## RMarkdown\_Demo\_1

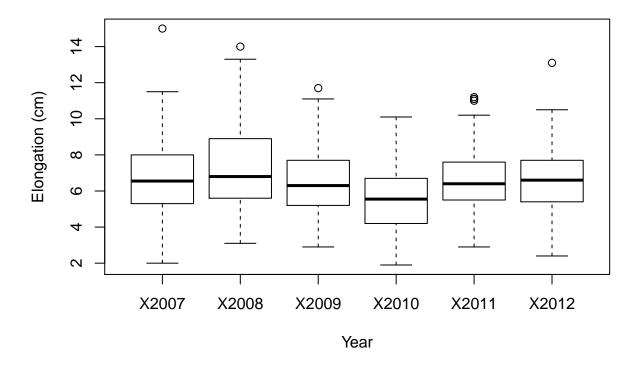
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```
#install and load the relevant packages
##install.packages("dplyr", "tidyr", "pander")
library(dplyr) #useful for data manipulation
## Warning: package 'dplyr' was built under R version 3.6.2
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
      filter, lag
## The following objects are masked from 'package:base':
##
      intersect, setdiff, setequal, union
library(tidyr) #useful to format data
## Warning: package 'tidyr' was built under R version 3.6.2
library(pander) #creates tables
## Warning: package 'pander' was built under R version 3.6.2
#set working directory to where data files are stored
#setwd()
#Import data from csv file in directory and assign data.frame to object 'elongation'
elongation <- read.csv("EmpetrumElongation.csv", sep = ",") #separated by commas
head(elongation)
    Zone Indiv X2007 X2008 X2009 X2010 X2011 X2012
##
## 1
          373
                5.1
                       5.1
                             4.8
                                   8.7
                                         6.3
                                               3.2
## 2
          379
       2
                 8.1 13.3
                             8.6
                                   4.9
                                        5.9
                                              6.3
## 3
       2
          383
                 9.3 8.5 11.7
                                   7.9
                                        8.0
                                              6.3
## 4
       2
          389 15.0 10.3
                             6.8
                                   6.9
                                        5.9 7.6
                                   3.8
## 5
           390
                 3.5 6.2
                             4.7
                                         3.5
                                               3.0
## 6
                       5.6
                                   4.5
                                        4.5 7.6
           395
                 6.1
                             4.4
```

```
#Tidy the data
#Put in long format with gather()
elongation_long <- gather(elongation,</pre>
                          Year, #name column
                          Length, #name column
                           c(X2007, X2008, X2009, X2010, X2011, X2012)) #Gather the lengths by year
head(elongation_long) #preview the data
     Zone Indiv Year Length
##
## 1
        2
            373 X2007
                         5.1
            379 X2007
## 2
                         8.1
## 3
            383 X2007
        2
                         9.3
## 4
            389 X2007
                         15.0
## 5
        2
            390 X2007
                         3.5
## 6
            395 X2007
                         6.1
#investigating the data
#create a boxplot of the 'elongation_long'
boxplot(Length ~ Year,
        data = elongation_long, #call data from data.frame
        xlab = 'Year', #x-axis title
        ylab = 'Elongation (cm)', #y-axis title
        main = "Annual growth of Empetrum") #main title
```

## **Annual growth of Empetrum**



```
# missing Germination.csv file
# germination of seeds subjected to toxic solutions
#Import data from csv file in directory and assign data.frame to object 'germination'
germination <- read.csv("Germination.csv", sep = ",") #separated by commas
# Use filter() to keep only the rows of `germination' for species `SR'
germinSR <- filter(germination, Species == 'SR')</pre>
#create histogram of germination of species 'SR' with 8 breaks
#use $ to access variables in column Nb_seeds_germin
hist(germinSR$Nb_seeds_germin, breaks = 8)
\# Use mutate() to create a new column of the germination percentage using the total number of seeds
# and the number of seeds that germinated
germin_percent <- mutate(germination, Percent = Nb_seeds_germin / Nb_seeds_tot * 100)</pre>
# Use a pipe to get a table of summary statistics for each Seed type
germin_summ <- germin_percent %>%
  group_by(Species) %>%
  summarise("Mean germination per" = mean(Nb_seeds_germin),
            "Max germination per" = max(Nb_seeds_germin),
            "Min germination per" = min(Nb_seeds_germin))
```