CS 636 Data Analytics with R Programming
Midterm Examination
Thursday, March 12, 2020
Form A

- This midterm examination consists of 10 pages (including this one), 7 questions, and 100 points. Please check to make sure you have all pages.
- This is a closed-book/notes exam, but an A4-sized cheating sheet is allowed.
- Write your answers on the given space for each question.
- Hand in this midterm examination with answers.
- You have 120 minutes to complete the exam.

On my honor, I pledge that I have not violated the provisions of the NJIT Academic Honor Code. I understand that if I do not include this pledge, as required by the instructor, with my signature, the instructor will not grade my work.

Last Name (printed): ____

First Name (printed): ____

UCID: ____

Signature: ____

Question	Score	Possible
1		10
2		20
3		10
4		10
5		10
6		20
7		20
Total		100

Problem 1 (10 pts): Please give the results of following commands (Note that Q1 and Q4 have two outputs):

1) rep(6:1, each=2);rep(5:12, times=2)

2) seq(10, 6, by=3)

3) order(10:20, decreasing=T)

4) print((1:4)<2|(1:4)%%2==0);
   print((3:6)>2&&(3:6)%%2==0);

5) x = c(1:10, "20");
   print(max(x))

Problem 2 (20 pts): Let gender = c(1,2,1,1,2,1,2,1,1,2); graduate = c(2,1,1,1,2,2,1,1,2,2); score=c(4:12, NA). A data frame is constructed as zz = data.frame(gender, graduate, score). Give the results of these R commands:

1) table(zz[,"gender"])

2) apply(zz[-1,], 2, max)

3) zz[zz[,3]>9,]

4) which.min(zz$score)

5) zz[order(zz["graduate"],zz["score"]),]

6) subset(zz, zz["gender"]==1)

7) tapply(zz$score, zz$graduate, mean, na.rm=T)

8) apply(zz[-10,], 1, sum)

Problem 3 (10 pts): Let mylist=list(sex = c(2,1,2,1,2,2,2,1,1,2), smoking = c(0,1,0,1,0,1,1,1,0,0), age=c(41:50)). Give the results of these R commands:

1) length(mylist)

2) lapply(mylist[1:2], function(addition){ addition+3})

3) sapply(mylist, max)

4) (mylist$sex-mylist$smoking)^3

Problem 4 (10 pts): Define zz=matrix(c(c(1,2,NA,4), seq(4,8), rep(5,6)), nrow = 3, ncol = 5). Use apply() function to compute the sum of each **row** and the average of each **column**(**ignore any missing value**).

Problem 5 (10 pts): Define geneExpr=data.frame(gene=LETTERS[1:10], expr1=c(6.1, 4.2, 2.8, 0.9, 0.1, 3.0, 2.6, 8.2, 3.4, 6.8), expr2=c(2.1, 4.5, 6.8, 7.9, 8.1, 5.0, 4.6, 3.2, 3.5, 7.8)). Give the results of the following R commands:

a)

```
counter<-0
for (i in 1:length(geneExpr[,2])) {
        if (geneExpr[i,3]<=4){
                counter<-counter+1
        }
}
print(counter)
```

b)

```
myMin<-function(x, k) { max(x[x<k]) }
apply(geneExpr[,-1],2, myMin, k=6)
```

Problem 6 (20 pts): Please complete the following questions:

a) Please write a function, similar as dnorm(), named fun_nd, to compute the normal distribution. Given three parameters, variable x, mean, and standard deviation, it is returned based on the following formula:

$$y = \frac{1}{\sqrt{2\pi}} e^{-(x-\mu)^2/2\sigma}$$

$\mu =$ Mean
$\sigma =$ Standard Deviation

The results should print out the value of y. Testing code and expected outputs are shown below:

```
> fun_nd(1.5, 1, 4)
[1] 0.09895942
```

b) Define a sequence as

$$a_n = 2 * a_{n-1} + a_{n-2}$$

starts with two 1s, $a_1 = 1, a_2 = 1$. Please write a function, Seq(n), which takes n as the input parameter and is supposed to return the n-th number in the defined sequence.

Problem 7 (20 pts): Please answer following questions：

a) Please write the results of the following R commands, library(stringr) already loaded:

1)
```
hw <- "Harry Potter";
str_sub(hw, end = 8);
```

2)
```
str_pad("a", 5, pad = c("*", "_", "0"))
```

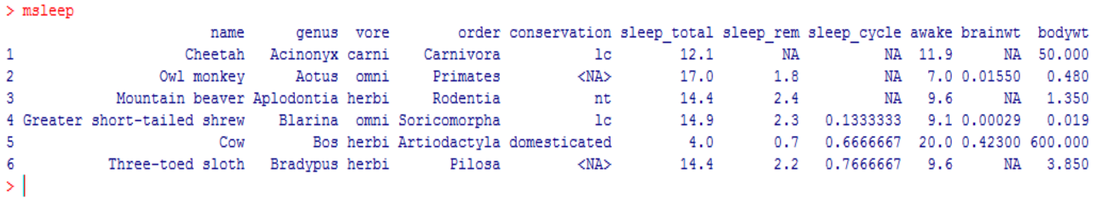
3)
```
fruit <- c("pinapple", "pear", "banana", "apple");
str_detect(fruit, "^p", negate = TRUE)
```

4)
```
x <- c("<a> <b>", "<a> <>", "<a>", "", NA);
str_match(x, "<(.*?)> <(.*?)>")
```

5)
```
fruits <- c("one apple", "two pears", "three bananas");
str_replace(fruits, "[aeiou]", c("1", "2", "3"))
```

b) Suppose we have a data frame named msleep

```
> library("dplyr")
> msleep <- read.csv("msleep_ggplot2.csv")
> msleep = head(msleep)
>msleep
```



```
> msleep
                        name      genus  vore        order conservation sleep_total sleep_rem sleep_cycle awake brainwt  bodywt
1                    Cheetah   Acinonyx carni    Carnivora           lc        12.1        NA          NA  11.9      NA  50.000
2                 Owl monkey      Aotus  omni     Primates         <NA>        17.0       1.8          NA   7.0 0.01550   0.480
3            Mountain beaver Aplodontia herbi     Rodentia           nt        14.4       2.4          NA   9.6      NA   1.350
4 Greater short-tailed shrew    Blarina  omni Soricomorpha           lc        14.9       2.3   0.1333333   9.1 0.00029   0.019
5                        Cow        Bos herbi Artiodactyla domesticated         4.0       0.7   0.6666667  20.0 0.42300 600.000
6           Three-toed sloth   Bradypus herbi       Pilosa         <NA>        14.4       2.2   0.7666667   9.6      NA   3.850
> |
```

Please rewrite the following commands using equivalent functions from ‘dplyr’ package, which is supposed to return the same results.

1) msleep[, grep("^sl", colnames(msleep))]

2) subset(msleep, sleep_total>10& !is.na(sleep_cycle))

3) msleep[order(msleep$sleep_total, decreasing= T),]

4) colnames(msleep)[colnames(msleep)=="sleep_total"] = "st"

5) msleep$sleep_total_min = msleep$sleep_total * 60