Bios 6301: Assignment 2

Erin Fey
04 October 2016

(informally) Due Tuesday, 20 September, 1:00 PM

50 points total.

This assignment won't be submitted until we've covered Rmarkdown. Create R chunks for each question and insert your R code appropriately. Check your output by using the Knit PDF 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)
- 2. Load the data set into R and make it a data frame called cancer.df. (2 points)

cancer.df <- read.csv("https://github.com/fonnesbeck/Bios6301/raw/master/datasets/cancer.csv", header=Thead(cancer.df)</pre>

```
year
                                     site
                                             state
                                                              race mortality
## 1 1999 Brain and Other Nervous System alabama Female
                                                             Black
                                                                         0.00
## 2 1999 Brain and Other Nervous System alabama Female Hispanic
                                                                         0.00
## 3 1999 Brain and Other Nervous System alabama Female
                                                                        83.67
## 4 1999 Brain and Other Nervous System alabama
                                                                         0.00
                                                     Male
                                                             Black
## 5 1999 Brain and Other Nervous System alabama
                                                     Male Hispanic
                                                                         0.00
## 6 1999 Brain and Other Nervous System alabama
                                                     Male
                                                             White
                                                                       103.66
     incidence population
            19
## 1
                   623475
## 2
             0
                    28101
## 3
           110
                   1640665
            18
                   539198
## 5
             0
                    37082
## 6
           145
                   1570643
```

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

```
nrow(cancer.df)

## [1] 42120

ncol(cancer.df)
```

[1] 8

3. Extract the names of the columns in cancer.df. (2)

```
colnames(cancer.df)
## [1] "year"
                                                                "race"
                      "site"
                                    "state"
                                                  "sex"
## [6] "mortality" "incidence"
                                    "population"
  4. Report the value of the 3000th row in column 6. (2)
cancer.df[3000, 6]
## [1] 350.69
  5. Report the contents of the 172nd row. (2)
cancer.df [172,]
##
                                         site state sex race mortality
## 172 1999 Brain and Other Nervous System nevada Male Black
       incidence population
## 172
                0
                        73172
  6. Create a new column that is the incidence rate (per 100,000) for each row.(3)
cancer.df$incidence_rate <- (cancer.df$incidence/cancer.df$population)*100000</pre>
  7. How many subgroups (rows) have a zero incidence rate? (2)
sum(cancer.df$incidence rate==0)
## [1] 23191
  8. Find the subgroup with the highest incidence rate.(3)
cancer.df[which.max(cancer.df$incidence rate),]
        year
                  site
                                        state sex race mortality incidence
## 5797 1999 Prostate district of columbia Male Black
                                                               88.93
                                                                            420
##
        population incidence_rate
## 5797
             160821
                           261.1599
  2. Data types (10 points)
  3. Create the following vector: x <- 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)
x \leftarrow c("5","12","7")
```

The characters are sorted according to their first digit, therefore 7>5>1 and you return the value "7"

max(x)

[1] "7"

sort(x)

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

Again the characters are sorted by their first digit 1<5<7, you return the values "12" "5" "7" sum(x)

Error, the class of vector x is a character and you can only sum numeric complex or logical values "' 2. For the next two commands, either explain their results, or why they should produce errors. (3 points)

Since "5" is a character, the whole vector is read as a character because it is the least flexible and you return the values "5" "7" "12"

$$y[2] + y[3]$$

Error, again here you are trying to take the sum of two characters because when you call y[2] you are returning the element found at the second position of y but it is returned in character form

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)
```

We get a data frame with z1 z2 and z3 the column names and 5 7 12 in the first row #since we have assigned z as a data frame, this function converts character variables to factors

[1] 19

Addition works here because the values are numeric and you return a value of 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)
- 4. (1, 2, 3, 4, 5, 6, 7, 8, 7, 6, 5, 4, 3, 2, 1)

$$x \leftarrow c(1:8,7:1)$$

2. (1,2,2,3,3,3,4,4,4,4,5,5,5,5,5)

$$x \leftarrow rep(1:5, c(1,2,3,4,5))$$

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

```
matrix(1, 3, 3) - diag(3)
```

```
## [,1] [,2] [,3]
## [1,] 0 1 1
## [2,] 1 0 1
## [3,] 1 1 0

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}
```

```
mx <- matrix(rep(1:4, 5),5,4,byrow = TRUE)
(mx <- mx ^ row(mx))</pre>
```

```
[,1] [,2] [,3] [,4]
##
## [1,]
           1
                 2
                      3
## [2,]
                 4
                      9
                           16
           1
## [3,]
           1
                 8
                     27
                           64
## [4,]
           1
                16
                     81
                          256
## [5,]
                32 243 1024
```

- 4. **Basic programming** (10 points)
- 5. 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. (5 points)

```
h <- function(x, n){
    sum = 0
    for (i in seq(n)){
        sum = sum + x^i
    }
    return(sum)
}</pre>
```

- 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)
- 3. Find the sum of all the multiples of 3 or 5 below 1,000. (3, [euler1])

```
sum <- function(x = 1000){
   sum = 0
   for (i in 1:x-1){
      if(i%%3 == 0 | i%%5 == 0)
        sum = sum + i
   }
   return(sum)
}</pre>
```

[1] 233168

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

```
sum <- function(x = 1000000){
  sum = 0
  for (i in 1:x-1){
    if(i%%4 == 0 | i%%7 == 0)
        sum = sum + i
  }
  return(sum)
}</pre>
```

[1] 178571071431

4. 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]) c(1,2,3,5,8,13,21,34,55,89)

```
count <- 1 sum <- 2 while (count < 15) { i <- i+1 x<-c(x,x[i]+x[i+1]) if (x[i+1]%%2==0) { count <- c(count,x[i+1]) sum <- sum+1 } sum "'
```