

Assignment 3 - Reproducibility

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Project Info

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GitHub Link: “https://github.com/bloopyploop/BIOL432_A3.git”

1. Loading Packages

```
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
```

2. Wrangling Data

```
Fallo_Data<- read.csv("InputData/FallopiaData.csv") %>%
  filter(Total >= 60) %>% # Remove rows with 'Total' biomass < 60
  select(Total, Taxon, Scenario, Nutrients) %>% # Reorder and remove all other columns
  mutate(TotalG = Total/1000, .before = Taxon, Total = NULL) # Make new column Total G which converts Total from
mg to g and replaces Total
```

Fallo_Data

```
##      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
```

Creating Custom Function

```
my.function <- function(dataframe = NULL, column = NULL, method = NULL){
  if(method == "Average"){
    return(mean(dataframe[, column]))} # If string2 is Average, calculate mean of column named in vector1
  if(method == "Sum"){
    return(sum(dataframe[, column]))} # If string2 is Sum, calculate sum of column named in vector1
  if(method == "Observation"){
    return(nrow(dataframe[, !is.na(column)]))} # If string2 is Observations, count number of columns in vector1
  else{
    print("ERROR") # If string2 is anything else, output Error
  }
}

# Column is input 1, a vector of data to process.
# Method is input 2, a string that defines what calculation to perform.
```

Testing Custom Function

```
Taxon_Obv <- my.function(Fallo_Data, "Taxon", "Observation") # Using function to count total number of observations in the Taxon column
```

Taxon_Obv

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

```
Avg_TotalG_LowNut <- my.function(Fallo_Data %>% filter(Nutrients == "low"), "TotalG", "Average") # Using function to calculate average TotalG for low Nutrient concentrations
```

Avg_TotalG_LowNut

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

```
Avg_TotalG_HighNut <- my.function(Fallo_Data %>% filter(Nutrients == "high"), "TotalG", "Average") # Using function to calculate average TotalG for high Nutrient concentrations
```

Avg_TotalG_HighNut

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

Saving New Data

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