Bios 6301: Assignment 2

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- 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)

```
library(tidyverse)
## -- Attaching packages -----
                                                                                                                             ----- tidyverse 1.3.2 --
## v ggplot2 3.3.6
                                                                    v purrr
                                                                                                   0.3.4
## v tibble 3.1.8
                                                                     v dplyr
                                                                                                   1.0.9
## v tidyr
                                 1.2.0
                                                               v stringr 1.4.1
## v readr
                                  2.1.2
                                                                     v forcats 0.5.2
## -- Conflicts -----
                                                                                                                                                ## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                                                               masks stats::lag()
library(dplyr)
setwd("C:/Users/choij33/OneDrive - Vanderbilt/Vanderbilt/Course/Statcomputing/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301-main/Bios6301
getwd()
## [1] "C:/Users/choij33/OneDrive - Vanderbilt/Vanderbilt/Course/Statcomputing/Bios6301-main/Bios6301-m
cancer.df<-read.csv("cancer.csv")</pre>
2. Determine the number of rows and columns in the data frame. (2)
rows: 42120, cols: 8
dim(cancer.df)
## [1] 42120
                                                   8
3. Extract the names of the columns in 'cancer.df'. (2)
colnames_cancer.df<-colnames(cancer.df)</pre>
colnames_cancer.df
## [1] "year"
                                                            "site"
                                                                                                    "state"
                                                                                                                                           "sex"
                                                                                                                                                                                   "race"
## [6] "mortality" "incidence"
                                                                                                   "population"
```

4. Report the value of the 3000th row in column 6. (2)

```
print(cancer.df[300, 6])
## [1] 47.27
5. Report the contents of the 172nd row. (2)
print(cancer.df[172,])
##
                                        site state sex race mortality incidence
## 172 1999 Brain and Other Nervous System nevada Male Black
##
       population
            73172
## 172
6. Create a new column that is the incidence *rate* (per 100,000) for each row. The incidence rate is to
cancer.df2<-cancer.df %>%
 mutate(rate=incidence/population * 100,000)
7. How many subgroups (rows) have a zero incidence rate? (2)
  sum(cancer.df2$rate==0)
"
## [1] 23191
  8. Find the subgroup with the highest incidence rate.(3)
cancer.df2[cancer.df2$rate == max(cancer.df2$rate), ]
##
                                       state sex race mortality incidence
        year
                  site
## 5797 1999 Prostate district of columbia Male Black
                                                             88.93
                                                                          420
        population
                         rate 0
            160821 0.2611599 0
## 5797
  2. Data types (10 points)
       1. Create the following vector: x \leftarrow c("5","12","7"). Which of the following commands will
         produce an error message? For each command, Either explain why they should be errors, or
         explain the non-erroneous result. (4 points)
          max(x)
          sort(x)
          sum(x)
x \leftarrow c("5","12","7")
max(x) #"7"
## [1] "7"
```

```
sort(x) # "12" "5" "7"
## [1] "12" "5" "7"
#sum(x) #reason: character type cannot be numerically summed
2. For the next two commands, either explain their results, or why they should produce errors. (3 point
        y \leftarrow c("5",7,12)
        y[2] + y[3]
y \leftarrow c("5",7,12)
\#y[2] + y[3] \#It cannot be calculated because 7 and 12 are considered as character because "5" is a character
3. For the next two commands, either explain their results, or why they should produce errors. (3 point
        z \leftarrow data.frame(z1="5", z2=7, z3=12)
        z[1,2] + z[1,3]
z \leftarrow data.frame(z1="5",z2=7,z3=12)
##
     z1 z2 z3
## 1 5 7 12
z[1,2] + z[1,3] # It can be calculated because data.frame can hold different types of data - so z2 and
## [1] 19
  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)
c(1:8, 7:1)
## [1] 1 2 3 4 5 6 7 8 7 6 5 4 3 2 1
2. $(1,2,2,3,3,3,4,4,4,4,5,5,5,5,5)$
rep(1:5, 1:5)
## [1] 1 2 2 3 3 3 4 4 4 4 5 5 5 5 5
3. $\begin{pmatrix}
  0 & 1 & 1 \\
  1 & 0 & 1 \\
  1 & 1 & 0 \\
\end{pmatrix}$
```

```
d<-matrix(data=rep(1,9), nrow=3, ncol=3)</pre>
diag(d)<-rep(0, length(diag(d)))</pre>
        [,1] [,2] [,3]
## [1,]
## [2,]
                0
           1
                      1
## [3,]
           1
4. $\begin{pmatrix}
  1 & 2 & 3 & 4 \\
  1 & 4 & 9 & 16 \\
  1 & 8 & 27 & 64 \\
  1 & 16 & 81 & 256 \\
  1 & 32 & 243 & 1024 \\
\end{pmatrix}$
d4 <- matrix(rep(1:4,4), nrow=4, ncol=4, byrow=TRUE)
for(i in 1:dim(d4)[1]){
  d4[i,] <- d4[i,]^i
}
d4
        [,1] [,2] [,3] [,4]
##
## [1,]
          1
              2
## [2,]
                          16
           1
                4
                      9
## [3,]
           1
                8
                     27
                          64
## [4,]
               16
           1
                     81
                         256
```

- 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
a <- 1
for(i in 1:n){
a <- a + x^i
}
a</pre>
```

[1] 31

- 1. If we list all the natural numbers below 10 that are multiples of 3 or 5, we get 3, 5, 6 and 9. The
 - 1. Find the sum of all the multiples of 3 or 5 below 1,000. (3, [euler1])

```
a1 <- 0
for (i in 1:999) {
   if (i %% 3 == 0 | i %% 5 == 0) {
      a1 <- a1 + i
   }
}
print(a1)</pre>
```

```
## [1] 233168
```

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

```
a2 <- 0
for (i in 1:999999) {
  if (i %% 4 == 0 | i %% 7 == 0) {
    a2 <- a2 + i
  }
}
print(a2)</pre>
```

[1] 178571071431

1. Each new term in the Fibonacci sequence is generated by adding the previous two terms. By starting w

```
fib_seq <- c(1,1)
  for (i in 3:60) {
    fib_seq[i] <- fib_seq[i-1] + fib_seq[i-2]
  }
fib_seq</pre>
```

```
## [1] 1.000000e+00 1.000000e+00 2.000000e+00 3.000000e+00 5.000000e+00 ## [6] 8.000000e+00 1.300000e+01 2.100000e+01 3.400000e+01 5.500000e+01 ## [11] 8.900000e+01 1.440000e+02 2.330000e+02 3.770000e+02 6.100000e+02 ## [16] 9.870000e+02 1.597000e+03 2.584000e+03 4.181000e+03 6.765000e+03 ## [21] 1.094600e+04 1.771100e+04 2.865700e+04 4.636800e+04 7.502500e+04 ## [26] 1.213930e+05 1.964180e+05 3.178110e+05 5.142290e+05 8.320400e+05 ## [31] 1.346269e+06 2.178309e+06 3.524578e+06 5.702887e+06 9.227465e+06 ## [36] 1.493035e+07 2.415782e+07 3.908817e+07 6.324599e+07 1.023342e+08 ## [41] 1.655801e+08 2.679143e+08 4.334944e+08 7.014087e+08 1.134903e+09 ## [46] 1.836312e+09 2.971215e+09 4.807527e+09 7.778742e+09 1.258627e+10 ## [51] 2.036501e+10 3.295128e+10 5.331629e+10 8.626757e+10 1.395839e+11 ## [56] 2.258514e+11 3.654353e+11 5.912867e+11 9.567220e+11 1.548009e+12
```

```
counter <-0; limit <- 15; summed <- 0
for (i in 1:length(fib_seq)){
   if (fib_seq[i]%2==0){
      summed <- summed + fib_seq[i]
      counter <- counter + 1
   }
   if (counter >= limit){
      break
   }
}
summed
```

[1] 1485607536

Some problems taken or inspired by projecteuler.