

Homework 7
MTH 3240, Spring 2020

Due Tuesday, Apr. 21

Reading: *Environmental Statistics*:

- Chapter 10 (but Sections **10.5** and **10.7** are **optional** in **Spring 2020**)

Problems: Please do the following problems from the Problems sections of *Environmental Statistics*:

Chapter in <i>Environmental Statistics</i>	Problems
Ch. 10	10.1, 10.2, 10.3, 10.4, 10.5* (skip parts <i>a</i> , <i>g</i> , and <i>h</i>), 10.6** (skip parts <i>a</i> , <i>g</i> , and <i>h</i>), 10.7*** (skip parts <i>a</i> , <i>g</i> , and <i>h</i>), 10.12**** (skip parts <i>a</i> , <i>g</i> , and <i>h</i>), 10.13***** (skip parts <i>a</i> , <i>g</i> , and <i>h</i>)

* For **Problem 10.5**, you can use the `aov()` function in R.

First, create a *data frame* in R that contains the data. There are two ways to do this.

The first is to use the `read.table()` function to read the data from the text file **Ch10Pr5Data.txt** (after saving it on your computer from the course website) by typing:

```
> my.data <- read.table(file.choose(), header = TRUE)
```

The second is to use the `data.frame()` function, for example by typing something like this:

```
> acid <- c("Mild", "Mild", "Mild", "Strong", "Strong", "Strong",  
           "Extreme", "Extreme", "Extreme")  
> biom <- c(1.35, 1.29, 1.24, 0.45, 0.36, 0.48, 0.91, 0.57, 0.51)  
> my.data <- data.frame(Acidification = acid, Biomass = biom)
```

Once you've created the *data frame*, you can carry out the ANOVA by typing:

```
> my.anova <- aov(Biomass ~ Acidification, data = my.data)  
> summary(my.anova)
```

** For **Problem 10.6**, you can use the `aov()` function in R.

First, create a *data frame* in R that contains the data either using the `read.table()` function (as described above but with the data from the text file `Ch10Pr6Data.txt`) or using the `data.frame()` function, for example by typing something like this:

```
> acid <- c("Mild", "Mild", "Mild", "Strong", "Strong", "Strong",  
           "Extreme", "Extreme", "Extreme")  
> mquot <- c(2.2, 0.78, 0.86, 4.8, 5.2, 2.4, 2.0, 3.8, 5.9)  
> my.data <- data.frame(Acidification = acid, MQuotient = mquot)
```

Once you've created the *data frame*, you can carry out the ANOVA by typing:

```
> my.anova <- aov(MQuotient ~ Acidification,  
                 data = my.data)  
> summary(my.anova)
```

*** For **Problem 10.7**, you can use the `aov()` function in R.

First, create a *data frame* in R that contains the data either using the `read.table()` function (as described above but with the data from the text file `Ch10Pr7Data.txt`) or using the `data.frame()` function, for example by typing something like this:

```
> conc <- c("Conc0", "Conc0", "Conc0", "Conc0", "Conc0",  
           "Conc5.6", "Conc5.6", "Conc5.6", "Conc5.6",  
           "Conc5.6", "Conc10", "Conc10", "Conc10", "Conc10",  
           "Conc10", "Conc18", "Conc18", "Conc18", "Conc18",  
           "Conc18", "Conc32", "Conc32", "Conc32", "Conc32",  
           "Conc32")  
> tbln <- c(19.58, 18.75, 19.14, 16.50, 17.93, 18.26, 16.25,  
           16.39, 18.70, 15.62, 13.31, 18.92, 15.62, 14.30,  
           15.29, 18.59, 12.88, 16.28, 15.38, 19.75, 12.54,  
           10.67, 15.95, 12.54, 11.66)  
> my.data <- data.frame(Concentration = conc, TubeLength = tbln)
```

Once you've created the *data frame*, you can carry out the ANOVA by typing:

```
> my.anova <- aov(TubeLength ~ Concentration,  
                 data = my.data)  
> summary(my.anova)
```

**** For **Problem 10.12**, you can use the `aov()` function in R.

First, create a *data frame* in R that contains the data either using the

