before
plot(x = gpacsv$HSGPA, y = gpacsv$CollegeGPA, xlab = "HS
      GPA", ylab = "College GPA", main = "College GPA vs.
      HS GPA", xlim = c(0,4.5), ylim = c(0,4.5), col =
      "red", pch = 1, cex = 1.0, panel.first = grid(col =
      "gray", lty = "dotted"))

# Puts the line  $y = a + bx$  on the plot
abline(a = mod.fit$coefficients[1], b =
      mod.fit$coefficients[2], lty = "solid", col =
      "blue", lwd = 2)

# Same scatter plot as before
plot(x = gpacsv$HSGPA, y = gpacsv$CollegeGPA, xlab = "HS
      GPA", ylab = "College GPA", main = "College GPA vs.
      HS GPA", xlim = c(0,4.5), ylim = c(0,4.5), col =
      "red", pch = 1, cex = 1.0, panel.first = grid(col =
      "gray", lty = "dotted"))

# Add line
# expr= math expression
curve(expr = mod.fit$coefficients[1] +
      mod.fit$coefficients[2]*x,
      xlim = c(min(gpacsv$HSGPA),max(gpacsv$HSGPA)),
      col= "blue", add = TRUE, lwd = 2)

```

- The `dev.new()` function can be used to open a new plotting window.
- The `abline()` function can be used to draw straight lines on a plot. In the format used here, the line $y = a + bx$ was drawn where a was the (intercept) and b was the (slope).
- In the second plot, the `curve()` function was used to draw the line on the plot. This was done to have the line within the range of the high school

GPA values.

Let's use function to automate what we have done.

```
my.reg.func <- function(x, y, data) {

  # Fit the simple linear regression model and save the results in mod.fit
  mod.fit <- lm(formula = y ~ x, data = data)

  # Open a new graphics window - do not need to
  dev.new(width = 6, height = 6, pointsize = 10)

  # Same scatter plot as before
  plot(x = x, y = y, xlab = "x", ylab = "y", main = "y vs. x", panel.first=grid(col = "gray", l
    "dotted"))

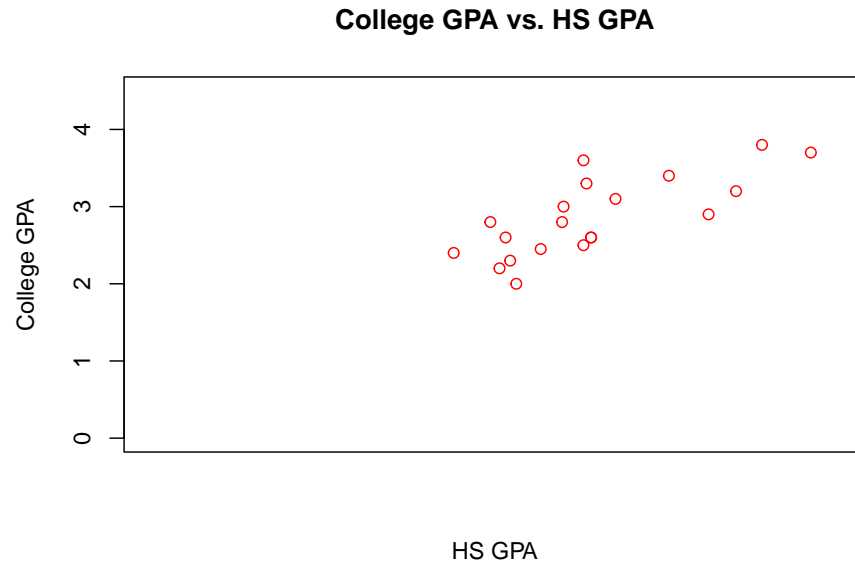
  # Plot model
  curve(expr = mod.fit$coefficients[1] +
    mod.fit$coefficients[2]*x, xlim = c(min(x),max(x)),
    col = "blue", add = TRUE)

  # This is the object returned
  mod.fit
}
```

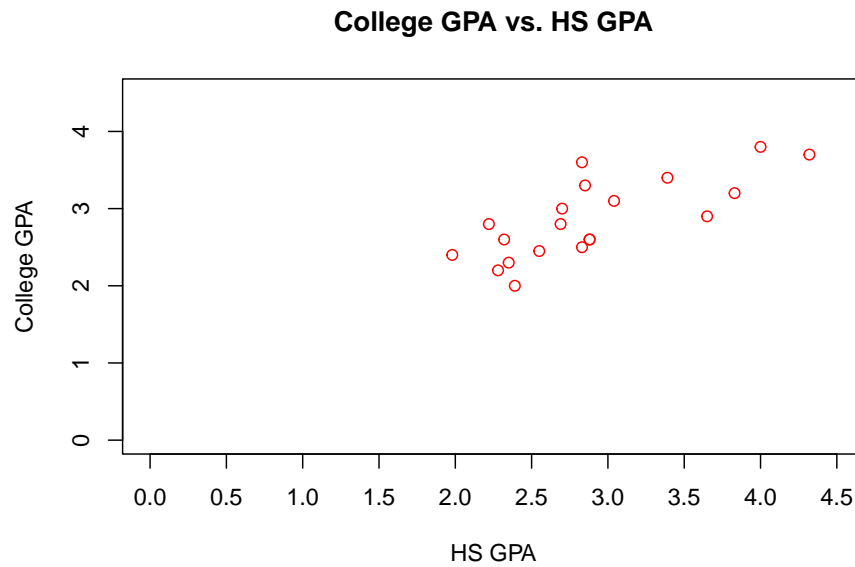
```
save.it <- my.reg.func(x = gpacsv$HSGPA, y =
  gpacsv$CollegeGPA, data = gpacsv)
```

To get specific x-axis or y-axis tick marks on a plot, use the `axis()` function. For example,

```
# Note that xaxt = "n" tells R to not give any labels on the
# x-axis (yaxt = "n" works for y-axis)
plot(x = gpacsv$HSGPA, y = gpacsv$CollegeGPA, xlab = "HS GPA",
  ylab = "College GPA", main = "College GPA vs. HS GPA",
  xaxt = "n", xlim = c(0, 4.5), ylim = c(0, 4.5), col =
  "red", pch = 1)
```



```
plot(x = gpacsv$HSGPA, y = gpacsv$CollegeGPA, xlab = "HS GPA",  
     ylab = "College GPA", main = "College GPA vs. HS GPA",  
     xaxt = "n", xlim = c(0, 4.5), ylim = c(0, 4.5), col =  
       "red", pch = 1)  
  
#Major tick marks  
axis(side = 1, at = seq(from = 0, to = 4.5, by = 0.5))
```

```
plot(x = gpacsv$HSGPA, y = gpacsv$CollegeGPA, xlab = "HS GPA",  
     ylab = "College GPA", main = "College GPA vs. HS GPA",  
     xaxt = "n", xlim = c(0, 4.5), ylim = c(0, 4.5), col =  
     "red", pch = 1)  
  
#Major tick marks  
axis(side = 1, at = seq(from = 0, to = 4.5, by = 0.5))  
  
#Minor tick marks  
axis(side = 1, at = seq(from = 0, to = 4.5, by = 0.1), tck  
     = 0.01, labels = FALSE)
```

