## Bios 6301: Assignment 2

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Due Tuesday, 20 September, 1:00 PM

50 points total.

Add your name as author to the file's metadata section.

Submit a single knitr file (named homework2.rmd) by email to tianyi.sun@vanderbilt.edu. Place your R code in between the appropriate chunks for each question. Check your output by using the Knit HTML button in RStudio.

- 1. Working with data In the datasets folder on the course GitHub repo, you will find a file called cancer.csv, which is a dataset in comma-separated values (csv) format. This is a large cancer incidence dataset that summarizes the incidence of different cancers for various subgroups. (18 points)
  - 1. Load the data set into R and make it a data frame called cancer.df. (2 points)

```
{\tt cancer.df \leftarrow read.csv("/Users/KatietheWise/Desktop/2022\_Fall/StatComp/Bios6301\_git/datasets/cancer.df \leftarrow read.csv("/Users/KatietheWise/Desktop/2022\_fall/StatComp/Bios6301\_git/dataset/Desktop/2022\_fall/StatComp/Bios6301\_fall
```

2. Determine the number of rows and columns in the data frame. (2)

```
dim(cancer.df) # directly reports row x column
## [1] 42120
str(cancer.df) # structure, including names of columns
## 'data.frame':
                   42120 obs. of 8 variables:
               $ year
                     "Brain and Other Nervous System" "Brain and Other Nervous System" "Brain and
   $ site
                     "alabama" "alabama" "alabama" ...
   $ state
               : chr
                      "Female" "Female" "Male" ...
##
   $ sex
               : chr
##
   $ race
               : chr
                     "Black" "Hispanic" "White" "Black" ...
  $ mortality : num
                     0 0 83.7 0 0 ...
   $ incidence : int
                     19 0 110 18 0 145 0 0 0 0 ...
                     623475\ 28101\ 1640665\ 539198\ 37082\ 1570643\ 12710\ 11664\ 220036\ 13900\ \dots
   $ population: int
42120 rows, 8 columns
 3. Extract the names of the columns in cancer.df. (2)
names(cancer.df)
## [1] "year"
                   "site"
                               "state"
                                            "sex"
                                                        "race"
## [6] "mortality" "incidence"
                               "population"
 4. Report the value of the 3000th row in column 6. (2)
cancer.df[3000,6] # data.frame[row, column]
```

5. Report the contents of the 172nd row. (2)

## [1] 350.69

```
cancer.df[172,]
                                         site state sex race mortality incidence
       year
## 172 1999 Brain and Other Nervous System nevada Male Black
##
       population
## 172
             73172
  6. Create a new column that is the incidence rate (per 100,000) for each row. The incidence
    rate is the (number of cases)/(population at risk), which in this case means (number of
    cases)/(population at risk) * 100,000. (3)
incidence_rate <- cancer.df$incidence/cancer.df$population</pre>
cancer.df[,9] <- incidence rate</pre>
colnames(cancer.df)[9] <- "incidence rate"</pre>
  7. How many subgroups (rows) have a zero incidence rate? (2)
colSums(cancer.df==0)[9] # had to input the entire dataframe, then select the 9th column
## incidence rate
##
             23191
  8. Find the subgroup with the highest incidence rate.(3)
max(cancer.df$"incidence rate") # I can't decide which of these I prefer
## [1] 0.002611599
max(cancer.df[,9])
## [1] 0.002611599
  1. Create the following vector: x \leftarrow c("5","12","7"). Which of the following commands will
```

- 2. **Data types** (10 points)
  - produce an error message? For each command, Either explain why they should be errors, or explain the non-erroneous result. (4 points)

```
x <- c("5","12","7")
```

max(x) - Each number in the vector is actually a string, which are sorted alphanumerically by default. '12' has the greatest numerical value, but because it begins with a '1' it is actually the "smallest" element in the vector. '7' comes after both '1' and '5' in this scheme and is therefore the maximum alphanumeric value in the vector.

sort(x) - See alphanumeric explanation above, numbers in "alphabetical" order begin with "1" and end with "9"

sum(x) - This operation will result in an error message, because the numbers are strings rather than numerical values and are therefore ineligible for mathematical operations.

```
max(x)
## [1] "7"
sort(x)
## [1] "12" "5" "7"
\#sum(x)
```

2. For the next two commands, either explain their results, or why they should produce errors. (3 points)

```
y < c("5",7,12)
```

• This command coerces the entered numeric values to strings, or characters. R prioritizes characters, so the data type of the first element was chosen and applied to all elements in the vector.

```
y[2] + y[3]
```

• This command will produce an error, because two characters cannot be added together.

```
y <- c("5",7,12) # warning, then coerced the numeric values to strings # elements of a vector must all have the same mode, or data type \#y[2] + y[3] \# error y # they were all changed to strings
```

```
## [1] "5" "7" "12"
```

3. For the next two commands, either explain their results, or why they should produce errors. (3 points)

```
z < -data.frame(z1="5", z2=7, z3=12)
```

• This command produces a 1x1 dataframe with each of the values listed. Dataframes allow multiple data types to exist, though they must be isolated to their own columns (ie, characters all in the same column).

```
z[1,2] + z[1,3]
```

• This command sums the values from columns 2 and 3, which are the same data type (numeric).

```
z \leftarrow data.frame(z1="5", z2=7, z3=12)
z[1,2] + z[1,3] # row 1, column 2 = 7
## [1] 19
```

```
# row 1, column 3 = 12
# 7 + 12 = 19
```

```
#dtype(z[1,2])
```

3. **Data structures** Give R expressions that return the following matrices and vectors (*i.e.* do not construct them manually). (3 points each, 12 total)

```
1. (1,2,3,4,5,6,7,8,7,6,5,4,3,2,1)

x <- seq(1,8,1)
c(x, rev(x[-8]))

## [1] 1 2 3 4 5 6 7 8 7 6 5 4 3 2 1
2. (1,2,2,3,3,3,4,4,4,4,5,5,5,5,5)

# 1 of 1, 2 of 2, etc
# repetitions = 1*1, 2*2, 3*3, 4*4

rep(1:5, times = 1:5)
```

**##** [1] 1 2 2 3 3 3 4 4 4 4 5 5 5 5 5

$$3. \begin{pmatrix} 0 & 1 & 1 \\ 1 & 0 & 1 \\ 1 & 1 & 0 \end{pmatrix}$$

```
diag(matrix1) = 0
  matrix1
           [,1] [,2] [,3]
  ##
  ## [1,]
              0
                    1
  ## [2,]
              1
                    0
  ## [3,]
              1
                    1
       1 8
                27
                      64
                     256
        1 16 81
           32 243 1024
  # first row is numbers
  # second row is squares of first row
  # third row is cubes of first row, etc
  # I know this isn't the most efficient solution, but I wasn't sure how to automatically iterate over
  base_vector \leftarrow c(1, 2, 3, 4)
  matrix2 <- matrix(c(base_vector, base_vector^2, base_vector^3, base_vector^4, base_vector^5), nrow=
  matrix2
           [,1] [,2] [,3] [,4]
  ##
  ## [1,]
              1
                    2
                         3
                               4
  ## [2,]
              1
                    4
                         9
                              16
  ## [3,]
              1
                    8
                        27
                              64
  ## [4,]
              1
                   16
                        81
                            256
  ## [5,]
              1
                   32
                      243 1024
4. Basic programming (10 points)
    1. Let h(x,n) = 1 + x + x^2 + \ldots + x^n = \sum_{i=0}^n x^i. Write an R program to calculate h(x,n) using a
       for loop. As an example, use x = 5 and n = 2. (5 points)
  x <- 5
  n <- 2
  vector \leftarrow c(1)
  for (i in 1:n) {
    new_value <- x^i</pre>
    vector <- c(vector, new_value)</pre>
    answer <- sum(vector) # will just give the last value when the loop breaks
  }
    2. If we list all the natural numbers below 10 that are multiples of 3 or 5, we get 3, 5, 6 and 9. The
       sum of these multiples is 23. Write an R program to perform the following calculations. (5 points)
        a. Find the sum of all the multiples of 3 or 5 below 1,000. (3, euler1)
  # 1000/3 = 333.33, call it 333x3 = 999
  \# 1000/5 = 200 even, must be less than 1000, call it 199x5 = 995
  # seq() to pick out the multiples, unique() to remove numbers in common (ex: 15 is divisible by 5
  sum(unique(c(seq(3, 999, 3), seq(5, 995, 5))))
  ## [1] 233168
```

# 0 on the diagonal

matrix1 <- matrix(seq(1, 1, length.out=9), nrow=3, ncol=3)</pre>

b. Find the sum of all the multiples of 4 or 7 below 1,000,000. (2)

```
# just an extension of the previous problem
# 1000000/4 = 250000 even, 249999x4 = 999996
# 1000000/7 = 142857.1, call it 142857x7 = 999999
sum(unique(c(seq(4, 999996, 4), seq(7, 999999, 7))))
```

## ## [1] 178571071431

3. Each new term in the Fibonacci sequence is generated by adding the previous two terms. By starting with 1 and 2, the first 10 terms will be (1, 2, 3, 5, 8, 13, 21, 34, 55, 89). Write an R program to calculate the sum of the first 15 even-valued terms. (5 bonus points, euler2)

```
fib <- c(1, 2) # define first two numbers
while (max(length(which(fib%%2 == 0))) < 15) {
# keep going until we get 15 even numbers
  fib <- c(fib, fib[length(fib) - 1] + fib[length(fib)])
}
first_fifteven <- sum(fib[fib%%2 == 0])
first_fifteven</pre>
```

## ## [1] 1485607536

Some problems taken or inspired by projecteuler.