Data Exploration

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# The following is an exploration of Stream Health Indicator correlation and comparison. The exploration will be structured as follows:

### Each dataframe (MIDO, NORO, and BICO) will be analyzed separately. Within each dataframe, there are data explaining biological indicator values, stream chemistry, and fecal indicators over time. The only group with multiple components is stream chemistry. I plan to do a series of correlative analysis showing if there is some sort of relationship between the three indicator types to help inform further analysis via principle component, multivariate analysis, etc. Therfore, the goal of this exploration is basically to summarize how these indicators correlate.

#### First, we need to load all the libraries we will need.

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

library(here)

## here() starts at C:/Data/Github/MADA/CARTERCOLEMAN\_MADA\_PROJECT

library(tidyverse)

## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.3.5 v purrr 0.3.4  
## v tibble 3.1.3 v stringr 1.4.0  
## v tidyr 1.1.3 v forcats 0.5.1  
## v readr 2.0.1

## -- Conflicts ------------------------------------------ tidyverse\_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()

library(tidyr)  
library(readr)  
library(stringr)

#### Loading the data from the processing script. Note that because you are loading a library at the beginning, it may either take a while or take several tries.

MIDO <- readRDS("../../data/processed\_data/MIDO.rds")  
NORO <- readRDS("../../data/processed\_data/NORO.rds")  
BICO <- readRDS("../../data/processed\_data/BICO.rds")

<- source(“processingscript.R”, local = knitr::knit\_global())

#### take a look at the data frames to make sure everything worked correctly.

view(MIDO)  
view(NORO)  
view(BICO)

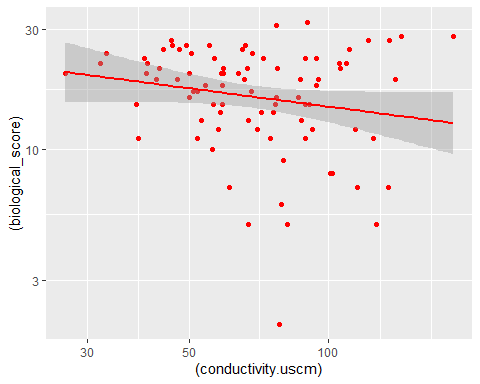
## MIDO

### *Biological Indicator:*

#### Biological Vs Conductivity

BS\_Con <- MIDO %>%   
 ggplot(aes(x=(conductivity.uscm),   
 y=(biological\_score))) +  
 geom\_point(color = "red") +  
 geom\_smooth(method=lm, color = "red") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
print(BS\_Con)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for BS\_Con.

BS\_Con\_lm <- lm(biological\_score ~ conductivity.uscm, data=MIDO)  
  
summary(BS\_Con\_lm)

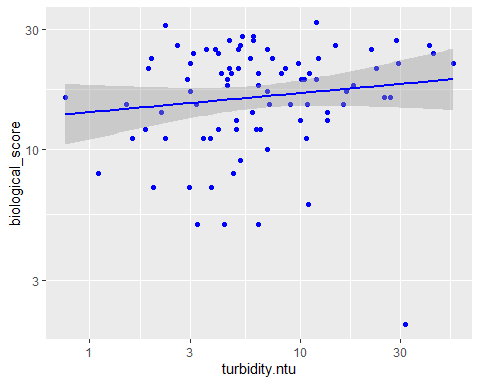
##   
## Call:  
## lm(formula = biological\_score ~ conductivity.uscm, data = MIDO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -15.6752 -5.0804 0.7546 5.0198 14.5213   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 19.00362 1.95783 9.706 1.8e-15 \*\*\*  
## conductivity.uscm -0.01694 0.02441 -0.694 0.489   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.721 on 86 degrees of freedom  
## Multiple R-squared: 0.005574, Adjusted R-squared: -0.005989   
## F-statistic: 0.482 on 1 and 86 DF, p-value: 0.4894

#### With *m = -0.017* and *p = 0.49*, there is a *negative*, *non-significant* correlation between *biological score* and *conductivity*.

#### Biological Vs Turbidity

BS\_Turb <- MIDO %>%  
 ggplot(aes(x=turbidity.ntu, y=biological\_score)) +  
 geom\_point(color = "blue") +  
 geom\_smooth(method=lm, color = "blue") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(BS\_Turb)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for BS\_Turb.

BS\_Turb\_lm <- lm(biological\_score ~ turbidity.ntu, data=MIDO)  
  
summary(BS\_Turb\_lm)

##   
## Call:  
## lm(formula = biological\_score ~ turbidity.ntu, data = MIDO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -18.2293 -4.9714 0.8791 4.9388 14.0396   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 16.70297 0.98476 16.961 <2e-16 \*\*\*  
## turbidity.ntu 0.11195 0.07386 1.516 0.133   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.652 on 86 degrees of freedom  
## Multiple R-squared: 0.02602, Adjusted R-squared: 0.01469   
## F-statistic: 2.297 on 1 and 86 DF, p-value: 0.1333

#### With *m = 0.11* and *p = 0.13*, there is a *positive*, *non-significant* correlation between *biological score* and *turbidity*.

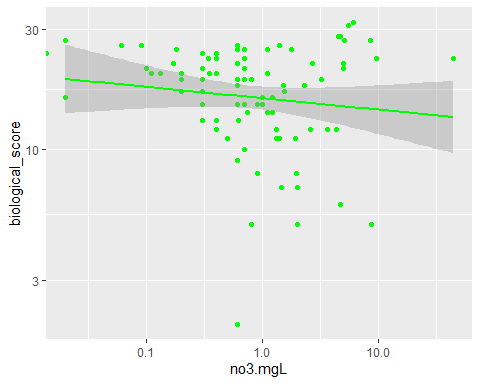
#### Biological Vs Nitrate Concentration

BS\_no3 <- MIDO %>%  
 ggplot(aes(x=no3.mgL, y=biological\_score)) +  
 geom\_point(color = "green") +  
 geom\_smooth(method=lm, color = "green") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(BS\_no3)

## Warning: Transformation introduced infinite values in continuous x-axis  
  
## Warning: Transformation introduced infinite values in continuous x-axis

## `geom\_smooth()` using formula 'y ~ x'

## Warning: Removed 1 rows containing non-finite values (stat\_smooth).



#### Now run linear regression for BS\_no3.

BS\_no3\_lm <- lm(biological\_score ~ no3.mgL, data=MIDO)  
  
summary(BS\_no3\_lm)

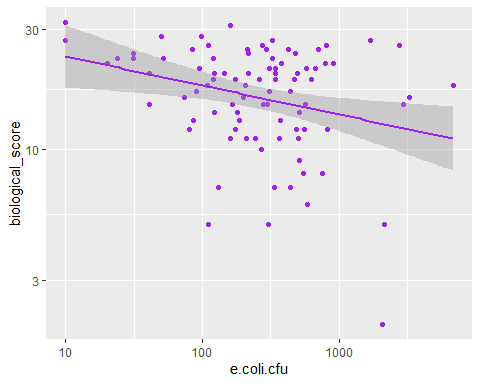
##   
## Call:  
## lm(formula = biological\_score ~ no3.mgL, data = MIDO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -15.5016 -4.7460 0.7879 4.7965 13.6079   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 17.4045 0.7737 22.496 <2e-16 \*\*\*  
## no3.mgL 0.1619 0.1451 1.116 0.268   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.692 on 86 degrees of freedom  
## Multiple R-squared: 0.01427, Adjusted R-squared: 0.002806   
## F-statistic: 1.245 on 1 and 86 DF, p-value: 0.2677

#### With *m = 0.11* and *p = 0.27*, there is a *positive*, *non-significant* correlation between *biological score* and *no3*.

#### Biological Vs E. Coli CFU

BS\_ECFU <- MIDO %>%  
 ggplot(aes(x=e.coli.cfu, y=biological\_score)) +  
 geom\_point(color = "purple") +  
 geom\_smooth(method=lm, color = "purple") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(BS\_ECFU)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for BS\_ECFU.

BS\_ECFU\_lm <- lm(biological\_score ~ e.coli.cfu, data=MIDO)  
  
summary(BS\_ECFU\_lm)

##   
## Call:  
## lm(formula = biological\_score ~ e.coli.cfu, data = MIDO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -14.686 -5.160 1.055 4.932 13.914   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 18.0924039 0.8243184 21.948 <2e-16 \*\*\*  
## e.coli.cfu -0.0006778 0.0007846 -0.864 0.39   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.711 on 86 degrees of freedom  
## Multiple R-squared: 0.008603, Adjusted R-squared: -0.002924   
## F-statistic: 0.7463 on 1 and 86 DF, p-value: 0.39

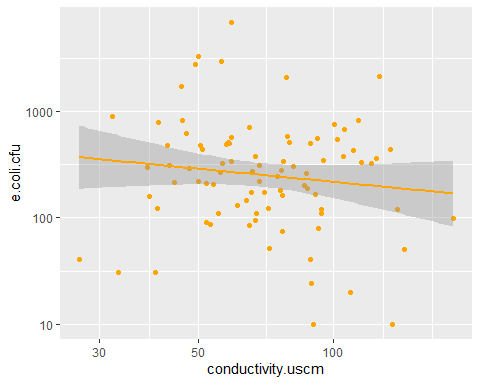
#### With *m = -0.0007* and *p = 0.39*, there really isn’t a relationship at all between *biological score* and *ECFU*.

### *E. Coli*

#### E. Coli Vs Conductivity

ECFU\_Con <- MIDO %>%  
 ggplot(aes(x=conductivity.uscm, y=e.coli.cfu)) +  
 geom\_point(color = "orange") +  
 geom\_smooth(method=lm, color = "orange") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(ECFU\_Con)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for ECFU\_Con.

ECFU\_Con\_lm <- lm(e.coli.cfu ~ conductivity.uscm, data=MIDO)  
  
summary(ECFU\_Con\_lm)

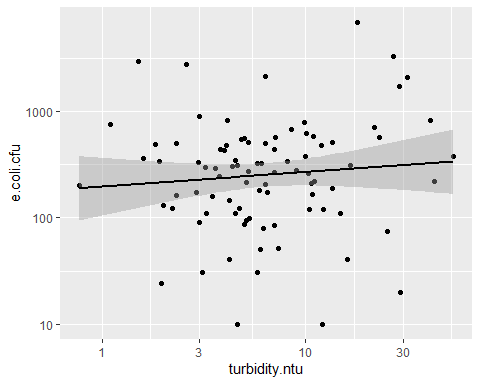
##   
## Call:  
## lm(formula = e.coli.cfu ~ conductivity.uscm, data = MIDO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -654.2 -392.3 -236.8 3.7 6288.2   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 793.308 266.825 2.973 0.00382 \*\*  
## conductivity.uscm -3.635 3.326 -1.093 0.27750   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 916 on 86 degrees of freedom  
## Multiple R-squared: 0.0137, Adjusted R-squared: 0.002229   
## F-statistic: 1.194 on 1 and 86 DF, p-value: 0.2775

#### With *m = -3.635* and *p = 0.28*, there is a *negative*, *non-significant* correlation between *ECFU* and *Conductivity*.

#### E. Coli Vs Turbidity

ECFU\_Turb <- MIDO %>%  
 ggplot(aes(x=turbidity.ntu, y=e.coli.cfu)) +  
 geom\_point(color = "black") +  
 geom\_smooth(method=lm, color = "black") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(ECFU\_Turb)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for ECFU\_Turb.

ECFU\_Turb\_lm <- lm(e.coli.cfu ~ turbidity.ntu, data=MIDO)  
  
summary(ECFU\_Turb\_lm)

##   
## Call:  
## lm(formula = e.coli.cfu ~ turbidity.ntu, data = MIDO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -961.2 -349.9 -206.9 22.6 6184.2   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 349.85 133.90 2.613 0.0106 \*  
## turbidity.ntu 18.60 10.04 1.852 0.0675 .  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 904.5 on 86 degrees of freedom  
## Multiple R-squared: 0.03835, Adjusted R-squared: 0.02717   
## F-statistic: 3.43 on 1 and 86 DF, p-value: 0.06746

#### With *m = 18.6* and *p = 0.07*, there is a *positive*, *non-significant* correlation between *ECFU* and *turbidity*.

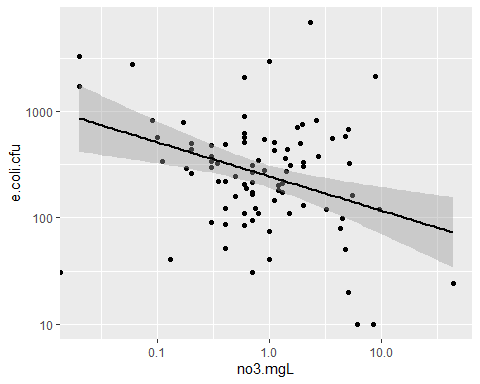
#### E. Coli Vs Nitrate Concentration

ECFU\_no3 <- MIDO %>%  
 ggplot(aes(x=no3.mgL, y=e.coli.cfu)) +  
 geom\_point(color = "black") +  
 geom\_smooth(method=lm, color = "black") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(ECFU\_no3)

## Warning: Transformation introduced infinite values in continuous x-axis  
  
## Warning: Transformation introduced infinite values in continuous x-axis

## `geom\_smooth()` using formula 'y ~ x'

## Warning: Removed 1 rows containing non-finite values (stat\_smooth).



#### Now run linear regression for ECFU\_no3.

ECFU\_no3\_lm <- lm(e.coli.cfu ~ no3.mgL, data=MIDO)  
  
summary(ECFU\_no3\_lm)

##   
## Call:  
## lm(formula = e.coli.cfu ~ no3.mgL, data = MIDO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -512.8 -390.1 -245.3 -26.1 6347.6   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 543.82 106.46 5.108 1.94e-06 \*\*\*  
## no3.mgL -10.61 19.97 -0.531 0.597   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 920.9 on 86 degrees of freedom  
## Multiple R-squared: 0.00327, Adjusted R-squared: -0.00832   
## F-statistic: 0.2821 on 1 and 86 DF, p-value: 0.5967

#### With *m = -10.61* and *p = 0.60*, there is a *negative*, *non-significant* correlation between *ECFU* and *no3*.

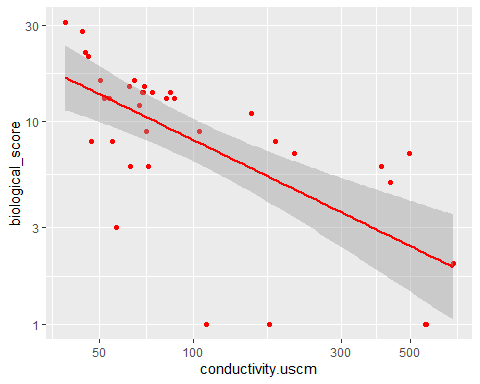
## NORO

### *Biological Indicator:*

#### Biological Vs Conductivity

N\_BS\_Con <- NORO %>%  
 ggplot(aes(x=conductivity.uscm, y=biological\_score)) +  
 geom\_point(color = "red") +  
 geom\_smooth(method=lm, color = "red") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(N\_BS\_Con)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for N\_BS\_Con.

N\_BS\_Con\_lm <- lm(biological\_score ~ conductivity.uscm, data=NORO)  
  
summary(N\_BS\_Con\_lm)

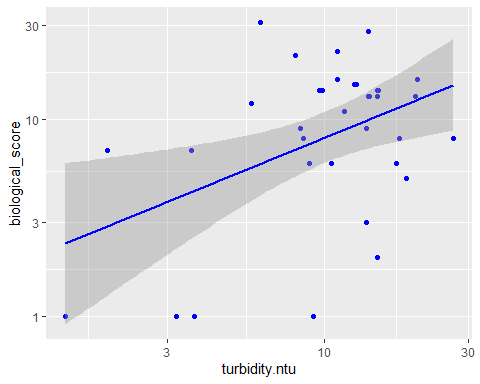
##   
## Call:  
## lm(formula = biological\_score ~ conductivity.uscm, data = NORO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -11.014 -2.907 0.296 1.978 17.353   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 14.541261 1.372711 10.593 3.75e-12 \*\*\*  
## conductivity.uscm -0.022931 0.005843 -3.924 0.000417 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.044 on 33 degrees of freedom  
## Multiple R-squared: 0.3182, Adjusted R-squared: 0.2975   
## F-statistic: 15.4 on 1 and 33 DF, p-value: 0.0004167

#### With *m = -0.023* and *p = 0.0004*, there is a *negative*, *significant* correlation between *biological score* and *conductivity*.

#### Biological Vs Turbidity

N\_BS\_Turb <- NORO %>%  
 ggplot(aes(x=turbidity.ntu, y=biological\_score)) +  
 geom\_point(color = "blue") +  
 geom\_smooth(method=lm, color = "blue") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(N\_BS\_Turb)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for N\_BS\_Turb.

N\_BS\_Turb\_lm <- lm(biological\_score ~ turbidity.ntu, data=NORO)  
  
summary(N\_BS\_Turb\_lm)

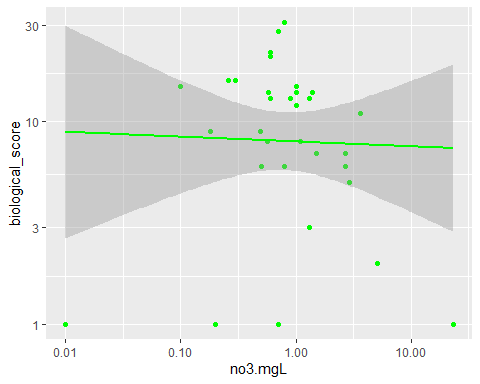
##   
## Call:  
## lm(formula = biological\_score ~ turbidity.ntu, data = NORO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -9.5326 -5.1174 0.0636 3.3833 20.9890   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 8.9848 2.8434 3.160 0.00337 \*\*  
## turbidity.ntu 0.1682 0.2204 0.763 0.45071   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 7.256 on 33 degrees of freedom  
## Multiple R-squared: 0.01735, Adjusted R-squared: -0.01243   
## F-statistic: 0.5826 on 1 and 33 DF, p-value: 0.4507

#### With *m = 0.17* and *p = 0.45*, there is a *positive*, *non-significant* correlation between *bilogical score* and *turbidity*.

#### Biological Vs Nitrate Concentration

N\_BS\_no3 <- NORO %>%  
 ggplot(aes(x=no3.mgL, y=biological\_score)) +  
 geom\_point(color = "green") +  
 geom\_smooth(method=lm, color = "green") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(N\_BS\_no3)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for N\_BS\_no3.

N\_BS\_no3\_lm <- lm(biological\_score ~ no3.mgL, data=NORO)  
  
summary(N\_BS\_no3\_lm)

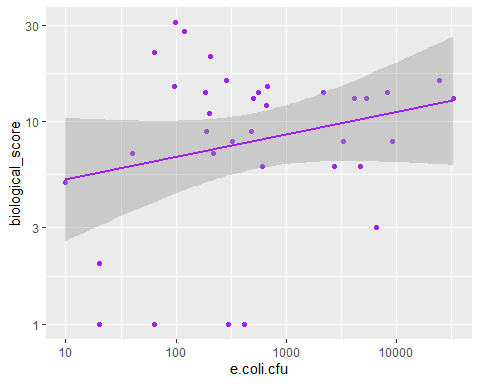
##   
## Call:  
## lm(formula = biological\_score ~ no3.mgL, data = NORO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -10.931 -4.254 1.091 2.736 19.514   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 11.9371 1.2970 9.203 1.24e-10 \*\*\*  
## no3.mgL -0.5632 0.3069 -1.835 0.0755 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.972 on 33 degrees of freedom  
## Multiple R-squared: 0.09262, Adjusted R-squared: 0.06512   
## F-statistic: 3.368 on 1 and 33 DF, p-value: 0.07548

#### With *m = -0.56* and *p = 0.08*, there is a *negative*, *non-significant* correlation between *biological score* and *no3*.

#### Biological Vs E. Coli CFU

N\_BS\_ECFU <- NORO %>%  
 ggplot(aes(x=e.coli.cfu, y=biological\_score)) +  
 geom\_point(color = "purple") +  
 geom\_smooth(method=lm, color = "purple") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(N\_BS\_ECFU)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for N\_BS\_ECFU.

N\_BS\_ECFU\_lm <- lm(biological\_score ~ e.coli.cfu, data=NORO)  
  
summary(N\_BS\_ECFU\_lm)

##   
## Call:  
## lm(formula = biological\_score ~ e.coli.cfu, data = NORO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -9.7460 -4.8366 -0.0854 3.2572 20.2770   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 1.072e+01 1.360e+00 7.880 4.39e-09 \*\*\*  
## e.coli.cfu 7.274e-05 1.830e-04 0.397 0.694   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 7.302 on 33 degrees of freedom  
## Multiple R-squared: 0.004765, Adjusted R-squared: -0.02539   
## F-statistic: 0.158 on 1 and 33 DF, p-value: 0.6936

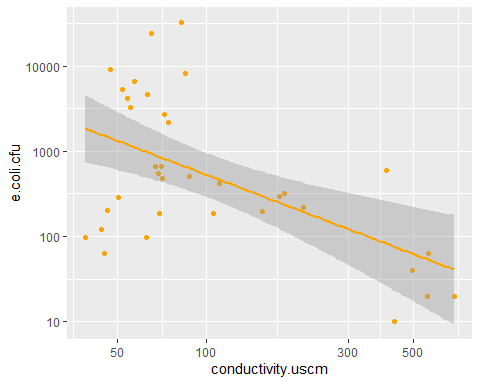
#### With *m = 7.274e-05* and *p = 0.69*, there is not relationship between *Bbiological score* and *ECFU*.

### *E. Coli*

#### E. Coli Vs Conductivity

N\_ECFU\_Con <- NORO %>%  
 ggplot(aes(x=conductivity.uscm, y=e.coli.cfu)) +  
 geom\_point(color = "orange") +  
 geom\_smooth(method=lm, color = "orange") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(N\_ECFU\_Con)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for N\_ECFU\_Con.

N\_ECFU\_Con\_lm <- lm(e.coli.cfu ~ conductivity.uscm, data=NORO)  
  
summary(N\_ECFU\_Con\_lm)

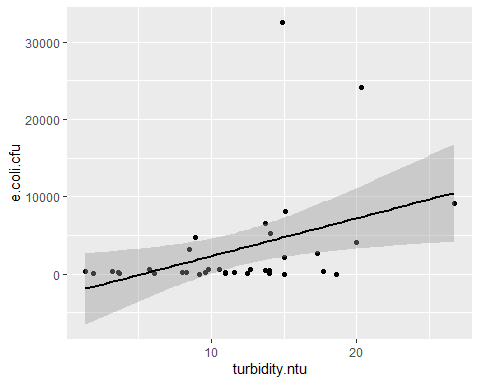
##   
## Call:  
## lm(formula = e.coli.cfu ~ conductivity.uscm, data = NORO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -4040.6 -3353.7 -2425.3 382.9 28807.5   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 4475.297 1537.659 2.910 0.00642 \*\*  
## conductivity.uscm -8.632 6.545 -1.319 0.19630   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6770 on 33 degrees of freedom  
## Multiple R-squared: 0.05007, Adjusted R-squared: 0.02128   
## F-statistic: 1.739 on 1 and 33 DF, p-value: 0.1963

#### With *m = -8.632* and *p = 0.20*, there is a *negative*, *non-significant* correlation between *ECFU* and *conductivity*.

#### E. Coli Vs Turbidity

N\_ECFU\_Turb <- NORO %>%  
 ggplot(aes(x=turbidity.ntu, y=e.coli.cfu)) +  
 geom\_point(color = "black") +  
 geom\_smooth(method=lm, color = "black")  
  
  
print(N\_ECFU\_Turb)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for N\_ECFU\_Turb.

N\_ECFU\_Turb\_lm <- lm(e.coli.cfu ~ turbidity.ntu, data=NORO)  
  
summary(N\_ECFU\_Turb\_lm)

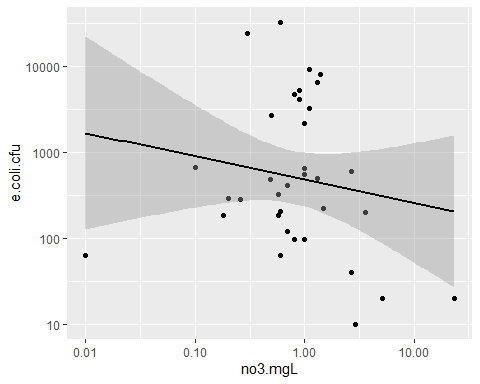
##   
## Call:  
## lm(formula = e.coli.cfu ~ turbidity.ntu, data = NORO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -6522 -3038 -1665 1171 27856   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -2582 2490 -1.037 0.307   
## turbidity.ntu 490 193 2.539 0.016 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6353 on 33 degrees of freedom  
## Multiple R-squared: 0.1634, Adjusted R-squared: 0.138   
## F-statistic: 6.444 on 1 and 33 DF, p-value: 0.01603

#### With *m = 490* and *p = 0.02*, there is a *positive*, *significant* correlation between *ECFU* and *Turbidity*.

#### E. Coli Vs Nitrate Concentration

N\_ECFU\_no3 <- NORO %>%  
 ggplot(aes(x=no3.mgL, y=e.coli.cfu)) +  
 geom\_point(color = "black") +  
 geom\_smooth(method=lm, color = "black") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(N\_ECFU\_no3)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for N\_ECFU\_no3.

N\_ECFU\_no3\_lm <- lm(e.coli.cfu ~ no3.mgL, data=NORO)  
  
summary(N\_ECFU\_no3\_lm)

##   
## Call:  
## lm(formula = e.coli.cfu ~ no3.mgL, data = NORO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -3431.7 -3157.8 -2728.8 399.7 29206.0   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 3496.9 1282.6 2.726 0.0102 \*  
## no3.mgL -213.1 303.5 -0.702 0.4875   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6895 on 33 degrees of freedom  
## Multiple R-squared: 0.01472, Adjusted R-squared: -0.01514   
## F-statistic: 0.493 on 1 and 33 DF, p-value: 0.4875

#### With *m = -213.1* and *p = 0.49*, there is a *negative*, *non-significant* correlation between *ECFU* and *no3*.

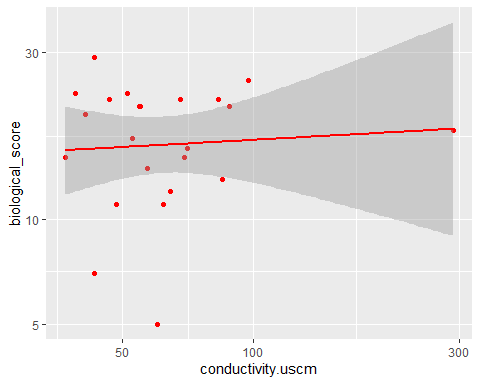
## BICO

### *Biological Indicator:*

#### Biological Vs Conductivity

B\_BS\_Con <- BICO %>%  
 ggplot(aes(x=conductivity.uscm, y=biological\_score)) +  
 geom\_point(color = "red") +  
 geom\_smooth(method=lm, color = "red") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(B\_BS\_Con)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for B\_BS\_Con.

B\_BS\_Con\_lm <- lm(biological\_score ~ conductivity.uscm, data=BICO)  
  
summary(B\_BS\_Con\_lm)

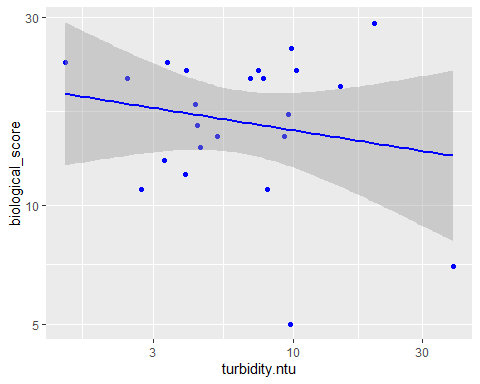
##   
## Call:  
## lm(formula = biological\_score ~ conductivity.uscm, data = BICO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -12.4765 -4.0273 -0.4428 4.4520 11.6024   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 17.199651 2.192576 7.844 1.13e-07 \*\*\*  
## conductivity.uscm 0.004614 0.025592 0.180 0.859   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.097 on 21 degrees of freedom  
## Multiple R-squared: 0.001546, Adjusted R-squared: -0.046   
## F-statistic: 0.03251 on 1 and 21 DF, p-value: 0.8586

#### With *m = 0.0046* and *p = 0.86*, there is a *positive*, *non-significant* correlation between *biological score* and *conductivity*.

#### Biological Vs Turbidity

B\_BS\_Turb <- BICO %>%  
 ggplot(aes(x=turbidity.ntu, y=biological\_score)) +  
 geom\_point(color = "blue") +  
 geom\_smooth(method=lm, color = "blue") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(B\_BS\_Turb)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for B\_BS\_Turb.

B\_BS\_Turb\_lm <- lm(biological\_score ~ turbidity.ntu, data=BICO)  
  
summary(B\_BS\_Turb\_lm)

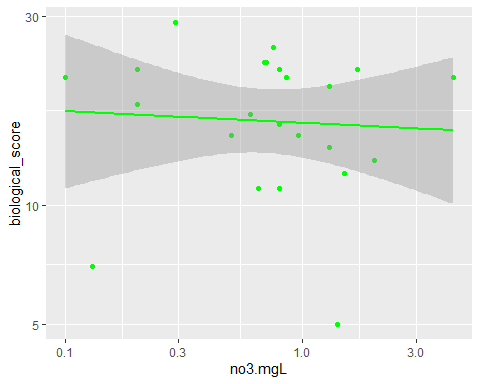
##   
## Call:  
## lm(formula = biological\_score ~ turbidity.ntu, data = BICO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -12.3528 -4.5901 -0.0402 4.1399 12.9672   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 18.5884 1.8365 10.122 1.57e-09 \*\*\*  
## turbidity.ntu -0.1278 0.1608 -0.795 0.436   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.012 on 21 degrees of freedom  
## Multiple R-squared: 0.0292, Adjusted R-squared: -0.01703   
## F-statistic: 0.6316 on 1 and 21 DF, p-value: 0.4357

#### With *m = -0.13* and *p = 0.44*, there is a *negative*, *non-significant* correlation between *biological score* and *turbidity*.

#### Biological Vs Nitrate Concentration

B\_BS\_no3 <- BICO %>%  
 ggplot(aes(x=no3.mgL, y=biological\_score)) +  
 geom\_point(color = "green") +  
 geom\_smooth(method=lm, color = "green") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(B\_BS\_no3)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for B\_BS\_no3.

B\_BS\_no3\_lm <- lm(biological\_score ~ no3.mgL, data=BICO)  
  
summary(B\_BS\_no3\_lm)

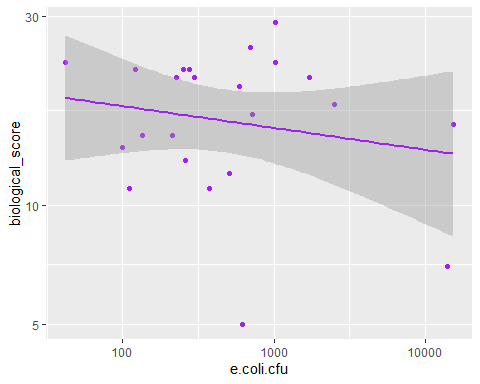
##   
## Call:  
## lm(formula = biological\_score ~ no3.mgL, data = BICO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -12.3950 -3.8197 0.2433 4.4531 11.2704   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 17.8170 1.9172 9.293 6.88e-09 \*\*\*  
## no3.mgL -0.3014 1.4653 -0.206 0.839   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.095 on 21 degrees of freedom  
## Multiple R-squared: 0.00201, Adjusted R-squared: -0.04551   
## F-statistic: 0.0423 on 1 and 21 DF, p-value: 0.839

#### With *m = -0.30* and *p = 0.84*, there is a *negative*, *non-significant* correlation between *biological score* and *no3*.

#### Biological Vs E. Coli CFU

B\_BS\_ECFU <- BICO %>%  
 ggplot(aes(x=e.coli.cfu, y=biological\_score)) +  
 geom\_point(color = "purple") +  
 geom\_smooth(method=lm, color = "purple") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(B\_BS\_ECFU)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for B\_BS\_ECFU.

B\_BS\_ECFU\_lm <- lm(biological\_score ~ e.coli.cfu, data=BICO)  
  
summary(B\_BS\_ECFU\_lm)

##   
## Call:  
## lm(formula = biological\_score ~ e.coli.cfu, data = BICO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -12.999 -4.678 1.989 3.855 11.162   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 18.2514270 1.3359266 13.662 6.43e-12 \*\*\*  
## e.coli.cfu -0.0004064 0.0003022 -1.345 0.193   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 5.854 on 21 degrees of freedom  
## Multiple R-squared: 0.07927, Adjusted R-squared: 0.03543   
## F-statistic: 1.808 on 1 and 21 DF, p-value: 0.1931

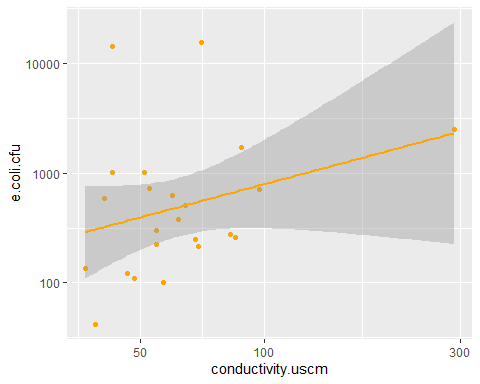
#### With *m = -0.00041* and *p = 0.19*, there is no relationship between *biological score* and *ECFU*.

### *E. Coli*

#### E. Coli Vs Conductivity

B\_ECFU\_Con <- BICO %>%  
 ggplot(aes(x=conductivity.uscm, y=e.coli.cfu)) +  
 geom\_point(color = "orange") +  
 geom\_smooth(method=lm, color = "orange") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(B\_ECFU\_Con)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for B\_ECFU\_Con.

B\_ECFU\_Con\_lm <- lm(e.coli.cfu ~ conductivity.uscm, data=BICO)  
  
summary(B\_ECFU\_Con\_lm)

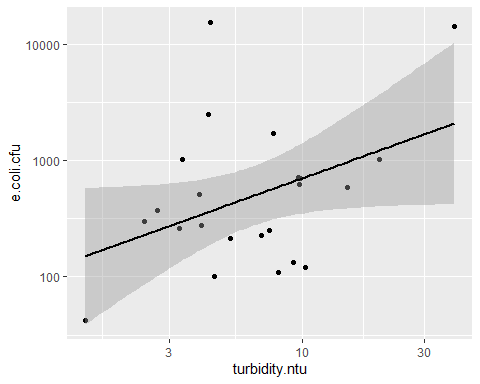
##   
## Call:  
## lm(formula = e.coli.cfu ~ conductivity.uscm, data = BICO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -1683.1 -1575.6 -1402.7 -885.4 13553.4   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 1636.516 1519.584 1.077 0.294  
## conductivity.uscm 2.278 17.737 0.128 0.899  
##   
## Residual standard error: 4225 on 21 degrees of freedom  
## Multiple R-squared: 0.0007846, Adjusted R-squared: -0.0468   
## F-statistic: 0.01649 on 1 and 21 DF, p-value: 0.899

#### With *m = 2.28* and *p = 0.90*, there is a *positive*, *non-significant* correlation between *ECFU* and *conductivity*.

#### E. Coli Vs Turbidity

B\_ECFU\_Turb <- BICO %>%  
 ggplot(aes(x=turbidity.ntu, y=e.coli.cfu)) +  
 geom\_point(color = "black") +  
 geom\_smooth(method=lm, color = "black") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(B\_ECFU\_Turb)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for B\_ECFU\_Turb.

B\_ECFU\_Turb\_lm <- lm(e.coli.cfu ~ turbidity.ntu, data=BICO)  
  
summary(B\_ECFU\_Turb\_lm)

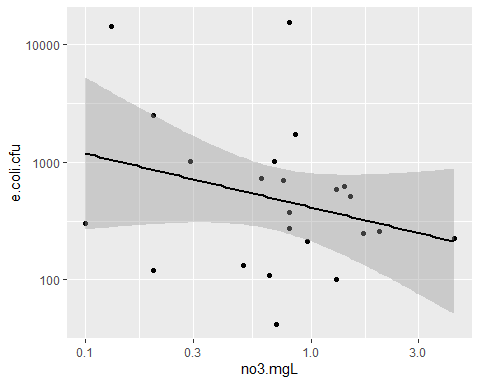
##   
## Call:  
## lm(formula = e.coli.cfu ~ turbidity.ntu, data = BICO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -3825.2 -1496.7 -689.4 58.8 14594.6   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -387.2 1114.8 -0.347 0.732   
## turbidity.ntu 261.5 97.6 2.679 0.014 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 3649 on 21 degrees of freedom  
## Multiple R-squared: 0.2547, Adjusted R-squared: 0.2192   
## F-statistic: 7.177 on 1 and 21 DF, p-value: 0.01405

#### With *m = 261.5* and *p = 0.01*, there is a *positive*, *significant* correlation between *ECFU* and *turbidity*.

#### E. Coli Vs Nitrate Concentration

B\_ECFU\_no3 <- BICO %>%  
 ggplot(aes(x=no3.mgL, y=e.coli.cfu)) +  
 geom\_point(color = "black") +  
 geom\_smooth(method=lm, color = "black") +  
 scale\_x\_continuous(trans = 'log10') +  
 scale\_y\_continuous(trans = 'log10')  
  
  
print(B\_ECFU\_no3)

## `geom\_smooth()` using formula 'y ~ x'



#### Now run linear regression for B\_ECFU\_no3.

B\_ECFU\_no3\_lm <- lm(e.coli.cfu ~ no3.mgL, data=BICO)  
  
summary(B\_ECFU\_no3\_lm)

##   
## Call:  
## lm(formula = e.coli.cfu ~ no3.mgL, data = BICO)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -2441.3 -1649.4 -1318.3 -646.8 13377.9   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 2759.0 1299.5 2.123 0.0458 \*  
## no3.mgL -983.6 993.2 -0.990 0.3333   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 4132 on 21 degrees of freedom  
## Multiple R-squared: 0.04462, Adjusted R-squared: -0.0008751   
## F-statistic: 0.9808 on 1 and 21 DF, p-value: 0.3333

#### With *m = -983.6* and *p = 0.33*, there is a *negative*, *non-significant* correlation between *ECFU* and *no3*.

### In summary, exploration of correlation of stream health indicators showed that most interactions were non-significant. However, it is to be noted that the ECFU and turbidity interaction was significantly positive. In further analysis, this may serve as a check to show that correlative analyses are robust enough with data provided. In aquatic microbiology, the positive relationship between ECFU growth and turbidity is generally accepted because the more bacteria that grow in the water column, the cloudier it will be.

### Additionally, there was a weird significant correlation between biological score and conductivity at the NORO site only. The relationship is negative, meaning that biological score decreased as conductivity increases, which make sense. However, NORO was the only site to show this interaction as significant.