# Homework #1

#### Madhav Viswesvaran

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```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr
          1.1.4
                     v readr
                                 2.1.5
## v forcats 1.0.0 v stringr
                                1.5.1
## v ggplot2 3.5.1
                      v tibble
                                  3.2.1
## v lubridate 1.9.4
                      v tidyr
                                  1.3.1
## v purrr
             1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                  masks stats::lag()
## i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to become error
##
## cols(
##
    season = col_character(),
##
    size = col_character(),
    speed = col_character(),
##
##
    mxPH = col_double(),
##
    mn02 = col_double(),
##
    C1 = col_double(),
##
    NO3 = col_double(),
##
    NH4 = col_double(),
##
    oPO4 = col_double(),
##
    PO4 = col_double(),
##
    Chla = col_double(),
##
    a1 = col_double(),
    a2 = col_double(),
##
##
    a3 = col_double(),
##
    a4 = col_double(),
    a5 = col_double(),
##
    a6 = col_double(),
##
    a7 = col_double()
## )
  1. Descriptive Summary Statistics
 a)
#number of observations in each season
library(dplyr)
algae %>%
 summarize(.by = season, n = n())
## # A tibble: 4 x 2
## season
   <chr> <int>
```

```
## 4 summer
                45
  b) There are missing values for some of the chemicals.
#Calculating mean and variance for each chemical
algae %>%
  summarize(across(c(4:11), list(mean = ~ mean(.x, na.rm = TRUE),
                                   var = ~ var(.x, na.rm = TRUE)))) %>%
  pivot_longer(cols = everything(),
               names_to = c("variable", "statistic"),
               names_sep = "_",
               values_to = "value") %>%
  mutate(value = format(value, scientific = FALSE, digits = 6))
## # A tibble: 16 x 3
##
      variable statistic value
##
      <chr>
                          <chr>>
               <chr>
##
   1 mxPH
               mean
                                  8.011734"
    2 mxPH
##
                                  0.357969"
               var
    3 mn02
                          11
##
               mean
                                  9.117778"
##
   4 \text{ mn}02
               var
                                  5.718089"
## 5 Cl
                          11
                                 43.636279"
               mean
## 6 Cl
               var
                              2193.171725"
                          11
## 7 NO3
                                  3.282389"
               mean
## 8 NO3
               var
                                 14.261756"
                          11
## 9 NH4
                                501.295828"
               mean
                          "3851584.684865"
## 10 NH4
               var
## 11 oP04
                                 73.590596"
               mean
## 12 oP04
                               8305.849930"
                var
## 13 PO4
                                137.882101"
               mean
## 14 PO4
                              16639.384545"
                var
## 15 Chla
                                 13.971197"
               mean
## 16 Chla
                          11
                                420.082735"
                var
It looks like NH4 has extremely large mean and variance relative to the other chemicals.
#Calculating median and mad for each chemical
algae %>%
  summarize(across(c(4:11), list(median = ~ median(.x, na.rm = TRUE),
                                   mad = \sim mad(.x, na.rm = TRUE)))) %>%
  pivot_longer(cols = everything(),
               names_to = c("variable", "statistic"),
```

```
## # A tibble: 16 x 3
## variable statistic value
## <chr> <chr> ## 1 mxPH median " 8.060000"
## 2 mxPH mad " 0.504084"
```

names\_sep = "\_",

values\_to = "value") %>%

mutate(value = format(value, scientific = FALSE, digits = 6))

## 1 winter

## 2 spring

## 3 autumn

62

53

40

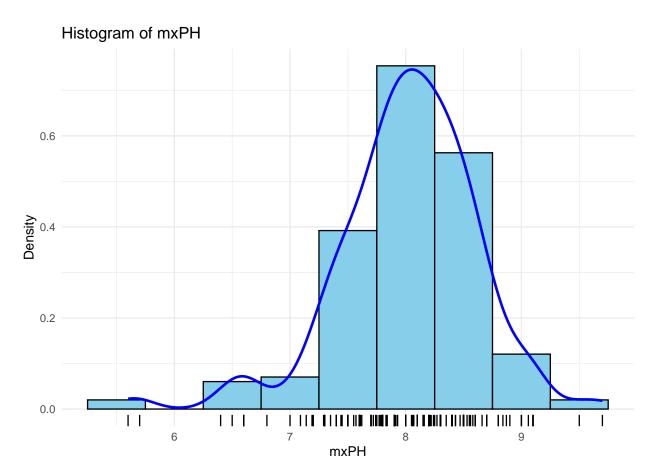
```
## 3 mnO2
                         " 9.800000"
               median
  4 mn02
                         " 2.053401"
##
               mad
  5 Cl
                         " 32.730000"
##
               median
                         " 33.249529"
  6 Cl
##
               mad
                         " 2.675000"
##
   7 NO3
               median
## 8 NO3
               mad
                         " 2.172009"
## 9 NH4
               median
                         "103.166500"
                         "111.617548"
## 10 NH4
               \mathtt{mad}
## 11 oPO4
               median
                         " 40.150000"
## 12 oPO4
               mad
                         " 44.045822"
## 13 PO4
               median
                         "103.285500"
## 14 PO4
                         "122.321172"
               mad
## 15 Chla
               median
                         " 5.475000"
                         " 6.671700"
## 16 Chla
               mad
```

The median and MAD tend to be pretty similar for the chemicals expect for mxPH and mnO2, with NH4 still having the biggest MAD and median

### 2 - Data visualization

a)

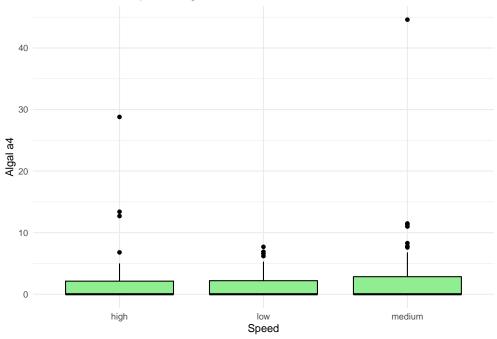
```
#creating a histogram
ggplot(algae, aes(x = mxPH)) +
  geom_histogram(aes(y = ..density..), binwidth = 0.5, fill = "skyblue", color = "black") +
  geom_density(color = "blue", linewidth = 1) +
  geom_rug() +
  ggtitle("Histogram of mxPH") +
  xlab("mxPH") +
  ylab("Density") +
  theme_minimal()
```



The distribution slightly skews left.  $\,$ 

```
#boxplot
ggplot(algae, aes(x = speed, y = a4)) +
  geom_boxplot(fill = "lightgreen", color = "black") +
  ggtitle("A Conditioned Boxplot of Algal a4") +
  xlab("Speed") +
  ylab("Algal a4") +
  theme_minimal()
```

### A Conditioned Boxplot of Algal a4



It appears that the

high and medium speeds have some outlier for algal a 4. ## 3 - Missing Values a)

```
#table with na values for each column
num_rows_with_na <- sum(apply(is.na(algae), 1, any))
num_rows_with_na</pre>
```

```
## [1] 16
```

```
algae %>%
  summarize(across(everything(), ~ sum(is.na(.)), .names = "count_{col}")) %>%
  pivot_longer(cols = everything(), names_to = "column", values_to = "na_count")
```

```
## # A tibble: 18 x 2
##
      column
                   na_count
##
      <chr>
                       <int>
##
   1 count_season
                           0
##
    2 count_size
                           0
##
    3 count_speed
                           0
   4 count_mxPH
                           1
##
                           2
##
   5 count_mn02
##
   6 count_Cl
                          10
                           2
##
    7 count_NO3
##
    8 count_NH4
                           2
   9 count_oPO4
                           2
                           2
## 10 count_PO4
                          12
## 11 count_Chla
## 12 count_a1
                           0
## 13 count_a2
                           0
## 14 count_a3
                           0
                           0
## 15 count_a4
## 16 count_a5
                           0
## 17 count a6
                           0
## 18 count_a7
```

b) 16 observations contain missing values, and the table shows the number of missing values by variable.

```
algae.del <- algae[complete.cases(algae), ]
#View(algae.del)</pre>
```

algae.del has 184 observations.

### 4 - Bias Variance Tradeoff

- a) The terms that represent reducible error are  $Var(\hat{f}(x_0))$  and  $[Bias(\hat{f}(x_0))]^2$  The term that represents irreducible error is Var(e)
- b) In the bias-variance tradeoff we know that the variance and bias are non-negative terms because they are squared, therefore even if the bias and variance are 0, the expected test error is still at least equal to the irreducible error, but in most cases it will be equal to the irreducible error plus some bias and variance since they are nonnegative.