

Git repository: [https://github.com/klynch416/BIOL432\\_A1](https://github.com/klynch416/BIOL432_A1) ([https://github.com/klynch416/BIOL432\\_A1](https://github.com/klynch416/BIOL432_A1))

```
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
```

*Import measurements.csv file*

```
MData <- read.csv("measurements.csv")
```

*Reformat species name in new column*

```
MData <- MData %>% mutate(Sp = sub("(\\D{1}).*\\s(\\w+)", "\\1. \\2", Species))
```

*New dataset with Organism column replaced by Sp column*

```
NData <- MData %>% select(!Species) %>% relocate(Sp, .after = X)
```

*Save new dataset to csv*

```
write.csv(NData, "MeasShort.csv")
```