

## Homework 1

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(Parts 1-3; 35 pts)

1. Investigate so-called vectorized operations. (8 pts)

- a. Create (and print) a vector of length 8 using whose elements are all 10. This can be done using the rep(.) function.

```
> elements <- c(rep(10,8))
> elements
[1] 10 10 10 10 10 10 10 10
> |
```

---

Creates vector that uses rep(.) to repeat 10, 8 times and assign it to elements

- b. Define (and print) a vector of length 3 whose elements are [0 1 2].

```
- -
> threeElements <- c(0,1,2)
> threeElements
[1] 0 1 2
> |
```

Creates vector and assign it values 0,1,2

- c. Provide the result of subtracting the vector in part (b) from the vector in part (a).

```
> subtract <- elements - threeElements
Warning message:
In elements - threeElements :
  longer object length is not a multiple of shorter object length
> subtract
[1] 10  9  8 10  9  8 10  9
> |
```

Uses subtraction operation to subtract elements vectors from previous question

- d. Consider the subtraction in the previous part. What does R do when told to perform a vectorized operation on vectors that have different lengths? Discuss both the printed warning message and the result of the subtraction.

R gives a warning message stating that the length of one of the vectors is longer than the shorter vectors.

As a result, R will just print the values by every 3 elements.

10-0, 10-1, 10-2 ... repeating until there's no more.

2. Define matrices **A** and **B**, vector **C**, and scalar **d** as shown below, and perform the indicated matrix operations using R commands. Note that **A'** denotes the transpose of matrix **A**. (8 pts)

$$A = \begin{bmatrix} 1 & 0 \\ 2 & 4 \\ -1 & 2 \end{bmatrix} \quad B = \begin{bmatrix} 1 & 2 & -1 \\ 0 & 3 & -4 \end{bmatrix} \quad C = \begin{bmatrix} 1 \\ 2 \\ 0 \end{bmatrix} \quad d = 2$$

a)  $C'A$

```
> firstOp <- t(C) %*% A
> firstOp
      [,1] [,2]
[1,]     5     8
> |
```

Perform transpose of matrix C multiply by matrix A

b)  $A'C$

```
> secondOp <- t(A) %*% C
> secondOp
      [,1]
[1,]     5
[2,]     8
> |
```

Perform transpose of matrix A multiply by matrix C

c)  $B' + dA$

```
> thirdOp <- D*A + t(B)
> thirdOp
      [,1] [,2]
[1,]     3     0
[2,]     6    11
[3,]    -3     0
> |
```

Perform transpose of matrix B and add it to scalar d multiply by matrix A

d)  $(BA)'$

```
> forthOp <- t((B%*%A))
> forthOp
      [,1] [,2]
[1,]     6    10
[2,]     6     4
~ |
```

Perform transpose of matrix B multiply A

3. Use a *while* loop (and brute force) to identify the first positive integer whose natural log is larger than 10. Outside the loop, set a numeric variable (call it  $x$ ) equal to 1. Inside the loop, print the value of  $\log(x)$ , and increase the value of  $x$  by 1. DO NOT submit the entirety of the output that is printed to the console. Instead, provide your code and the value of  $x$  that causes the loop to terminate. (4 pts)

```
x <- 1
while(log(x) < 10){
  print(paste("At", x, "the log value is", log(x)))
  x <- x + 1
}
```

```
[1] "At 22026 the log value is 9.99997885272489"
```

Creates x variable and assign it to 1. Create a while loop with condition  $\log(x) < 10$ . Inside we print the value of  $\log(x)$  and increase x by 1.

At  $x = 22026$ , the loop will terminate

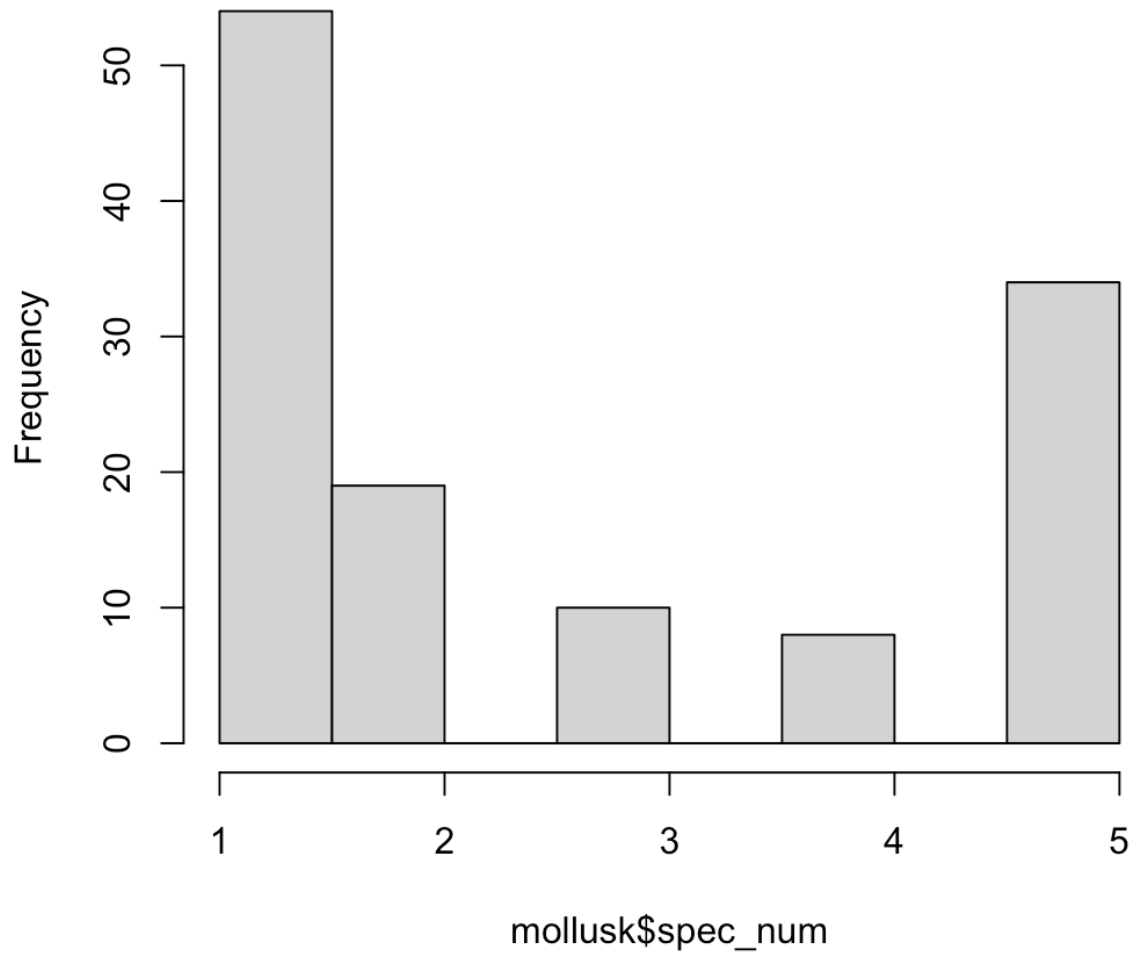
4. The data set mollusk.txt (UBLearns) contains data about five species of mollusk. (10 pts)
- a) Obtain the frequency distribution (counts and percentages) of the Species Number variable.

Obtained the counts and percentages of the species number variable and display both in a histogram.

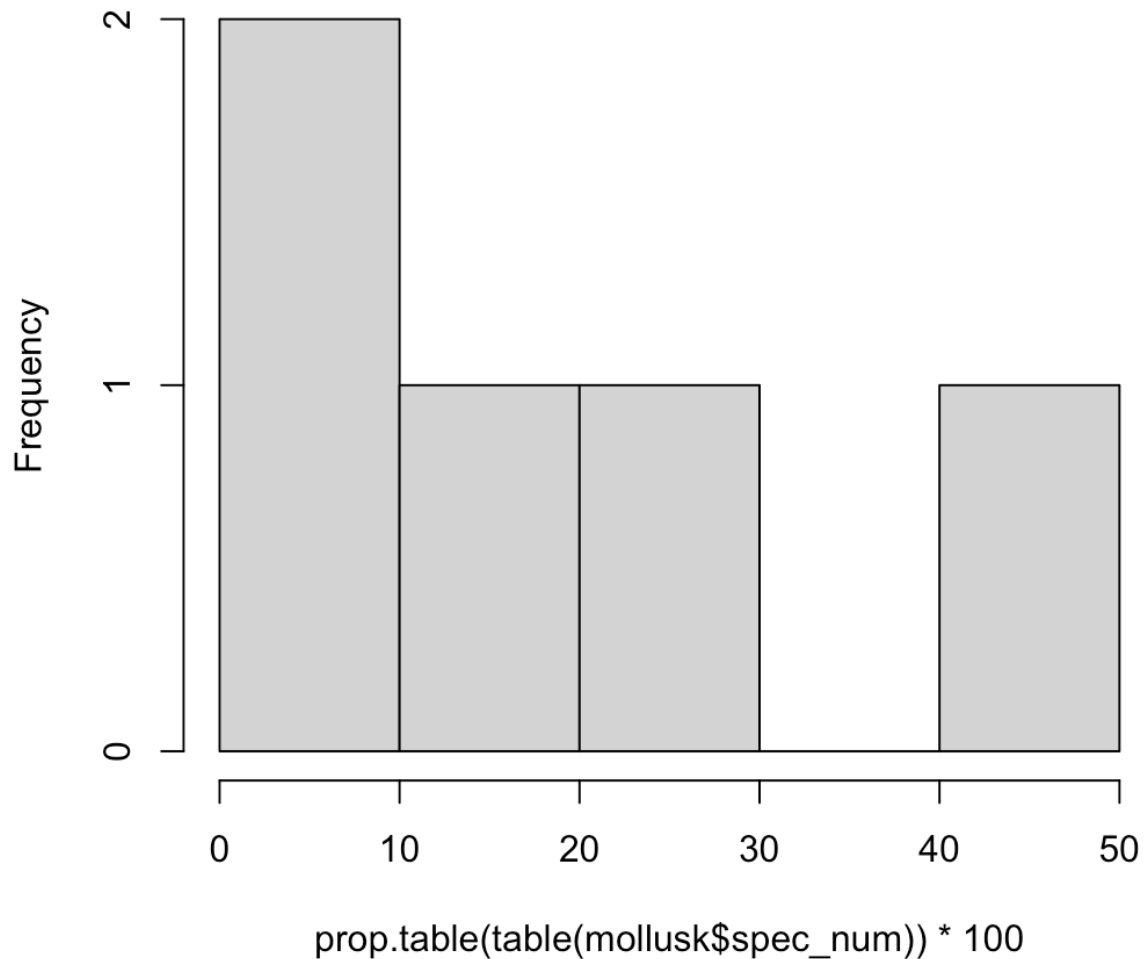
```
  1  2  3  4  5
54 19 10  8 34
> hist(mollusk$spec_num)
> prop.table(table(mollusk$spec_num)) * 100

  1    2    3    4    5
43.2 15.2  8.0  6.4 27.2
> hist(prop.table(table(mollusk$spec_num)) * 100 )
> |
```

**Histogram of mollusk\$spec\_num**



### Histogram of $\text{prop.table}(\text{table}(\text{mollusk\$spec\_num})) * 100$



b) Report the sample mean and sample standard deviation of the Impulse Rate variable.

```
> mean <- mean(mollusk$impulse)
> sd <- sd(mollusk$impulse)
> mean
[1] 173.8722
> sd
[1] 176.131
> |
```

Report the mean and standard deviation

- c) Use the `ifelse(.)` function to define a vector called **fast** which classifies each mollusk's response time. The value of **fast** should be set to TRUE if a mollusk's recorded value of Impulse Rate is less than 100. Mollusks with Impulse Rate greater than or equal to 100 should have their value of **fast** set to FALSE.

```
> mollusk$fast <- ifelse(mollusk$impulse < 100, TRUE, FALSE)
> mollusk$fast
[1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[24] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[47] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE TRUE TRUE FALSE FALSE FALSE FALSE FALSE TRUE TRUE FALSE
[70] FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[93] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[116] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
>
```

Assign vector `fast` and uses `ifelse(.)`, to check if the mollusk's recorded value of Impulse Rate is less than 100. It should show TRUE or FALSE

- d) Create a logical vector equivalent to the one produced in part (c). Instead of populating the vector using `ifelse(.)`, use an inequality sign directly.

```
> mollusk$fast2 <- mollusk$impulse < 100
> mollusk$fast2
[1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[24] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[47] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[70] FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE TRUE TRUE FALSE
[93] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[116] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
>
```

Uses logical vector equivalent to the one produced in part (c).

- e) Verify that the two vectors from parts (c) and (d) are equivalent using the `identical(.)` function.

```
> ?identical()
> identical(mollusk$fast, mollusk$fast2)
[1] TRUE
>
```

Uses `identical` function to check if previous two vectors are equivalent.

- f) Give the total number of mollusks in the data set having **fast** equal to TRUE.

```
> sum(mollusk$fast == TRUE)
[1] 71
>
```



Use sum function and pass in `mollusk$fast == TRUE` to get the total number of mollusks with Impulse Rate is less than 100.

5. A graduate student is writing a program that requires 100 objects to be defined in advance, each of them a vector of length 5. For simplicity, the objects can be named `obj_1`, `obj_2`, ..., `obj_100`. (5 pts)

- a) The student considers use of the `paste(.)` function to combine the text string “obj” with the digit 1, separated by an underscore. Refer to the `paste(.)` function’s help file, and use the function to produce the character string “obj\_1.”

```
> ?paste()
> obj1 <- paste ("obj", 1, sep = "_", collapse = NULL, recycle0 = FALSE)
> obj1
[1] "obj_1"
> |
```

Create `obj1` and assign it to “obj\_1” using paste function

- b) The student realizes that printing the characters “obj\_1” to the console is insufficient; he intended to have a stored object in memory called **obj\_1**, which he could set equal to an empty numeric vector of length 5. After some online reading, he discovers the `assign(.)` function, which allows the user to give both a variable name and the value assigned to that variable. Use the `assign(.)` function to create **obj\_1**, and demonstrate the following result in console:

```
obj_1
[1] 0 0 0 0 0
```

```
> ?assign(.)
> obj_1 <- assign("obj_1", numeric(5))
> obj_1
[1] 0 0 0 0 0
> |
```

Create `obj_1` and use assign function to object in memory called “obj\_1” with vector length 5

- c) Adapt the code from part (b) to execute in a *for* loop, so that `obj_1`, `obj_2`, ..., `obj_100` are all created in memory, each equal to an empty numeric vector of length 5. No output is required for this part; just your code block.

```
"""
c) Adapt the code from part (b) to execute in a for loop, so that obj_1, obj_2, ..., obj_100 are all created in memory,
each equal to an empty numeric vector of length 5. No output is required for this part; just your code block.
"""
```

```
for (x in 1:100) {
  obj_x <- assign(paste("obj", x), numeric(5))
  print(paste("obj", x, "is created in memory"))
  print(obj_x)
}
```

## Complete R code:

###1. Investigate so-called vectorized operations. (8 pts)

"""

a. Create (and print) a vector of length 8 using whose elements are all 10.

This can be done using the rep(.) function.

"""

```
elements <- c(rep(10,8))
```

```
elements
```

"""

b. Define (and print) a vector of length 3 whose elements are [0 , 1, 2].

"""

```
threeElements <- c(0,1,2)
```

```
threeElements
```

"""

c. Provide the result of subtracting the vector in part (b) from the vector in part (a).

"""

```
subtract <- elements - threeElements
```

```
subtract
```

"""

2. Define matrices A and B, vector C, and scalar d as shown below, and perform the indicated matrix operations using R commands. Note that A' denotes the transpose of

matrix A. (8 pts)

"""

```
A <- matrix(c(1,2,-1,0,4,2), nrow = 3, ncol = 2)
```

```
B <- matrix(c(1,0,2,3,-1,-4), nrow = 2, ncol = 3)
```

```
C <- matrix(c(1,2,0), nrow = 3, ncol = 1)
```

```
D <- 2
```

A

B

C

"""

a.  $C'A$

"""

```
firstOp <- t(C) %*% A
```

```
firstOp
```

"""

b.  $A'C$

"""

```
secondOp <- t(A) %*% C
```

```
secondOp
```

"""

c.  $B'+dA$

"""

```
thirdOp <- D*A + t(B)
```

thirdOp

"""

d. (BA)'

"""

```
forthOp <- t((B%*%A))
```

forthOp

"""

3. Use a while loop (and brute force) to identify the first positive integer whose natural log is larger than 10. Outside the loop, set a numeric variable (call it x) equal to 1. Inside the loop, print the value of log(x), and increase the value of x by 1. DO NOT submit the entirety of the output that is printed to the console. Instead, provide your code and the value of x that causes the loop to terminate. (4 pts)

"""

```
x <- 1
```

```
while(log(x) < 10){
```

```
  print(paste("At", x, "the log value is", log(x)))
```

```
  x <- x + 1
```

```
}
```

"""

4. The data set mollusk.txt (UBLeans) contains data about five species of mollusk. (10 pts)

```
"""
```

```
"""
```

a) Obtain the frequency distribution (counts and percentages) of the Species Number variable.

```
"""
```

```
mollusk <- read.csv("~/Documents/STA 361/mollusk.txt", sep="")
```

```
View(mollusk)
```

```
table(mollusk$spec_num)
```

```
hist(mollusk$spec_num)
```

```
prop.table(table(mollusk$spec_num)) * 100
```

```
hist(prop.table(table(mollusk$spec_num)) * 100 )
```

```
"""
```

b) Report the sample mean and sample standard deviation of the Impulse Rate variable.

```
"""
```

```
mean <- mean(mollusk$impulse)
```

```
sd <- sd(mollusk$impulse)
```

```
mean
```

```
sd
```

```
"""
```

c) Use the ifelse(.) function to define a vector called fast which classifies each mollusk's response time.

The value of fast should be set to TRUE if a mollusk's recorded value of Impulse Rate is less than 100.

Mollusks with Impulse Rate greater than or equal to 100 should have their value of fast set to FALSE.

```
"""
```

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mollusk$fast <- ifelse(mollusk$impulse < 100, TRUE, FALSE)
```

```
mollusk$fast
```

```
"""
```

d) Create a logical vector equivalent to the one produced in part (c). Instead of populating the vector using ifelse(),

use an inequality sign directly.

```
"""
```

```
mollusk$fast2 <- mollusk$impulse < 100
```

```
mollusk$fast2
```

```
"""
```

e) Verify that the two vectors from parts (c) and (d) are equivalent using the identical(.) function.

```
"""
```

```
identical(mollusk$fast, mollusk$fast2)
```

```
"""
```

f) Give the total number of mollusks in the data set having fast equal to TRUE.

```
"""
```

```
sum(mollusk$fast == TRUE)
```

"""

A graduate student is writing a program that requires 100 objects to be defined in advance, each of them a vector of length 5.

For simplicity, the objects can be named `obj_1`, `obj_2`, ..., `obj_100`. (5 pts)

"""

"""

a) The student considers use of the `paste(.)` function to combine the text string “obj” with the digit 1, separated by an underscore.

Refer to the `paste(.)` function’s help file, and use the function to produce the character string “obj\_1.”

"""

```
obj1 <- paste ("obj", 1, sep = "_", collapse = NULL, recycle0 = FALSE)
```

```
obj1
```

"""

b) The student realizes that printing the characters “obj\_1” to the console is insufficient; he intended to have a stored object

in memory called `obj_1`, which he could set equal to an empty numeric vector of length 5.

After some online reading, he discovers the `assign(.)` function, which allows the user to give both a



variable name and the value assigned to that variable. Use the `assign(.)` function to create `obj_1`, and

demonstrate the following result in console:

```
""""
```

```
obj_1 <- assign("obj_1", numeric(5))
```

```
obj_1
```

```
""""
```

c) Adapt the code from part (b) to execute in a for loop, so that `obj_1`, `obj_2`, ..., `obj_100` are all created in memory,

each equal to an empty numeric vector of length 5. No output is required for this part; just your code block.

```
""""
```

```
for (x in 1:100) {
```

```
  obj_x <- assign(paste("obj", x), numeric(5))
```

```
  print(paste("obj", x, "is created in memory"))
```

```
  print(obj_x)
```

```
}
```