R_Intermediate_Assignment

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```
data(iris)
head(iris)
```

```
##
     Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1
                           3.5
                                                          setosa
## 2
              4.9
                           3.0
                                        1.4
                                                     0.2 setosa
## 3
              4.7
                           3.2
                                        1.3
                                                     0.2 setosa
## 4
                           3.1
              4.6
                                        1.5
                                                     0.2 setosa
## 5
              5.0
                           3.6
                                                     0.2 setosa
                                        1.4
## 6
              5.4
                           3.9
                                        1.7
                                                     0.4 setosa
```

```
##create unique vector of species names
sp ids = unique(iris$Species)
##make an empty matrix that is 3x4
output = matrix(0, nrow=length(sp_ids), ncol=ncol(iris)-1)
##assign the species ids as the rownames of the output
rownames(output) = sp ids
##assign measurements (Sepal.Length Sepal.Width Petal.Length Petal.Width) as the column
names of the output
colnames(output) = names(iris[ , -ncol(iris)])
##create a loop
for(i in seq along(sp ids)) {
  ##subset the measurements so that "Species" is not listed
    iris sp = subset(iris, subset=Species == sp ids[i], select=-Species)
   ##identify each column
    for(j in 1:(ncol(iris sp))) {
       x = 0
        y = 0
        ##for every value that is greater than 0 (everything)
        if (nrow(iris sp) > 0) {
          ##identify sum of rows and sum of traits for each column
            for(k in 1:nrow(iris sp)) {
                x = x + iris_sp[k, j]
                y = y + 1
           ##the sum of the values divided by the number of observations
            output[i, j] = x / y
        }
    }
}
output
```

```
##
              Sepal.Length Sepal.Width Petal.Length Petal.Width
## setosa
                     5.006
                                  3.428
                                               1.462
                                                            0.246
## versicolor
                     5.936
                                  2.770
                                               4.260
                                                            1.326
## virginica
                     6.588
                                  2.974
                                               5.552
                                                            2.026
```

- 1. Describe the values stored in the object output. In other words what did the loops create? The loop created means for each trait for each species.
- 2. Describe using pseudo-code how output was calculated. See comments in code above
- 3. The variables in the loop were named so as to be vague. How can the objects <code>output</code>, <code>x</code>, and <code>y</code> could be renamed such that it is clearer what is occurring in the loop. Output can be descibed as the "means" for each measurement. Y could be described as the sum of all of the observations (number of rows), this could be called "sum_rows". X could be described as the sum of all the measurements for each trait, this could be called "sum_trait"
- 4. It is possible to accomplish the same task using fewer lines of code? Please suggest one other way to calculate output that decreases the number of loops by 1.

```
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
## filter, lag

## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union

iris %>%
    group_by(Species) %>%
    summarise_if(is.numeric, mean)
```

```
## # A tibble: 3 x 5
##
    Species
               Sepal.Length Sepal.Width Petal.Length Petal.Width
    <fct>
                       <dbl>
                                   <dbl>
                                                <dbl>
##
## 1 setosa
                       5.01
                                    3.43
                                                 1.46
                                                            0.246
## 2 versicolor
                        5.94
                                    2.77
                                                 4.26
                                                            1.33
## 3 virginica
                        6.59
                                    2.97
                                                 5.55
                                                            2.03
```

5. You have a vector \mathbf{x} with the numbers 1:10. Write a for loop that will produce a vector \mathbf{y} that contains the sum of \mathbf{x} up to that index of \mathbf{x} . So for example the elements of \mathbf{x} are 1, 2, 3, and so on and the elements of \mathbf{y} would be 1, 3, 6, and so on.

```
x<-c(1:10)
y=NULL
for (i in x) {
   y[i]=sum(x[1:i])
}
y</pre>
```

```
## [1] 1 3 6 10 15 21 28 36 45 55
```

6. Modify your for loop so that if the sum is greater than 10 the value of y is set to NA

```
x<-c(1:10)
y=NULL
for (i in x) {
    y[i]=sum(x[1:i])
        if (y[i]>10) {
            y[i] <- 'NA'
        }
}</pre>
```

```
## [1] "1" "3" "6" "10" "NA" "NA" "NA" "NA" "NA" "NA"
```

7. Place your for loop into a function that accepts as its argument any vector of arbitrary length and it will return y

```
sum_seq <- function(p) {
    d <- NULL
    for(i in p) {
        d[i] = sum(p[1:i])
     }
    print(d)
}
sum_seq(x)</pre>
```

```
## [1] 1 3 6 10 15 21 28 36 45 55
```