

# BIOL432 Assignment 4 - Caroline Tang (20115082)

## Project info

Date: Jan 31, 2022

Github username: carolinetang77

## Data science

Load libraries

```
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
```

Load in measurements data from week 1 as MData

```
MData <- read.csv("../InputData/A4_Caroline_Tang.csv")
```

Create a new dataset that is a copy of MData but with Sp instead of Organism, formatted as (G. species)

```
(short <- MData %>% mutate(Sp = gsub("(\\w)\\w+\\s+(\\w+)", "\\1. \\2", MData$Organism)) %>%  
  select(Sp, Limb.length, Limb.width, Observer))
```

```
##           Sp Limb.length Limb.width Observer  
## 1      P. lotor           1         1.0 Olivier R  
## 2    P. pygmaeus           2         1.0      Han S  
## 3 P. cancrivorus           3         1.0      Luke S  
## 4      P. lotor           4         1.0 Olivier R  
## 5    P. pygmaeus           5         1.0 Olivier R  
## 6 P. cancrivorus           6         1.0      Han S  
## 7      P. lotor           7         1.0      Luke S  
## 8    P. pygmaeus           8         1.0      Luke S  
## 9 P. cancrivorus           9         1.0      Han S
```

## 10	H. sapiens	101	1.0	Olivier R
## 11	P. pygmaeus	1	0.1	Han S
## 12	P. pygmaeus	2	0.1	Luke S
## 13	P. lotor	3	0.1	Han S
## 14	P. pygmaeus	4	0.1	Olivier R
## 15	P. cancrivorus	5	0.1	Luke S
## 16	P. lotor	6	0.1	Han S
## 17	P. pygmaeus	7	0.1	Luke S
## 18	P. cancrivorus	8	0.1	Han S
## 19	P. lotor	9	0.1	Luke S

Save new dataset as MeasShort.csv

```
write.csv(short, "./Output/MeasShort.csv")
```