

Assignment 4 - Regex

Cecilia Ho

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Project Info

Name: “Cecilia Ho”

Student ID: “20068106”

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GitHub UserName: “bloopyploop”

GitHub Link: “<https://github.com/bloopyploop/BIOL432.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

```
MData <- read.csv("InputData/measurements.csv") %>% # Importing .csv file  
  mutate(Sp = sub("(\\w)(\\w+)", "\\1\\.", Organism), Organism = NULL, .before = Limb.width) #Shortening genus nam  
e, removing Organism column, moving Sp column to where Organism column was
```

MData

```
##           Sp Limb.width Limb.length  Observer  
## 1      I. scapularis      0.01      0.20 Victoria X  
## 2        H. sapiens      3.28     38.00      Hans P  
## 3        H. amphibius    68.09    112.54    Ashley A  
## 4  G. camelopardalis    29.13     88.41     Bobby B  
## 5        S. domesticus    16.92     29.37    Cedric C  
## 6        C. hoffmani     11.81     61.90    Darren D  
## 7        P. cinereus      5.09     21.02    Elijah E  
## 8        U. maritimus    14.05    100.91    Fatima F  
## 9         E. lutris       4.77     14.08    Georgia G  
## 10       C. lupus       36.17    104.20     Juice J
```

3. Saving New Dataset

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