BIOL432 Assignment 4 - Caroline Tang (20115082)

Project info

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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/measurements.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")
```