

## stats 380 A2

Sooyong Choi

10/09/2020

### Question 1

```
triDiag = function(diagonal, upper, lower, nrow , ncol ) {  
  
  if (missing(nrow) & missing(ncol)) {  
    my_matrix = matrix(0, nrow = length(diagonal), ncol = length(diagonal))  
    diag(my_matrix) = diagonal  
    my_matrix[row(my_matrix) - col(my_matrix) == 1] = lower  
    my_matrix[col(my_matrix) - row(my_matrix) == 1] = upper  
    my_matrix  
  }  
  
  else {  
    my_matrix = matrix(0, nrow = nrow, ncol = ncol)  
    min = min(nrow, ncol)  
    my_matrix[row(my_matrix) == col(my_matrix)] = rep(diagonal, min)[1:min]  
    my_matrix[row(my_matrix) - col(my_matrix) == 1] = lower  
    my_matrix[col(my_matrix) - row(my_matrix) == 1] = upper  
    my_matrix  
  }  
}
```

```

> triDiag(c(1,2,3,4), -2, 8 , 3 , 5)
      [,1] [,2] [,3] [,4] [,5]
[1,]     1    -2     0     0     0
[2,]     8     2    -2     0     0
[3,]     0     8     3    -2     0
> triDiag(2, 5, -1 , 4, 4)
      [,1] [,2] [,3] [,4]
[1,]     2     5     0     0
[2,]    -1     2     5     0
[3,]     0    -1     2     5
[4,]     0     0    -1     2
> triDiag(c(1,2,3,4), -2, 8)
      [,1] [,2] [,3] [,4]
[1,]     1    -2     0     0
[2,]     8     2    -2     0
[3,]     0     8     3    -2
[4,]     0     0     8     4

```

## Question 2a

```

stratified.hist = function(Sepal.Width, Species, xlab, title) {
  plot.new()
  plot.window(xlim = c(2, 4.8), c(0, 30))
  hist = hist(Sepal.Width, breaks = 20, ylim = c(0, 30), xlab = xlab, main =
title)
  legend("topright", legend = c("setosa", "versicolor", "virginica"), col = h
cl(c(240, 180, 0)), lty = 1, lwd = 10)

  table = table(Sepal.Width, Species)
  virginica_table = table[, "virginica"]
  versicolor_table = table[, "versicolor"]
  setosa_table = table[, "setosa"]

  # remove 0
  hist_counts = hist$counts[which(hist$counts != 0)]
  # difference between count and virginica for ybottom of light green rectang
le
  ybottom_versicolor = virginica_table
  ybottom_versicolor[which(virginica_table == 0)] = 0
  # difference between count and setosa for ytop of light green rectangle
  ytop_versicolor = ybottom_versicolor + versicolor_table
  # light green rectangle

  rect(xleft = seq(2, 3.3, by = 0.1), ybottom = ybottom_versicolor, xright =
seq(2.1, 3.4, by = 0.1), ytop = ytop_versicolor , col = hcl(180), border = NA
)

```

```

# light pink rectangle

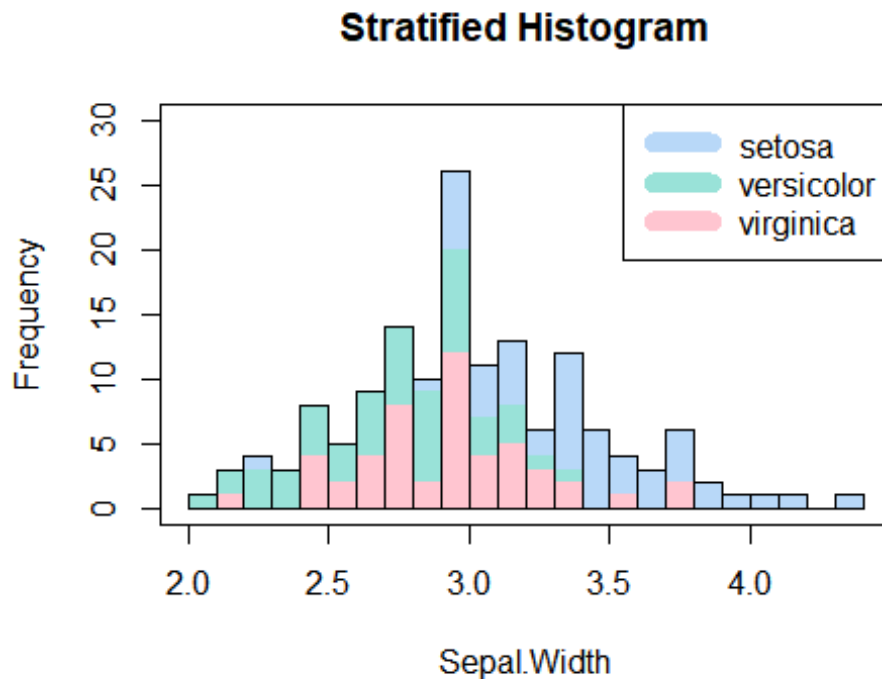
ytop_virginica = virginica_table[which(virginica_table != 0)]
sequence = seq(2, 4.2, by = 0.1)
x_axis_virginica = c(sequence[-2.1], 4.4)
x_axis_virginica = sequence[which(virginica_table != 0)]
rect(xleft = x_axis_virginica, ybottom = 0, xright = x_axis_virginica + 0.1
, ytop = ytop_virginica , col = hcl(0), border = NA)

# light blue rectangle
sequence_setosa = seq(2.8, 4.3, by = 0.1)
x_axis_setosa = c(2.2, sequence_setosa)
x_axis_setosa = x_axis_setosa[-16]

ybottom_setosa = versicolor_table[which(setosa_table != 0)] + virginica_table[which(setosa_table != 0)]
ybottom_setosa[8:16] = virginica_table[which(setosa_table != 0 & versicolor_table == 0)]
ytop_setosa = hist_counts[which(setosa_table != 0)]
rect(xleft = x_axis_setosa, ybottom = ybottom_setosa, xright = x_axis_setosa + 0.1, ytop = ytop_setosa, col = hcl(240), border = NA)

# colourless rectangle with border
rect(xleft = hist$breaks[-length(hist$breaks)], ybottom = 0, xright = hist$breaks[-length(hist$breaks)] + 0.1, ytop = hist$counts, col = NA)
# add a frame
box()
}
with (iris, stratified.hist(Sepal.Width, Species, xlab="Sepal.Width", title = "Stratified Histogram"))

```



## Question 2b

```
setosa_length = iris$Sepal.Length[1:50]
versicolor_length = iris$Sepal.Length[51:100]
virginica_length = iris$Sepal.Length[101:150]
setosa_width = iris$Sepal.Width[1:50]
versicolor_width = iris$Sepal.Width[51:100]
virginica_width = iris$Sepal.Width[101:150]

plot.new()
plot.window(xlim = c(2,8), ylim = c(0,12))
par(mar = rep(2,4))
layout(matrix(1:6, nr = 2, byrow = TRUE))

# top histograms
hist(setosa_length, xlim = c(min(setosa_length), 8), ylim = c(0, 12), col = hcl(240), main = "", axes = TRUE)
axis(side = 1, seq(4.5, 8, by = 0.5))
axis(side = 2, seq(0, 12, by = 1))
rect(xleft = 4.4, ybottom = 0, xright = 8, ytop = 0 )

hist(versicolor_length, xlim = c(4.5, 8), ylim = c(0, 10), col = hcl(180), breaks = 11, main = "Histogram for iris$Sepal.Length", axes = T)
rect(xleft = 4.4, ybottom = 0, xright = 8, ytop = 0 )
```

```

hist(virginica_length, xlim = c(4.5, 8), ylim = c(0, 11), col = hcl(0), break
s = 14, main = "")
axis(side = 1, seq(4.5, 8, by = 0.5))
axis(side = 2, seq(0, 10, by = 1))
rect(xleft = 4.4, ybottom = 0, xright = 8, ytop = 0 )

# bottom histograms
hist(setosa_width, xlim = c(2, 4.4), ylim = c(0, 9), col = hcl(240), breaks =
20, main = "")
rect(xleft = 2, ybottom = 0, xright = 4.4, ytop = 0 )

hist(versicolor_width, xlim = c(2, 4), ylim = c(0, 8), col = hcl(180), breaks
= 15, main = "Histogram for iris$Sepal.Width")
rect(xleft = 2, ybottom = 0, xright = 4.5, ytop = 0 )

hist(virginica_width, xlim = c(2, 4), ylim = c(0, 12), col = hcl(0), breaks =
20, main = "")
rect(xleft = 2, ybottom = 0, xright = 4.5, ytop = 0 )

```

