Homework07

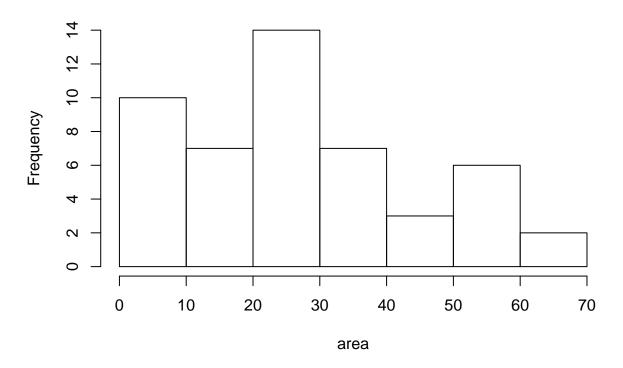
Ahilan Subbaian

4/30/2020

"I pledge my honor that I have abided by the Stevens Honor System" 10.32) a.

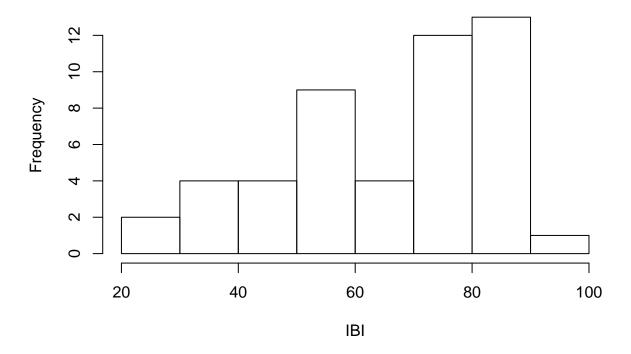
```
library(readxl)
data <-read.csv("Water-Quality.csv")</pre>
area<- data$Area
IBI<-data$IBI
forest<-data$Forest</pre>
chrt <- matrix(c(mean(IBI),sd(IBI),median(IBI),max(IBI),min(IBI),</pre>
                  mean(area), sd(area), median(area), max(area), min(area)), ncol=5, byrow=TRUE)
colnames(chrt) <- c("mean", "standard deviation", "median", "max", "min")</pre>
rownames(chrt) <- c("IBI", "area")</pre>
tabl <- as.table(chrt)</pre>
chrt
##
             mean standard deviation median max min
## IBI 65.93878
                            18.27955
                                           71 91
## area 28.28571
                             17.71417
                                           26 70
summary(area)
##
      Min. 1st Qu.
                     Median
                                Mean 3rd Qu.
                                                 Max.
##
      2.00
             16.00
                      26.00
                               28.29
                                        34.00
                                                70.00
summary(IBI)
##
      Min. 1st Qu. Median
                                Mean 3rd Qu.
                                                 Max.
     29.00
            55.00
                     71.00
                               65.94
##
                                        82.00
                                                91.00
hist(area, main = "Area's Histogram")
```

Area's Histogram



hist(IBI, main = "IBI's Histogram")

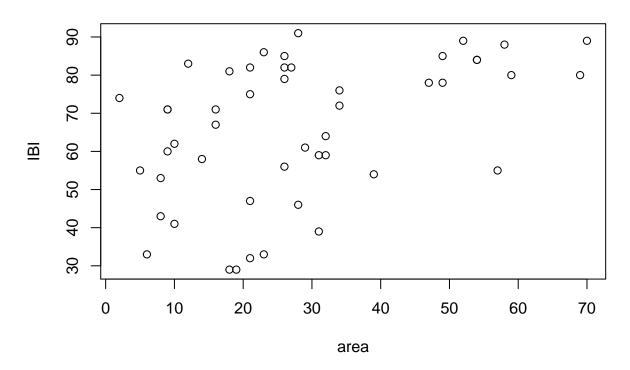
IBI's Histogram



Because the sample size is greater than 30 we can assume that both distributions are normal. Area is right skewed and IBI is left skewed. Area has multiple outliers while IBI has no outliers. b.

```
plot(area, IBI, main = "Scatterplot of Area vs. IBI")
```

Scatterplot of Area vs. IBI



There appears to be no outliers or unusual patters. There is a weak positive relationship between area and IBI and more variance in smaller values of area.

```
c. for i in 1:49 let yi = b0 + b1 * xi + ei d. h0: b1 = 0 ha: b1 != 0 e.
```

summary(lm(IBI~area))

```
##
## Call:
## lm(formula = IBI ~ area)
##
## Residuals:
##
       Min
                1Q
                   Median
                                3Q
                                       Max
   -32.666 -8.887
                     3.432
##
                            12.414
##
##
   Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                52.9230
                            4.4835
                                    11.804 1.17e-15 ***
                 0.4602
                            0.1347
                                     3.415 0.00132 **
## area
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 16.53 on 47 degrees of freedom
```

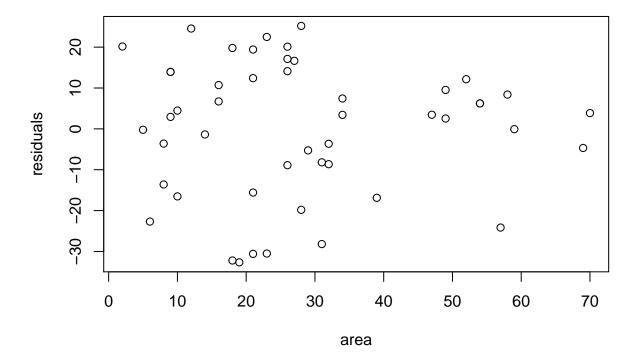
```
## Multiple R-squared: 0.1988, Adjusted R-squared: 0.1818 ## F-statistic: 11.67 on 1 and 47 DF, p-value: 0.001322
```

The coefficient of multiple determination is .1988, so 19.88% of the changes in IBI is caused by Area. the coefficient of area is .4602, so for every increase of 1 in area, IBI increases by .4602.

f.

```
residuals<- resid(lm(IBI~area))
plot(area, residuals, main = "Area vs. Residuals")</pre>
```

Area vs. Residuals

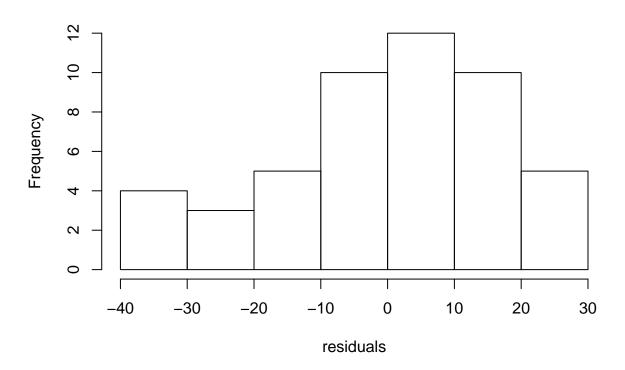


Nothing unusual, there appears to be no pattern

g.

```
hist(residuals, main = "Area vs. Residuals")
```

Area vs. Residuals



The residuals appear approximately normal because the scatterplot did not seem to have any relationship and the histogram is approximately normal.

h. My assumptions from c seem reasonable as the residuals appear to be independent of area.

```
10.33) a.
```

##

##

Min. 1st Qu.

55.00

29.00

Median

71.00

```
chrt1 <- matrix(c(mean(IBI),sd(IBI),median(IBI),max(IBI),min(IBI),</pre>
                  mean(forest),sd(forest),median(forest),max(forest),min(forest)),ncol=5,byrow=TRUE)
colnames(chrt1) <- c("mean", "standard deviation", "median", "max", "min")</pre>
rownames(chrt1) <- c("IBI", "Forest")</pre>
tabl1 <- as.table(chrt1)
chrt1
##
               mean standard deviation median max min
## IBI
           65.93878
                               18.27955
                                             71
                                                 91
## Forest 39.38776
                               32.20431
                                             33 100
summary(IBI)
```

Max.

91.00

Mean 3rd Qu.

82.00

65.94

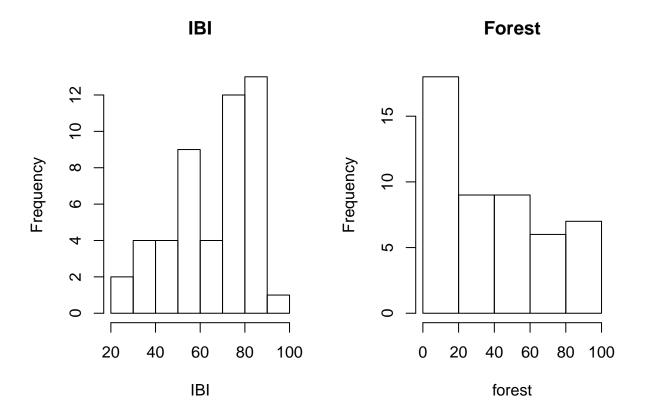
summary(forest)

```
## Min. 1st Qu. Median Mean 3rd Qu. Max.

## 0.00 10.00 33.00 39.39 63.00 100.00

par(mfrow=c(1,2))
```

```
hist(IBI, main = "IBI")
hist(forest, main = "Forest")
```

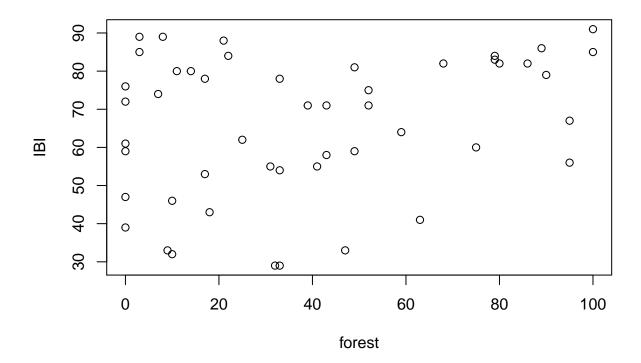


Because the sample size is larger than 30 we can assume that the distributions are normal. Forest is right skewed and IBI is left skewed. Niether seem to have an outlier.

b.

```
plot(forest, IBI, main = "Forest vs. IBI")
```

Forest vs. IBI



There seems to be a very weak positive relationship between forest and IBI, and no weird patters.

```
c. for i in 1:49 let yi = a0 + a1 * xi + ei ei is independant and normally distributed at mean 0 d. h0 b1 = 0 ha b1 != 0 e.
```

summary(lm(IBI ~ forest))

```
##
## Call:
## lm(formula = IBI ~ forest)
##
## Residuals:
##
                1Q
                    Median
                                3Q
                                       Max
##
   -35.961 -11.186
                     4.508
                           13.021
                                    28.633
##
##
   Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
  (Intercept) 59.90725
                           4.03957
                                             <2e-16 ***
##
                                    14.830
## forest
                0.15313
                           0.07972
                                     1.921
                                             0.0608 .
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.79 on 47 degrees of freedom
## Multiple R-squared: 0.07278,
                                    Adjusted R-squared: 0.05305
```

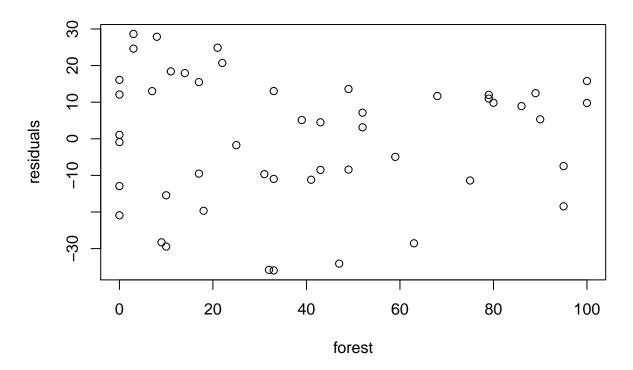
```
## F-statistic: 3.689 on 1 and 47 DF, p-value: 0.06084
```

the coefficient of multiple determination is .07278 so 7.27% of the change in IBI is explained by forest. and the coefficient of forest is .15313 so for every 1 change in forest there is a .15313 change in IBI

f.

```
residuals<- resid(lm(IBI~forest))
plot(forest, residuals, main = "Forest vs. Residuals")</pre>
```

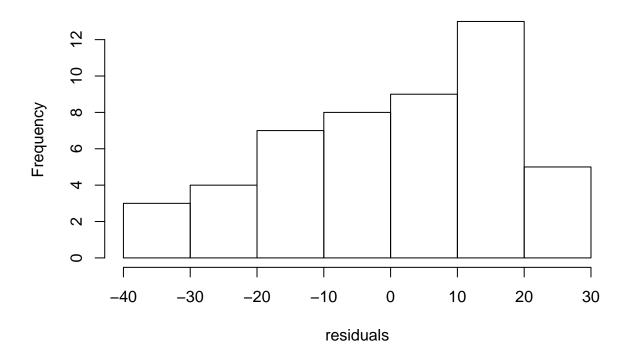
Forest vs. Residuals



there does not appear to be a pattern in the scatterplot

g.

Forest vs. Residuals



the histogram appears to be left skewed

- h. the assumption is not reasonable because the residuals appear to be left skewed showing a pattern in the data.
- 10.34) I pick area because it has a higher r squared so it explains more change and has a lower p value.
- 10.35) a. Because the relationship between the two variables is almost significant at the alpha level of 0.05, an observation with 0% forest would decrease the p value The regression equation is IBI = 51.3 + 0.483 Area
 - b. Because the relationship between the two variables is almost significant at the alpha level of 0.05, an observation with 100% forest would increase the p value The regression equation is IBI = 51.0 + 0.462 Area

10.36) a.

```
71.4735 - (-2.011) * sqrt( 314.34 * ((1/49) + (40-25*4)^(2) / (-4272069)))
```

[1] 76.4607

```
71.4735 + (-2.011) * sqrt( 314.34 * ((1/49) + (40-25*4)^2/ (-4272069)))

## [1] 66.4863
(66.4863, 76.4607)
b.

71.4735 + (-2.011) * sqrt( 314.34 * (1 + (1/49) + (40-25*4)^2/ (-4272069)))

## [1] 35.47209

71.4735 - (-2.011) * sqrt( 314.34 * (1+ (1/49) + (40-25*4)^2/ (-4272069)))

## [1] 107.4749

(35.47209, 107.4749)
```

- c. the confidence interval tell us that we are 90% confident that the true population mean is between 66.48 and 76.46. and the prediction interval tell us that we are 95% confident that the true prediction response lies between 35.47 and 107.47
- d. We cannot use this data for other streams in Arkansas or other states because we dont know if other streams will have the same conditions.

10.37) At an area of 10, the prediction index of biotic integrity was 57.52. At 63% forest produced a predicted value of 69.55. This has a very large range of change in values, because they both use different base data.