BIOL432 Assignment 3

Project Info

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Project link (https://github.com/carolinetang77/biol432-assignment3)

Data Wrangling

```
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
```

Reading in the data

```
dat <- read.csv("./InputData/FallopiaData.csv")
```

Filtering, Selecting, Adding a new column

```
wrangled <- dat %>%
  #remove rows with Total < 60
  filter(Total >= 60) %>%
  #select Total, Taxon, Scenario, Nutrients in that order and remove all other columns
  select(Total, Taxon, Scenario, Nutrients) %>%
  #replace total (currently in mg) with total in grams
  mutate(Total = Total/1000) %>%
  #name this new column TotalG
  rename(TotalG = Total)
print(wrangled)
```

```
##     TotalG Taxon    Scenario Nutrients
## 1  0.06706 japon         low       low
## 2  0.06108 japon         low       low
## 3  0.06082 japon        high      high
## 4  0.06674 japon        high      high
## 5  0.06318 japon        high      high
## 6  0.06131 japon        high      high
## 7  0.06471 bohem        high      high
## 8  0.06106 bohem        high      high
## 9  0.06420 bohem        high      high
## 10 0.06855 bohem        high      high
## 11 0.06660 bohem        high      high
## 12 0.07482 bohem        high      high
## 13 0.06606 japon     gradual      high
## 14 0.06701 japon     gradual      high
## 15 0.07041 japon     gradual      high
## 16 0.06343 japon     gradual      high
## 17 0.07705 japon     gradual      high
## 18 0.06179 japon     gradual      high
## 19 0.06256 bohem     gradual      high
## 20 0.06954 bohem     gradual      high
## 21 0.07591 bohem     gradual      high
## 22 0.06497 bohem     gradual      high
## 23 0.06071 bohem     gradual      high
## 24 0.06744 japon     extreme      high
## 25 0.07774 japon     extreme      high
## 26 0.06568 japon     extreme      high
## 27 0.07107 japon     extreme      high
## 28 0.06770 bohem     extreme      high
## 29 0.06086 bohem     extreme      high
## 30 0.06219 bohem     extreme      high
## 31 0.06553 bohem     extreme      high
## 32 0.06089 bohem     extreme      high
## 33 0.06037 bohem     extreme      high
## 34 0.06786 bohem     extreme      high
## 35 0.06900 japon fluctuations      high
## 36 0.06540 japon fluctuations      high
## 37 0.06308 japon fluctuations      high
## 38 0.06093 japon fluctuations      high
## 39 0.06873 japon fluctuations      high
## 40 0.06988 japon fluctuations      high
## 41 0.06948 japon fluctuations      high
## 42 0.06680 bohem fluctuations      high
## 43 0.06296 bohem fluctuations      high
## 44 0.07880 bohem fluctuations      high
## 45 0.06425 bohem fluctuations      high
```

Custom Function

```
calculate <- function(x, calculation) {
  if (calculation == "Average") { #if string is "Average" calculate the mean
    cat("Calculating mean...\n")
    result <- mean(x, na.rm = T)

  } else if (calculation == "Sum") { #if string is "Sum" calculate the sum
    cat("Calculating sum...\n")
    result <- sum(x, na.rm = T)

  } else if (calculation == "Observations") { #if string is "Observations" count number of obser
vations
    cat("Counting up observations...\n")
    result <- length(x)
  } else {
    stop(message("Calculation not recognized"))
  }
  return(result)
}
```

Testing the function

Counting observations in Taxon column

```
calculate(wrangled$Taxon, "Observations")
```

```
## Counting up observations...
```

```
## [1] 45
```

Calculating average TotalG for the high nutrient group

```
calculate(wrangled$TotalG[wrangled$Nutrients == "high"], "Average")
```

```
## Calculating mean...
```

```
## [1] 0.06646674
```

Calculating average TotalG for the low nutrient group

```
calculate(wrangled$TotalG[wrangled$Nutrients == "low"], "Average")
```

```
## Calculating mean...
```

```
## [1] 0.06407
```

Saving the new data

```
write.csv(wrangled, file = "./Output/WrangledData.csv", row.names = F)
```