

Ammonia Model

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Setup

```
#load packages  
library(here)
```

```
## here() starts at /Users/summerheshong/Stats_Group_Project
```

```
library(tidyverse)
```

```
## -- 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 (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(nlme)
```

```
##  
## Attaching package: 'nlme'  
##  
## The following object is masked from 'package:dplyr':  
##  
## collapse
```

```
wetlands <- read.csv(here('Data/Processed/Combined_Data_NArm.csv'))
```

Step 1 - Research Question: What predicts ammonium levels in wetlands

Step 2 - Examine Data

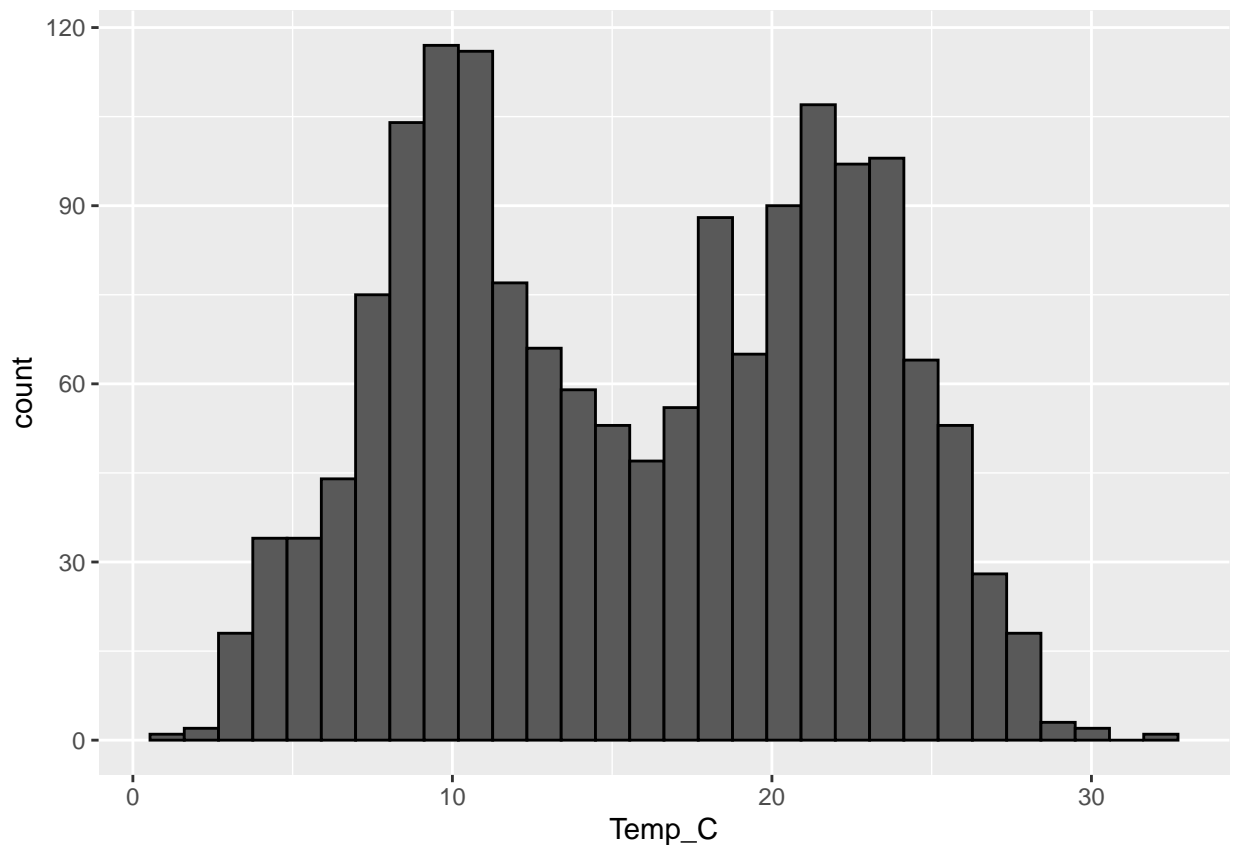
Display raw counts and distributions of data

```
#remove outliers using Nicole's code
wetlands <- wetlands %>%
  mutate(across(where(is.numeric),
    ~ ifelse(abs
      (., - mean
      (., na.rm = TRUE))) > 3 * sd
      (., na.rm = TRUE), NA, .)))

#create histograms
ggplot(wetlands, aes(x = Temp_C)) +
  geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

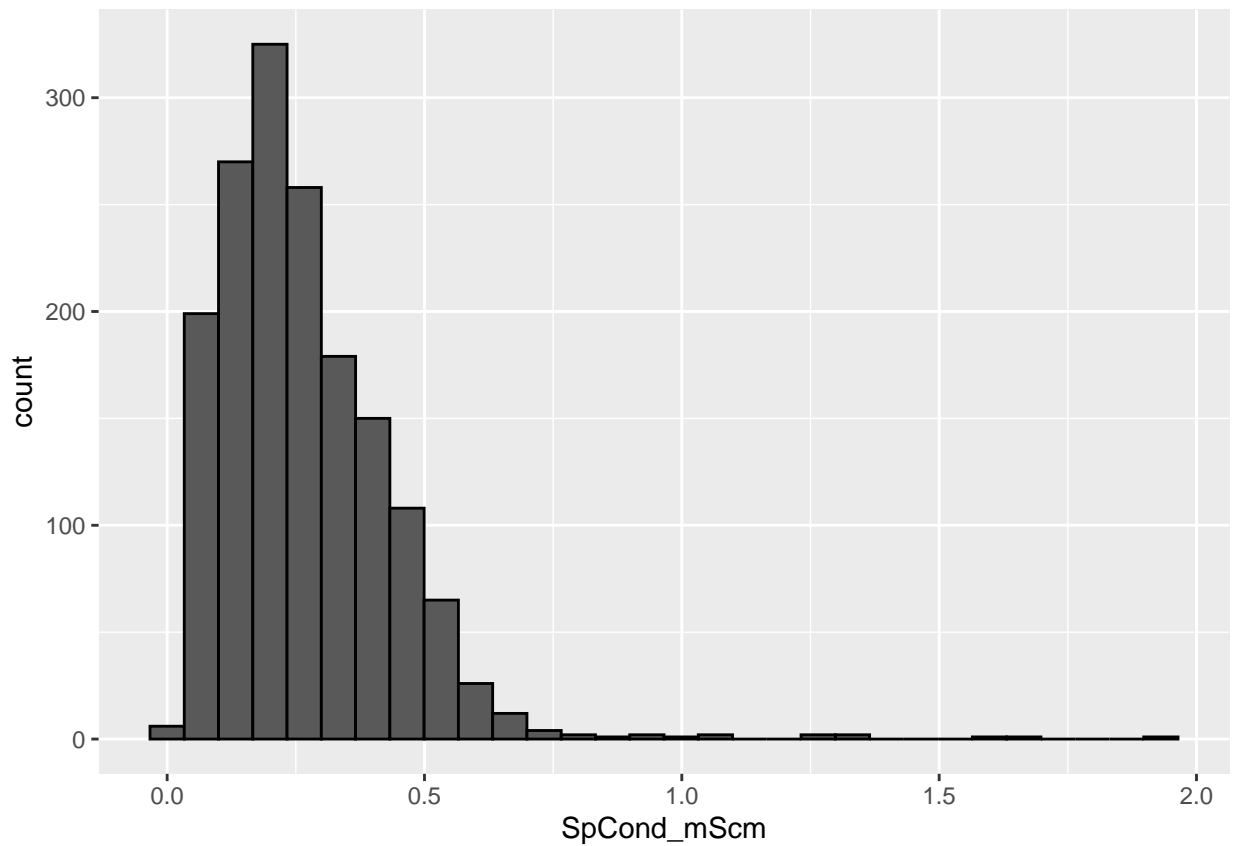
```
## Warning: Removed 1 row containing non-finite outside the scale range
## ('stat_bin()').
```



```
ggplot(wetlands, aes(x = SpCond_mScm)) +  
geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

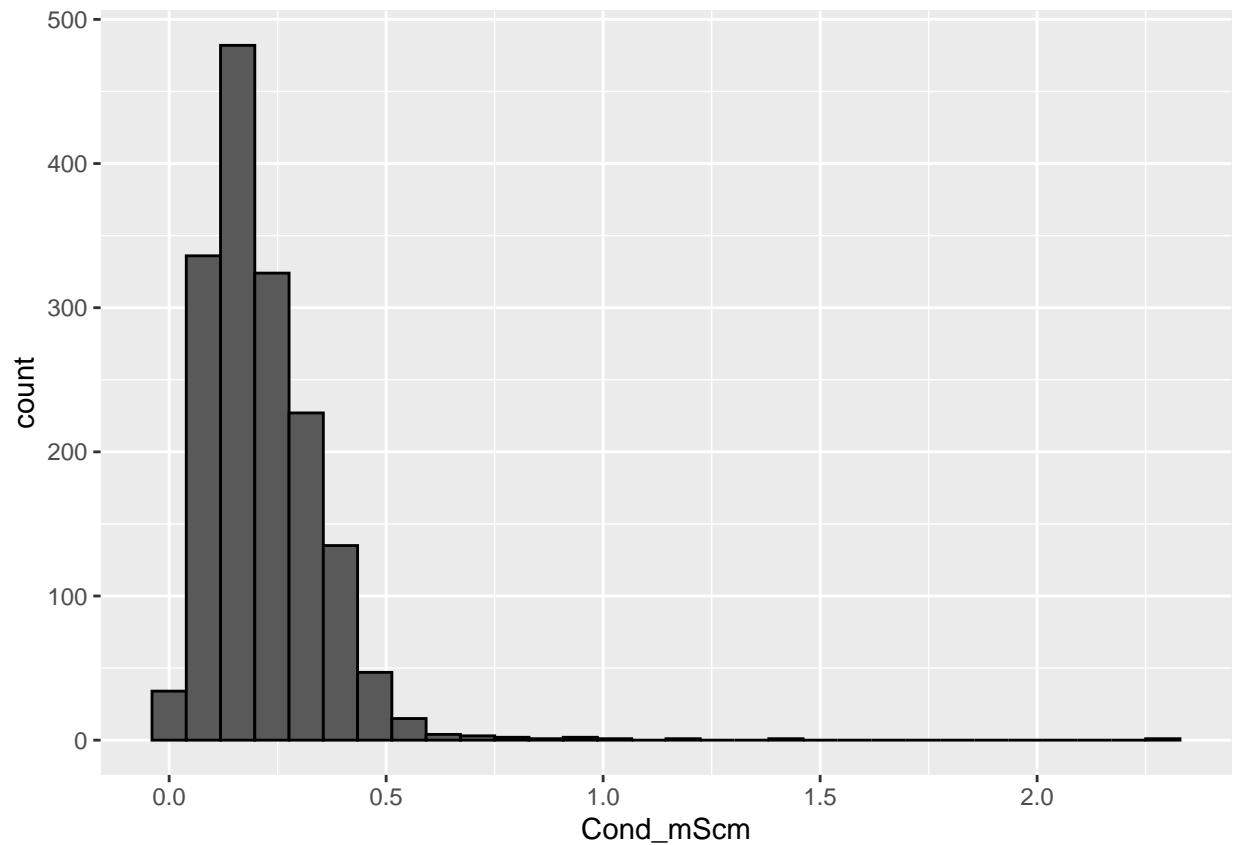
```
## Warning: Removed 1 row containing non-finite outside the scale range  
## ('stat_bin()').
```



```
ggplot(wetlands, aes(x = Cond_mScm)) +  
geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

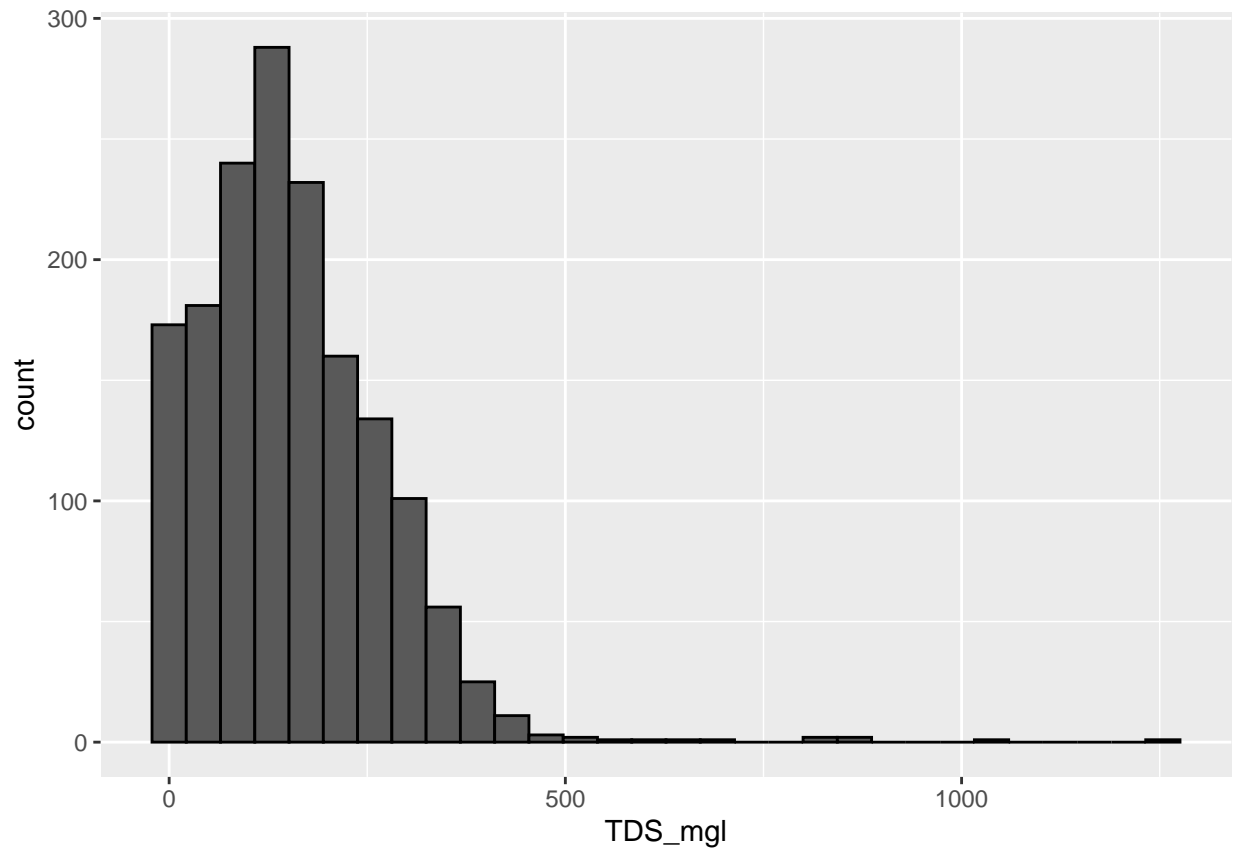
```
## Warning: Removed 2 rows containing non-finite outside the scale range  
## ('stat_bin()').
```



```
ggplot(wetlands, aes(x = TDS_mgl)) +  
geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

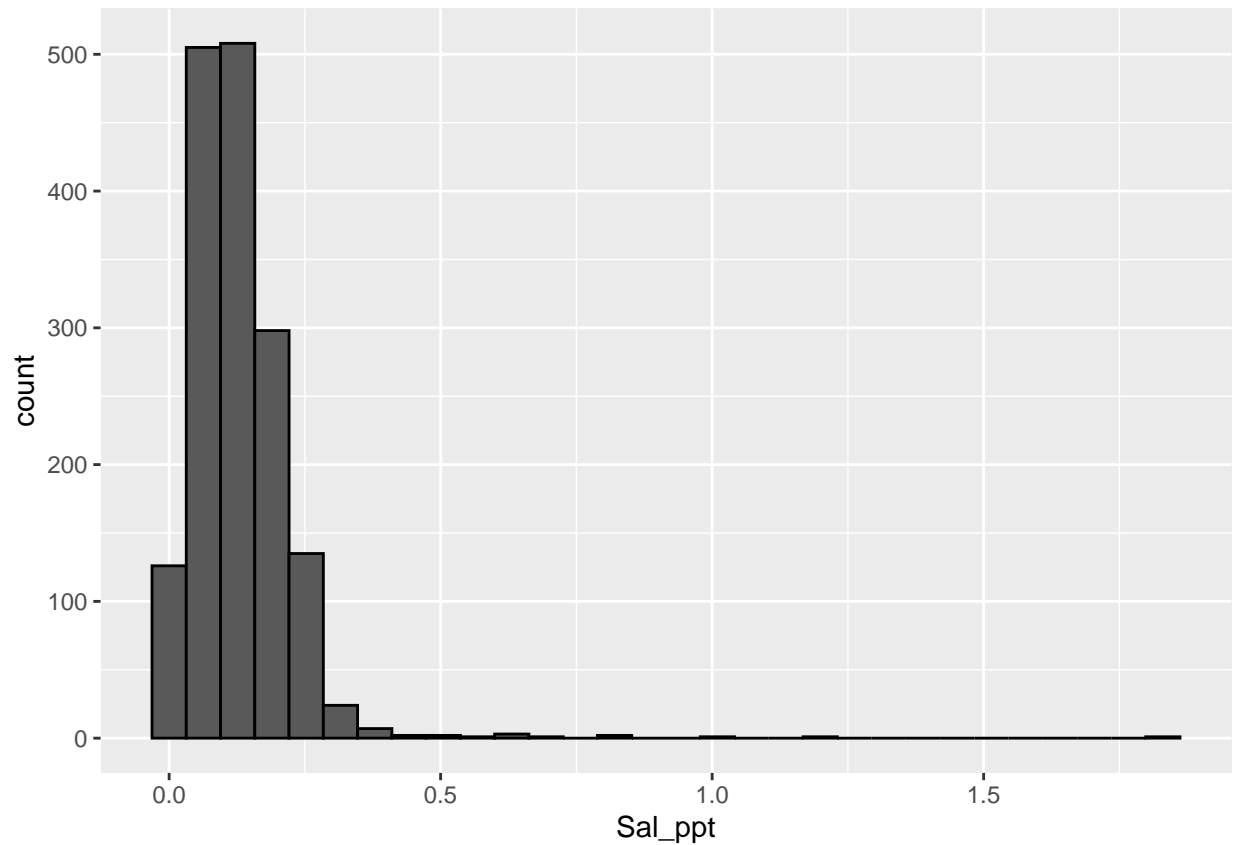
```
## Warning: Removed 2 rows containing non-finite outside the scale range  
## ('stat_bin()').
```



```
ggplot(wetlands, aes(x = Sal_ppt)) +  
geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

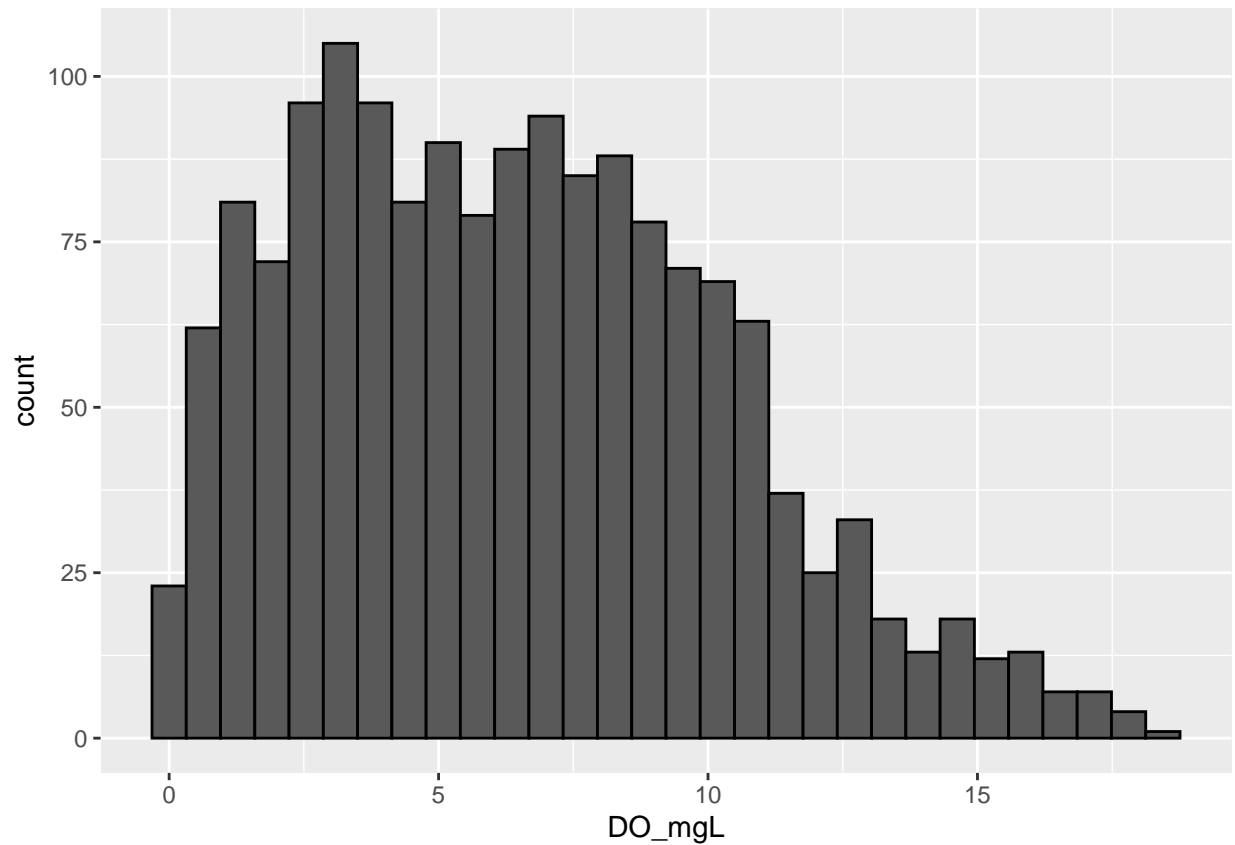
```
## Warning: Removed 1 row containing non-finite outside the scale range  
## ('stat_bin()').
```



```
ggplot(wetlands, aes(x = DO_mgL)) +  
geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

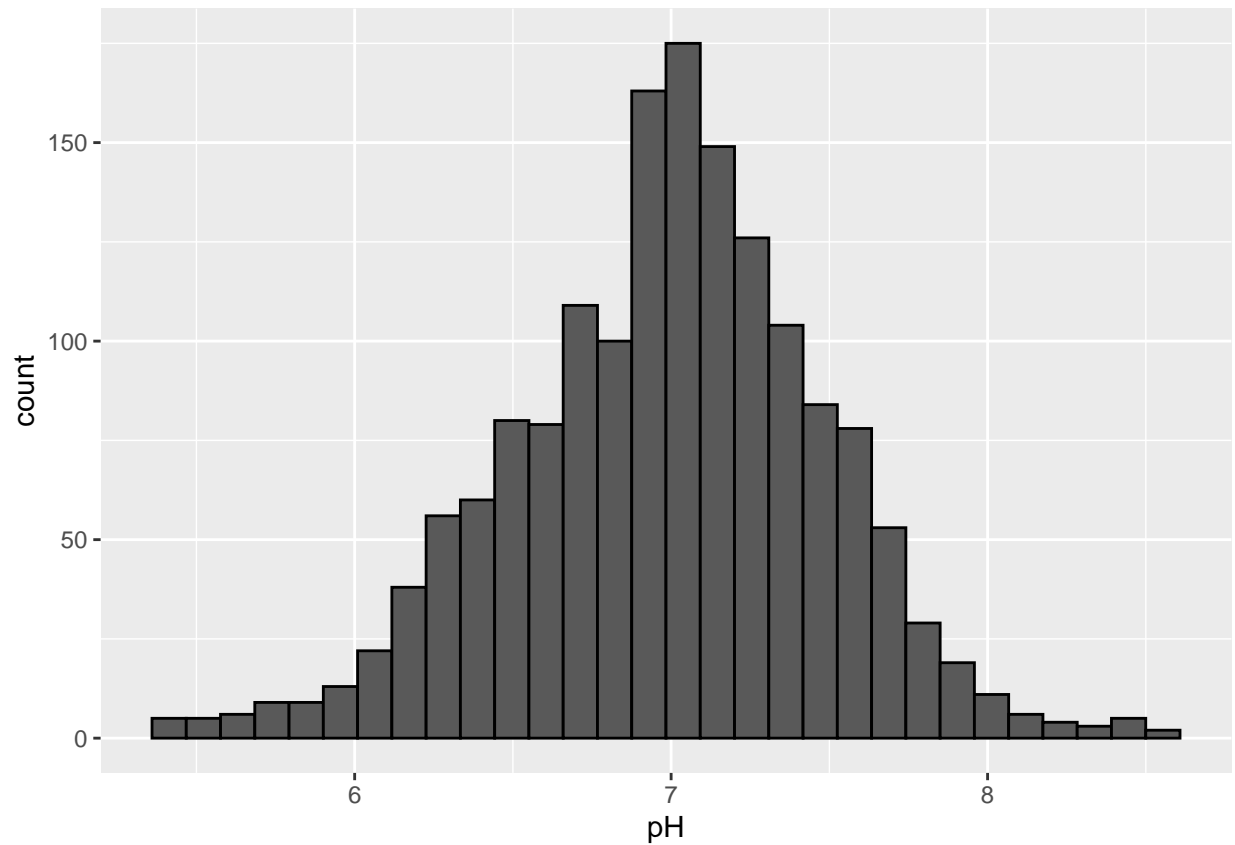
```
## Warning: Removed 8 rows containing non-finite outside the scale range  
## ('stat_bin()').
```



```
ggplot(wetlands, aes(x = pH)) +  
geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

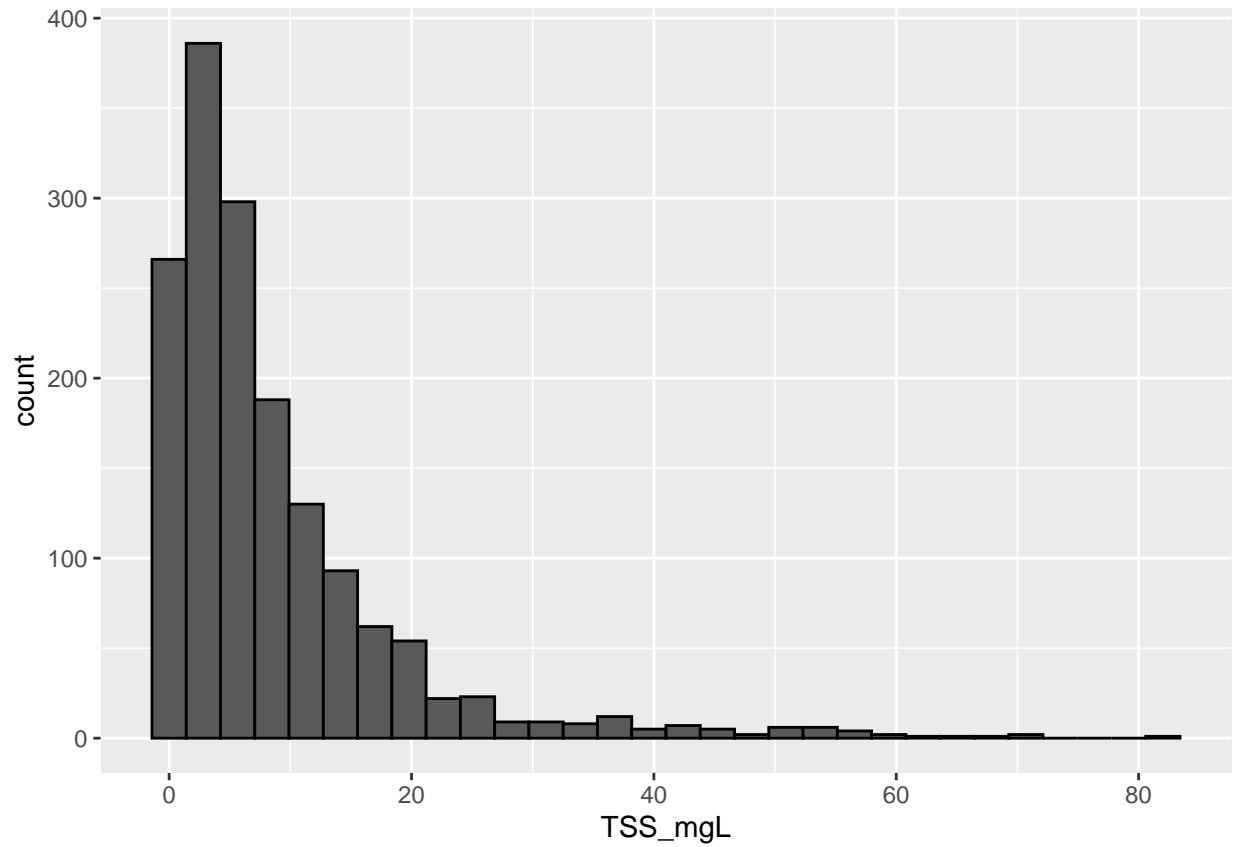
```
## Warning: Removed 16 rows containing non-finite outside the scale range  
## ('stat_bin()').
```



```
ggplot(wetlands, aes(x = TSS_mgL)) +  
geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

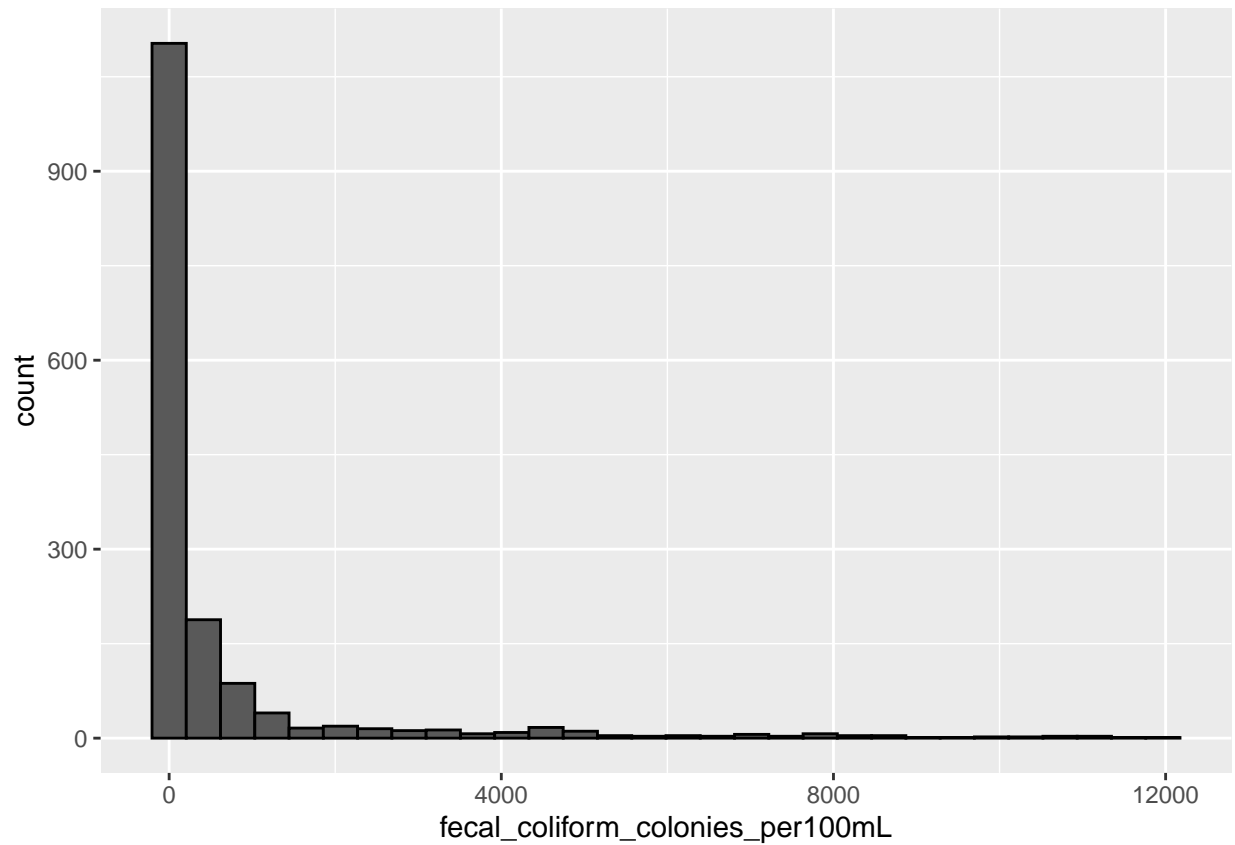
```
## Warning: Removed 15 rows containing non-finite outside the scale range  
## ('stat_bin()').
```

```
ggplot(wetlands, aes(x = fecal_coliform_colonies_per100mL)) +  
geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

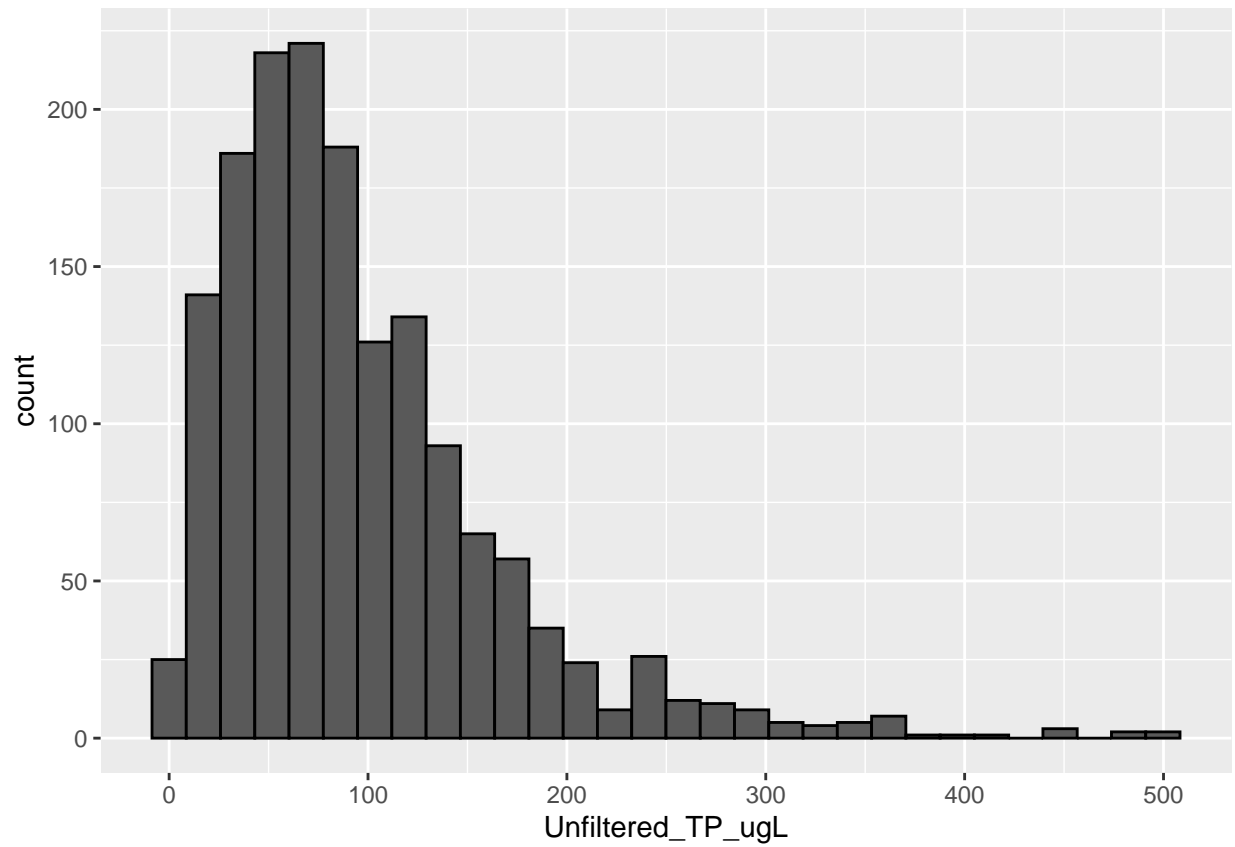
```
## Warning: Removed 29 rows containing non-finite outside the scale range  
## ('stat_bin()').
```



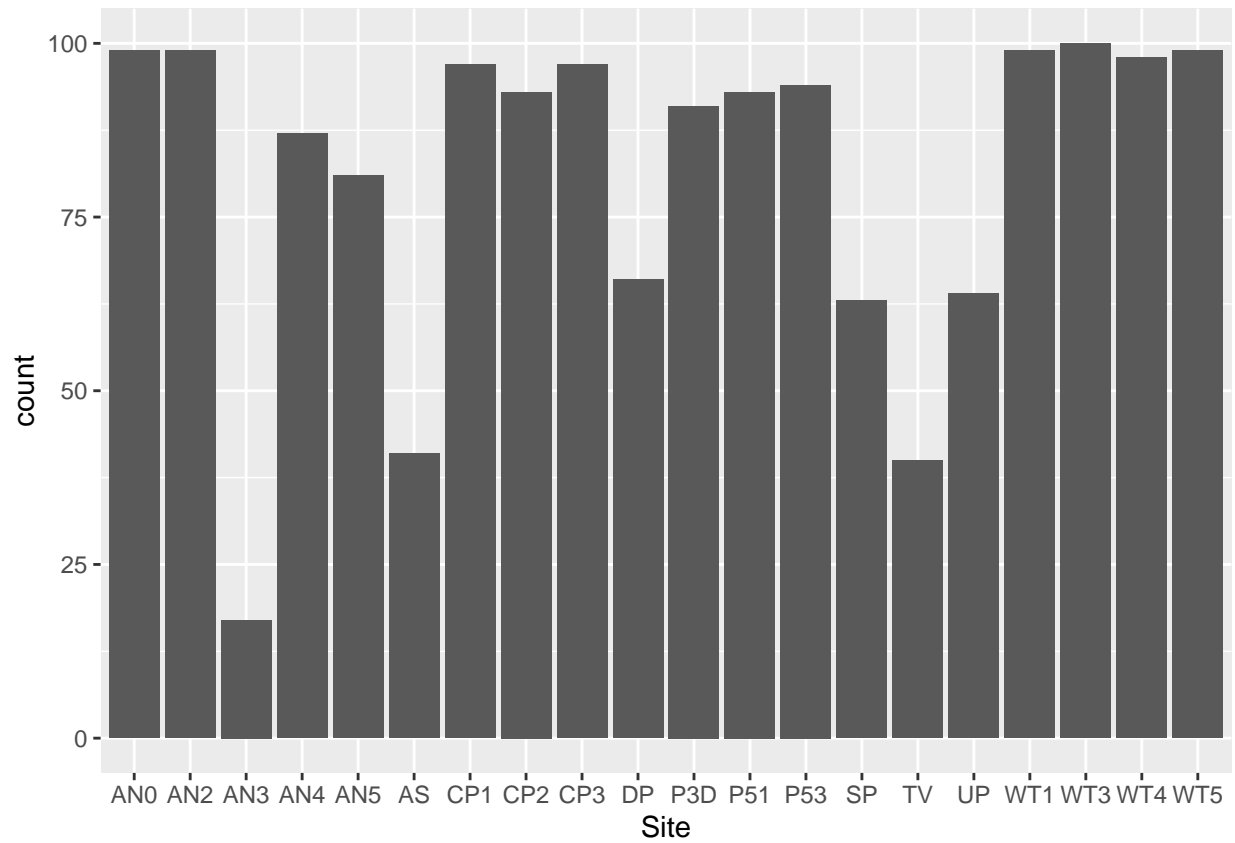
```
ggplot(wetlands, aes(x = Unfiltered_TP_ugL)) +  
geom_histogram(color = 'black')
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

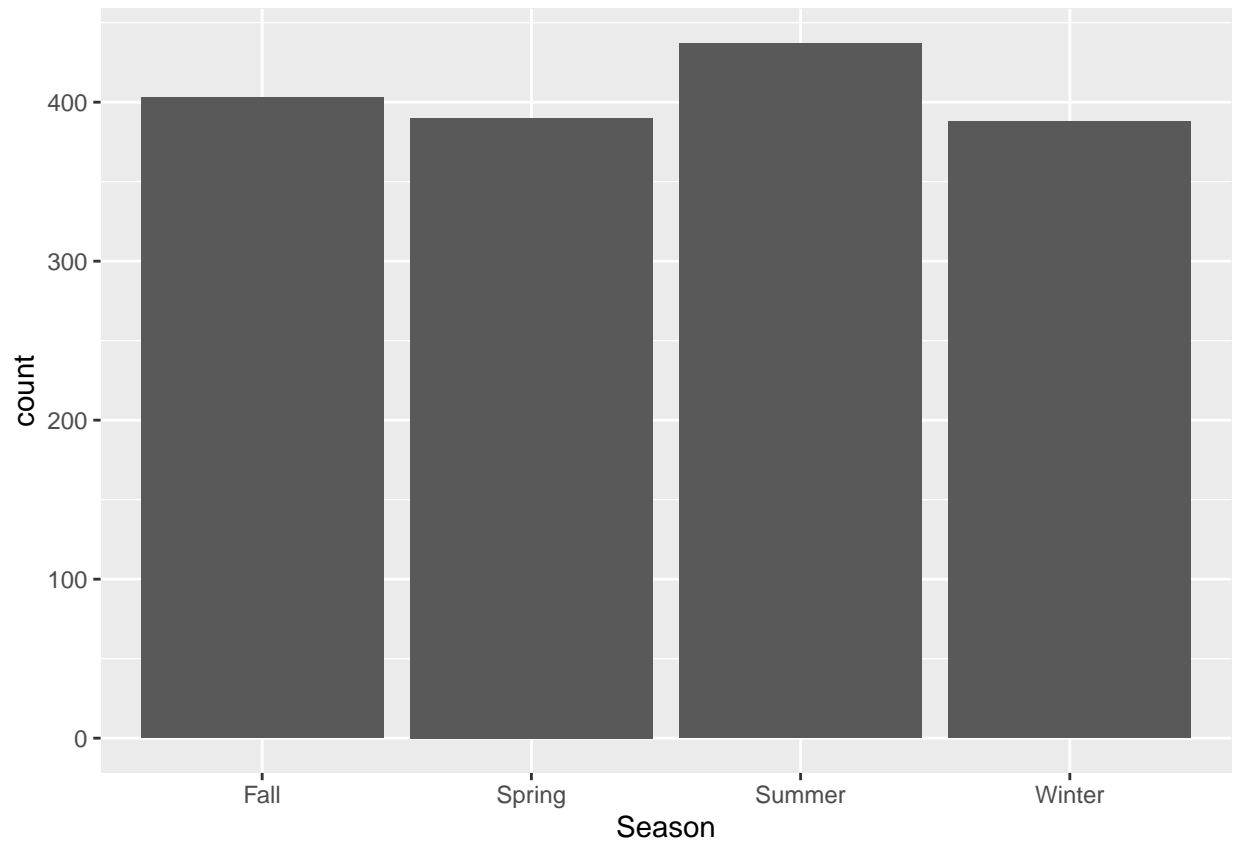
```
## Warning: Removed 7 rows containing non-finite outside the scale range  
## ('stat_bin()').
```



```
ggplot(wetlands, aes(x = Site)) +  
geom_bar()
```



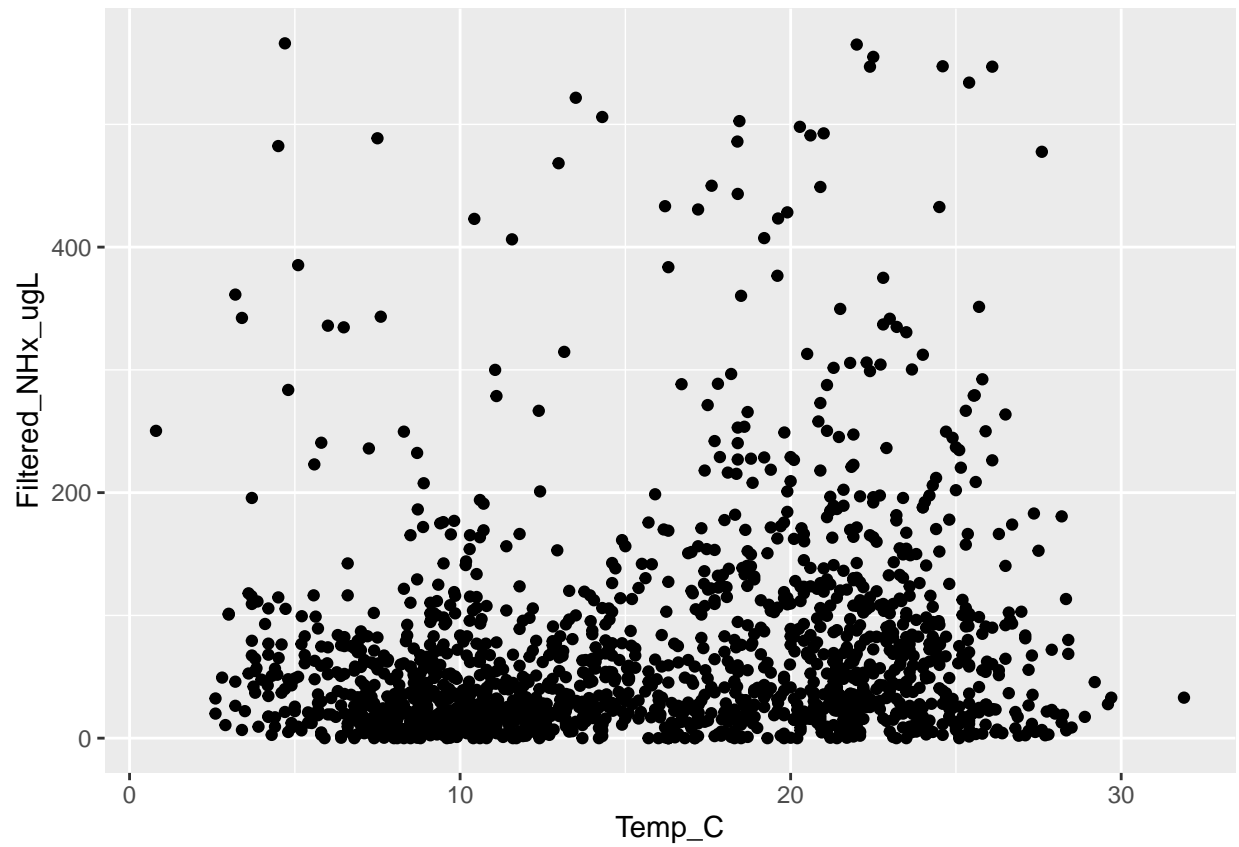
```
ggplot(wetlands, aes(x = Season)) +  
geom_bar()
```



Display relationships between predictor variables and outcome variable

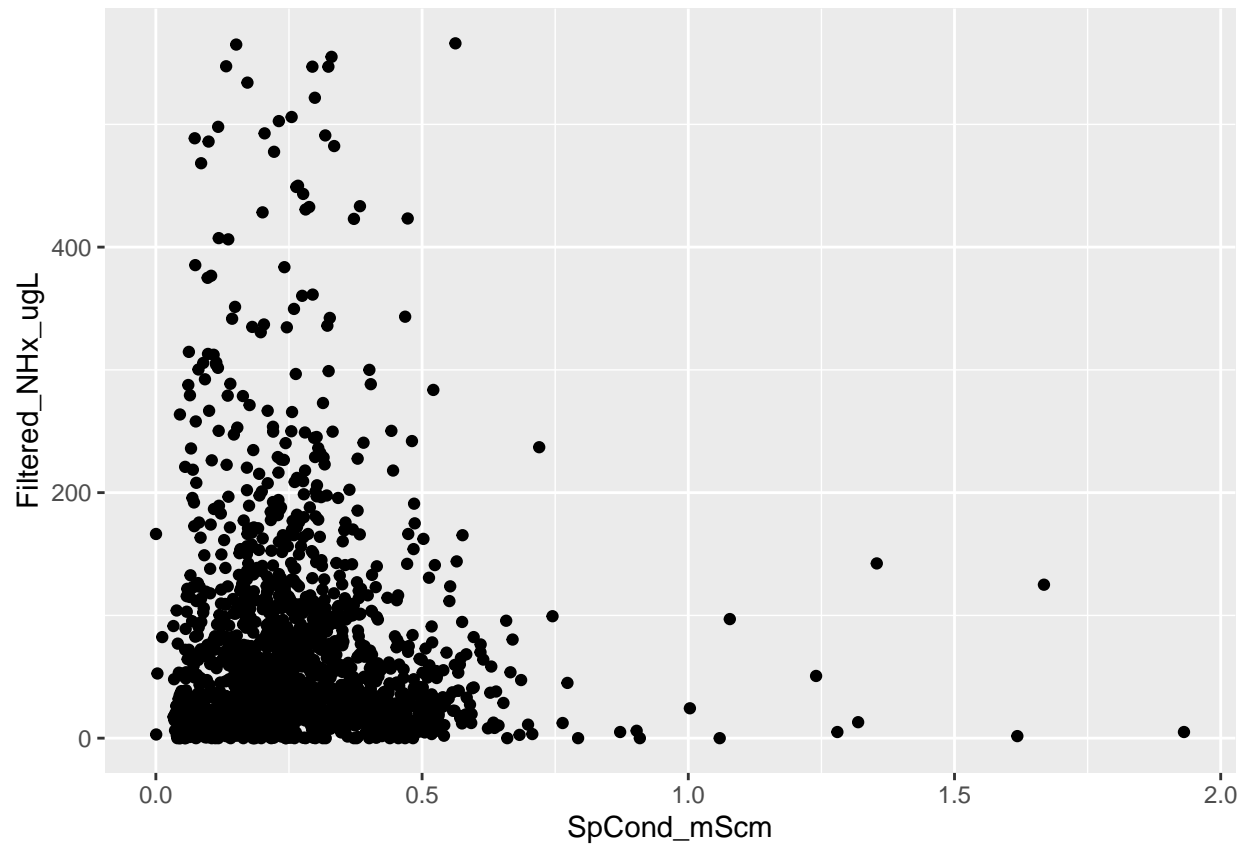
```
#create scatterplots  
ggplot(wetlands, aes(x = Temp_C, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 24 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



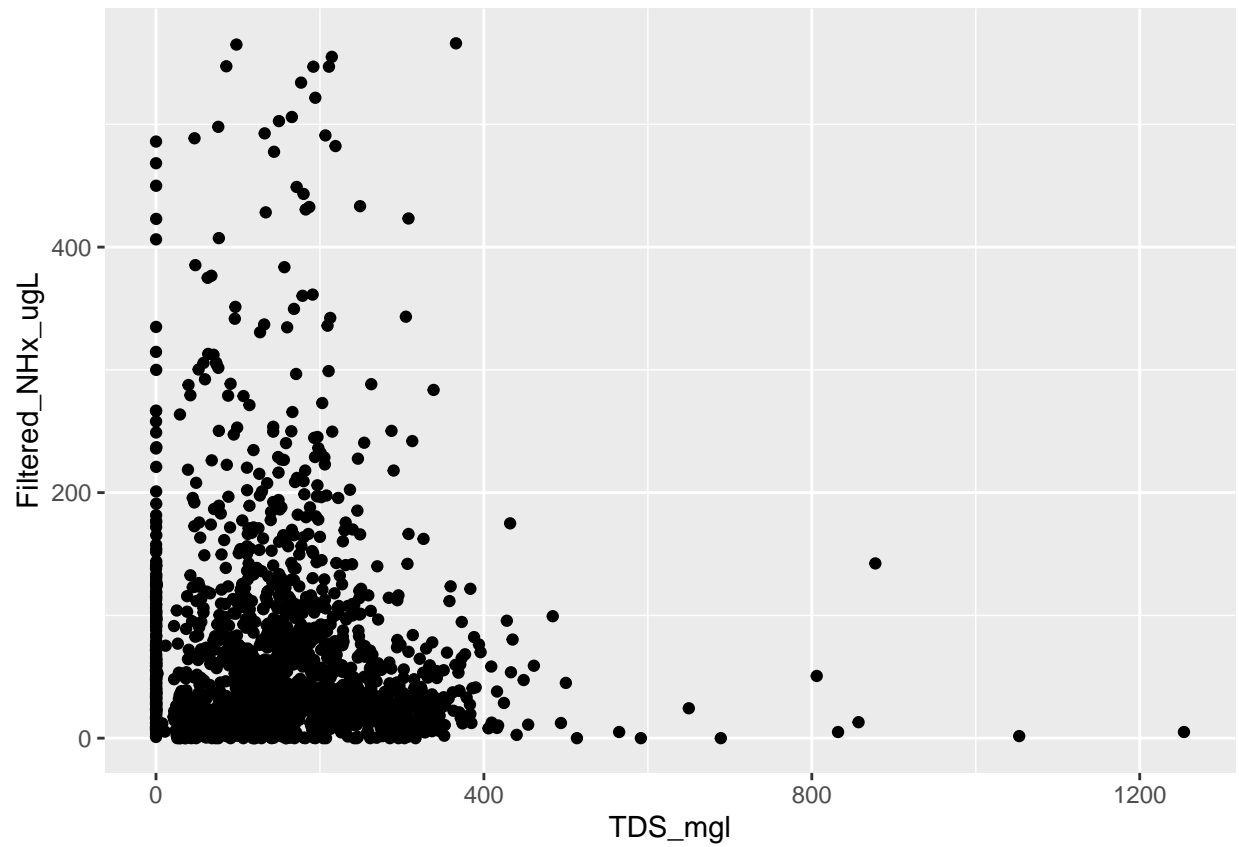
```
ggplot(wetlands, aes(x = SpCond_mScm, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 23 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



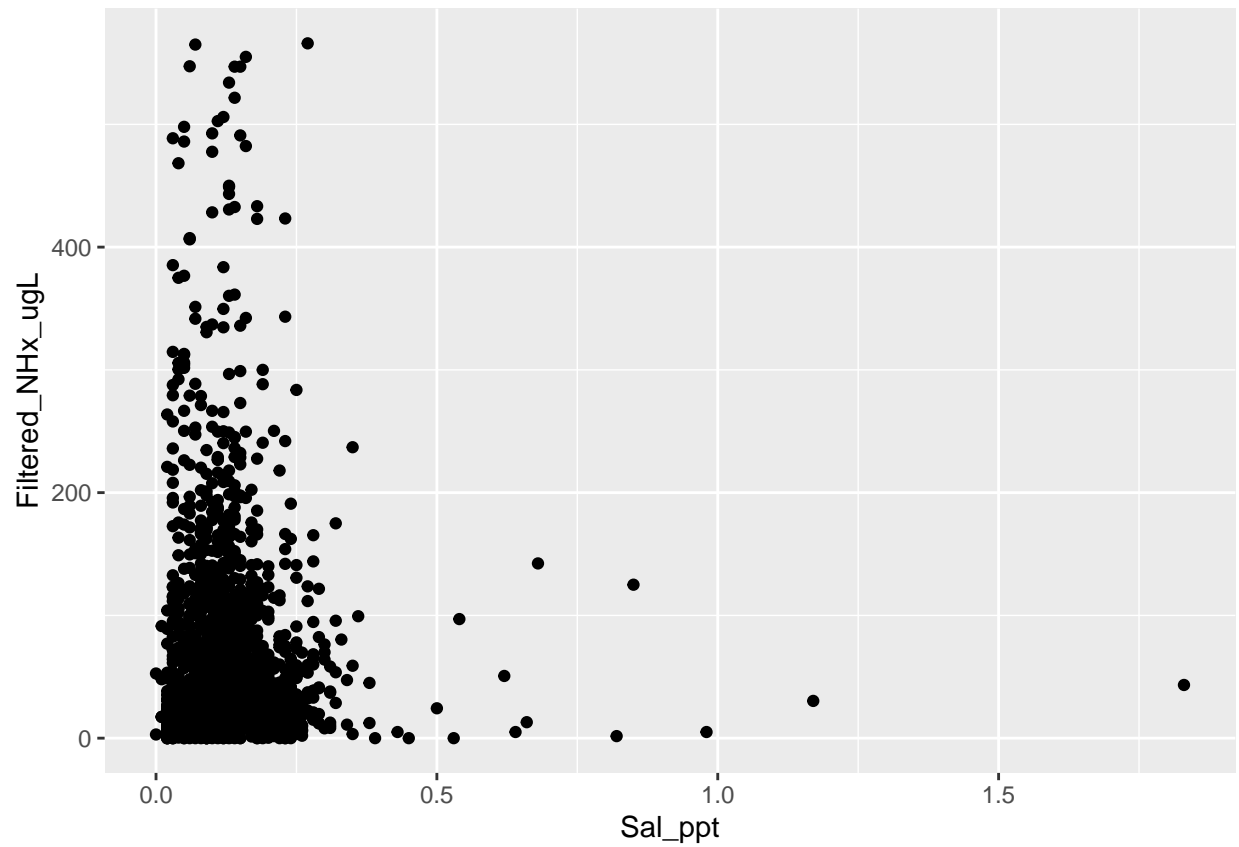
```
ggplot(wetlands, aes(x = TDS_mgl, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 24 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



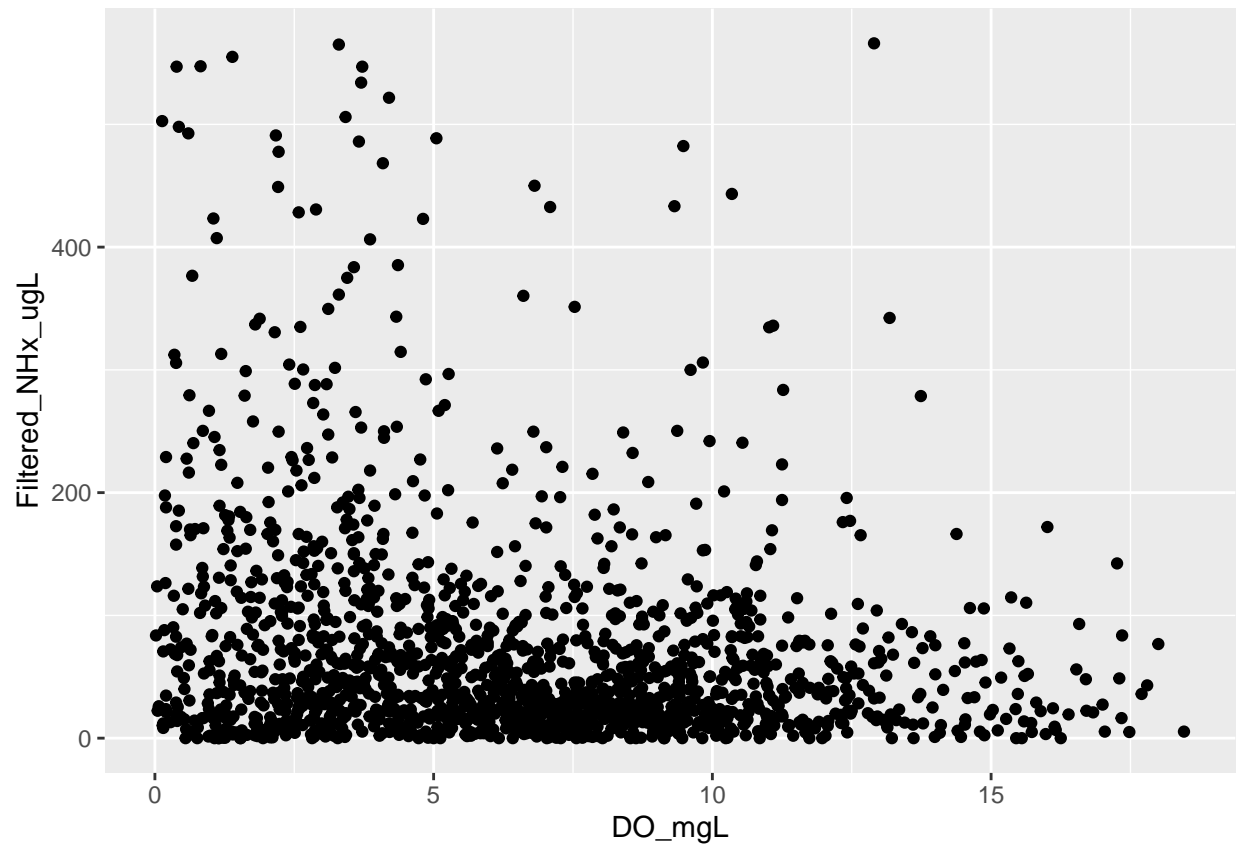
```
ggplot(wetlands, aes(x = Sal_ppt, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 23 rows containing missing values or values outside the scale range  
## ('geom_point()').
```

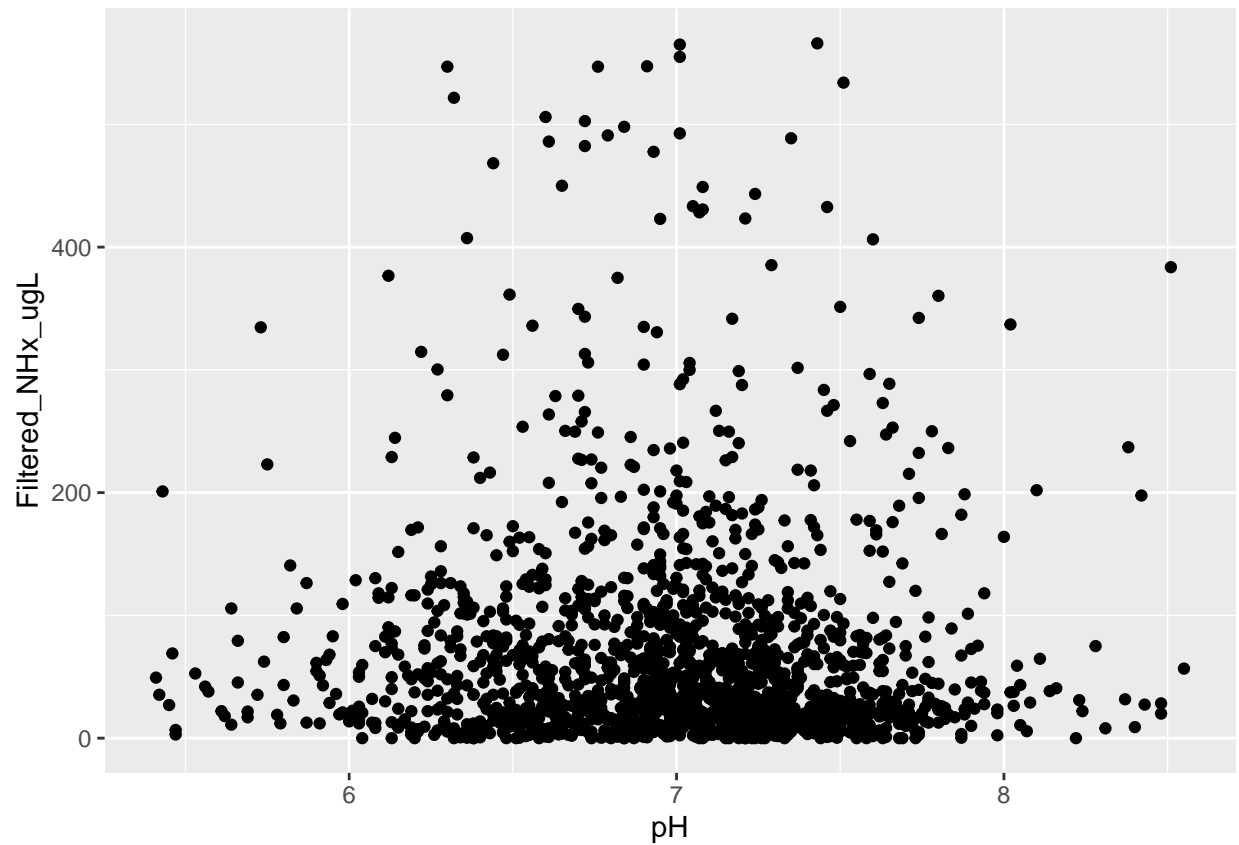
```
ggplot(wetlands, aes(x = DO_mgL, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 31 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



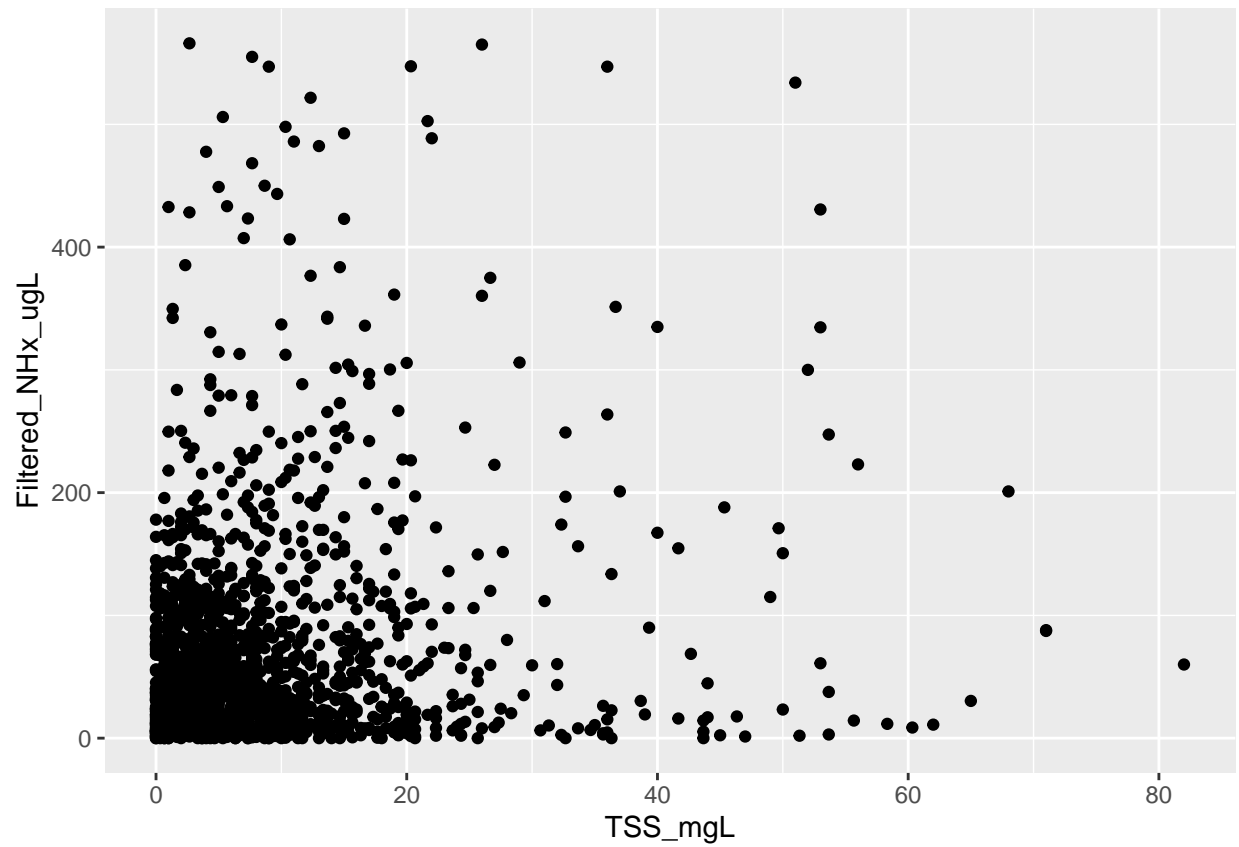
```
ggplot(wetlands, aes(x = pH, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 39 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



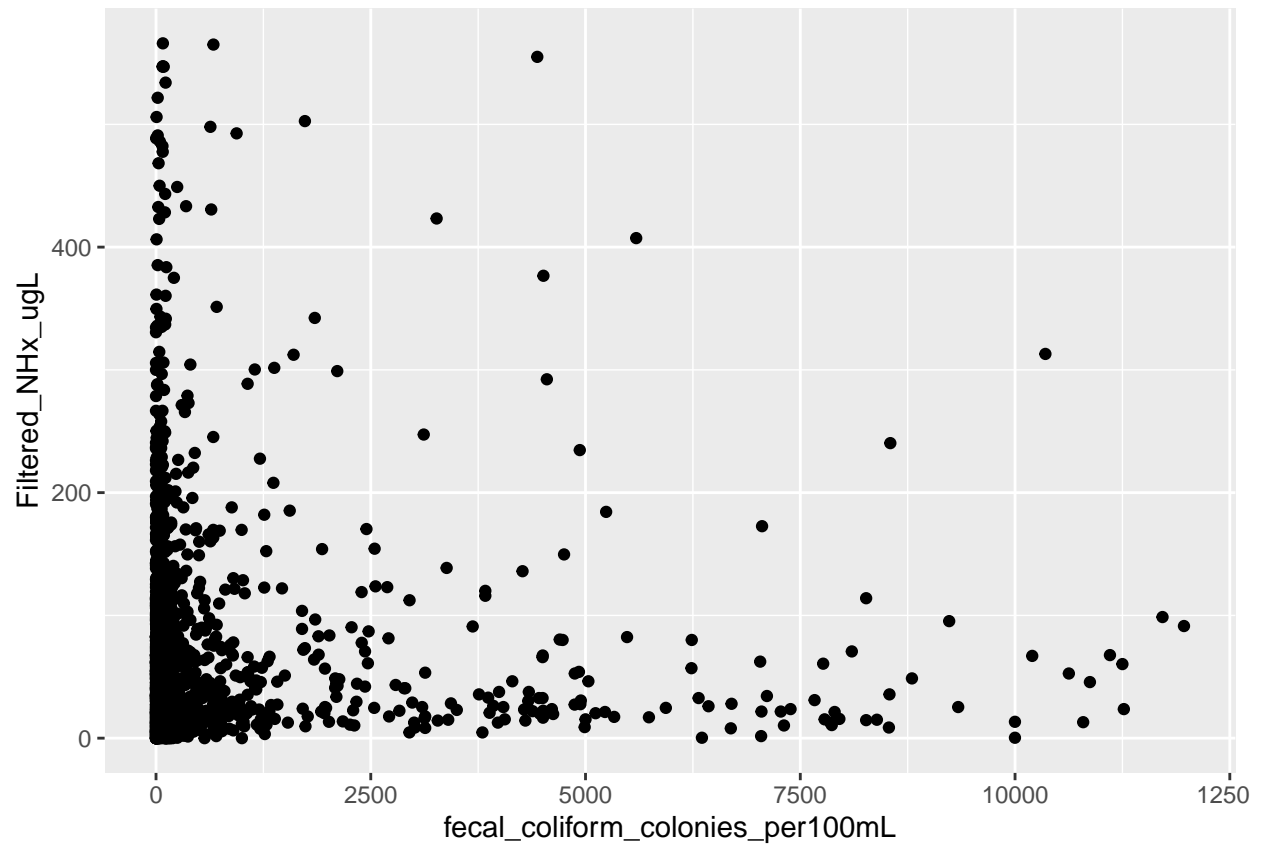
```
ggplot(wetlands, aes(x = TSS_mgL, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 33 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



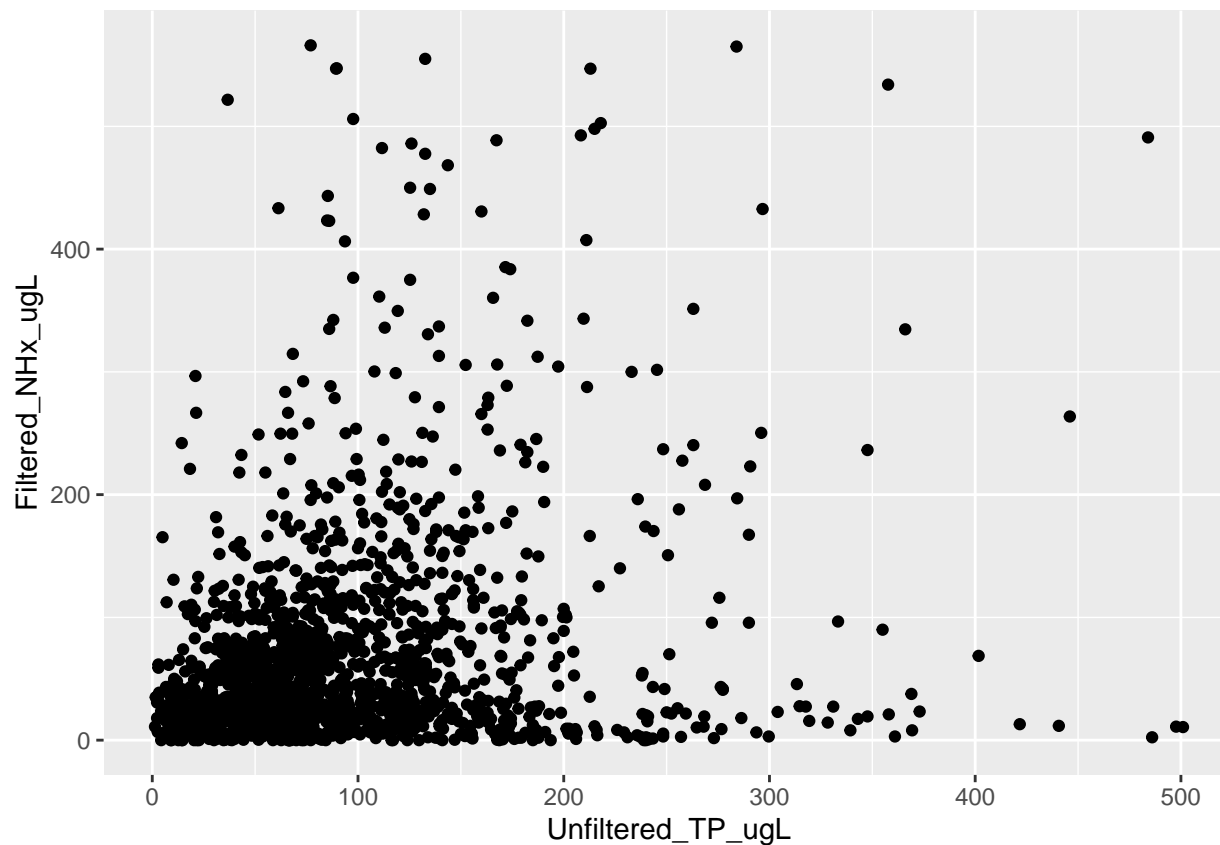
```
ggplot(wetlands, aes(x = fecal_coliform_colonies_per100mL, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 51 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



```
ggplot(wetlands, aes(x = Unfiltered_TP_ugL, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 26 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



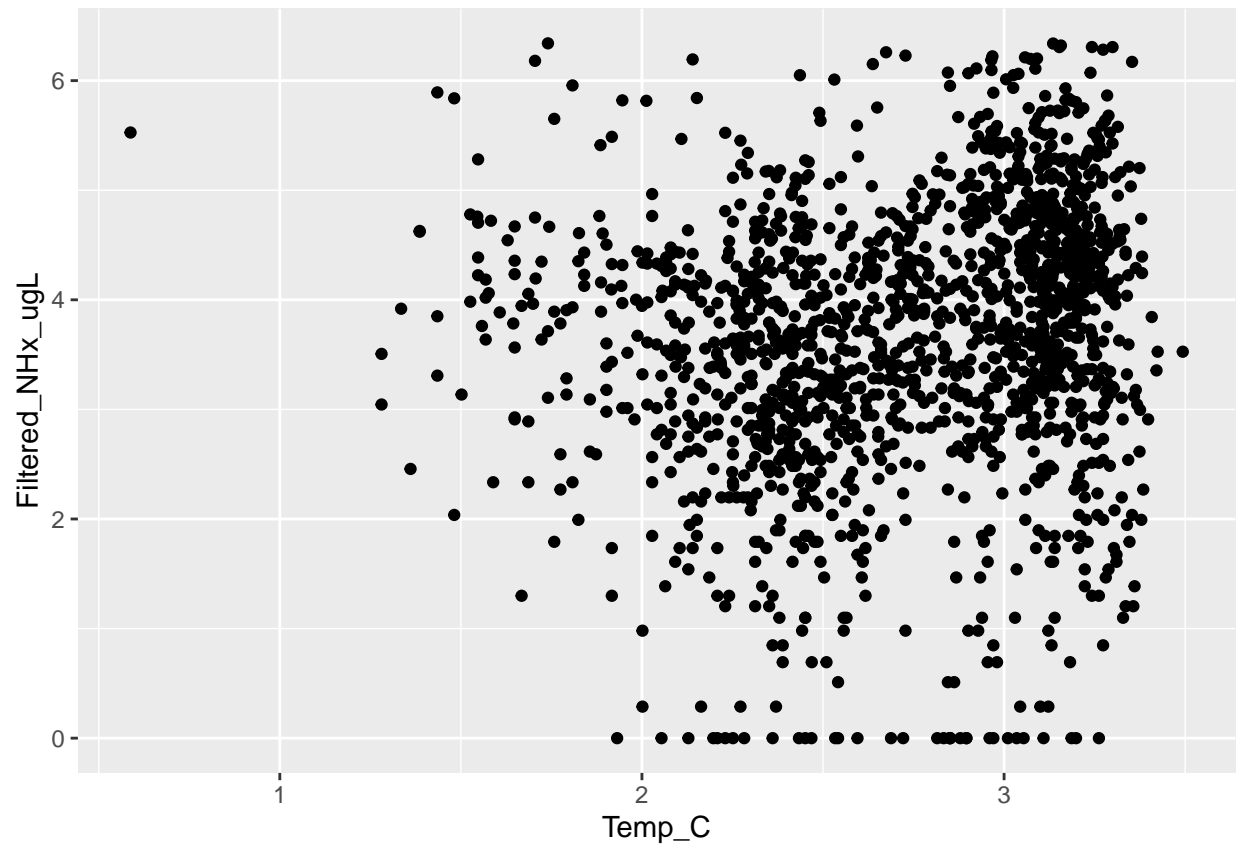
everything needs to be log transformed?

```
#log transform everything except DO
log_wetland <- wetlands %>%
  mutate(across(c(Temp_C, SpCond_mScm, Cond_mScm,
                  TDS_mgl, Sal_ppt, pH,
                  Filtered_NHx_ugL, TSS_mgL,
                  fecal_coliform_colonies_per100mL, Unfiltered_TP_ugL),
    ~ log(.+1)))

#re-vistualize data

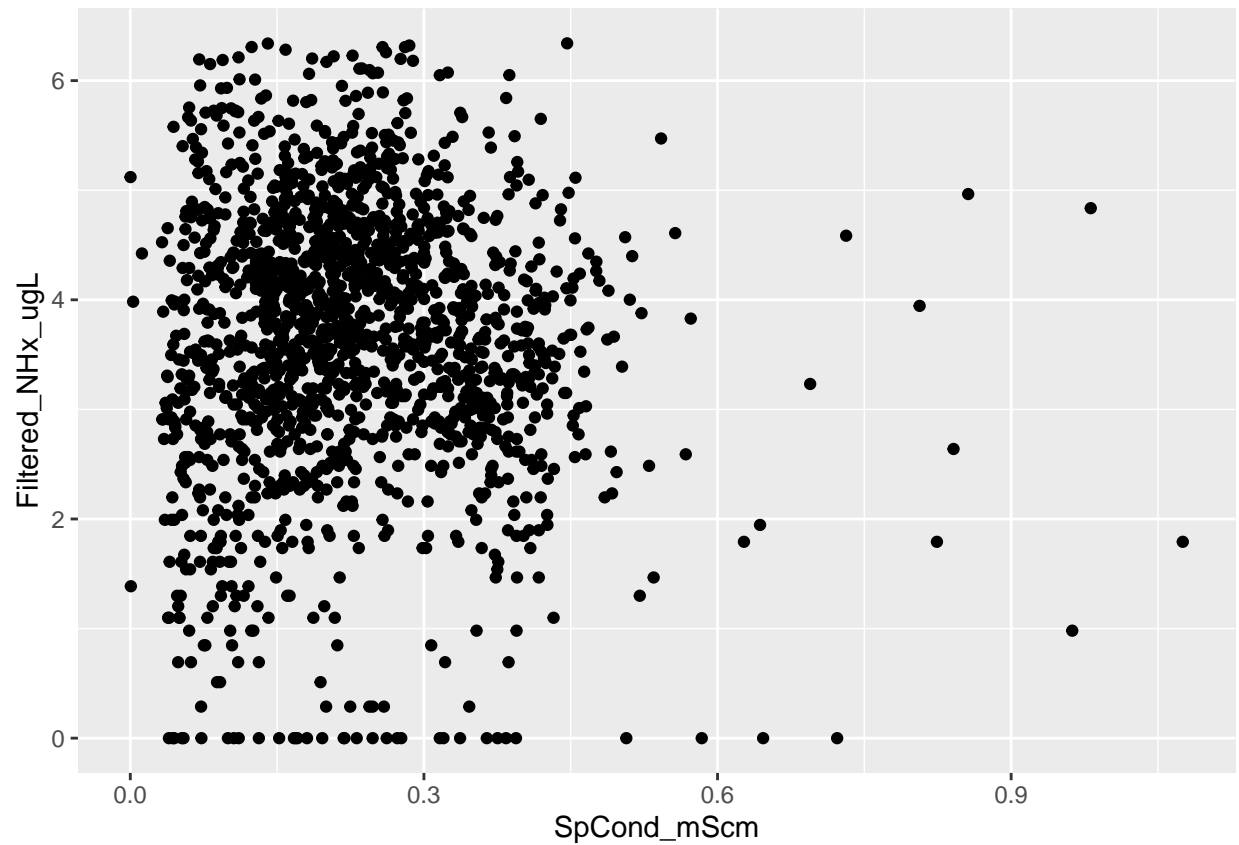
ggplot(log_wetland, aes(x = Temp_C, y = Filtered_NHx_ugL)) +
  geom_point()
```

```
## Warning: Removed 24 rows containing missing values or values outside the scale range
## ('geom_point()').
```



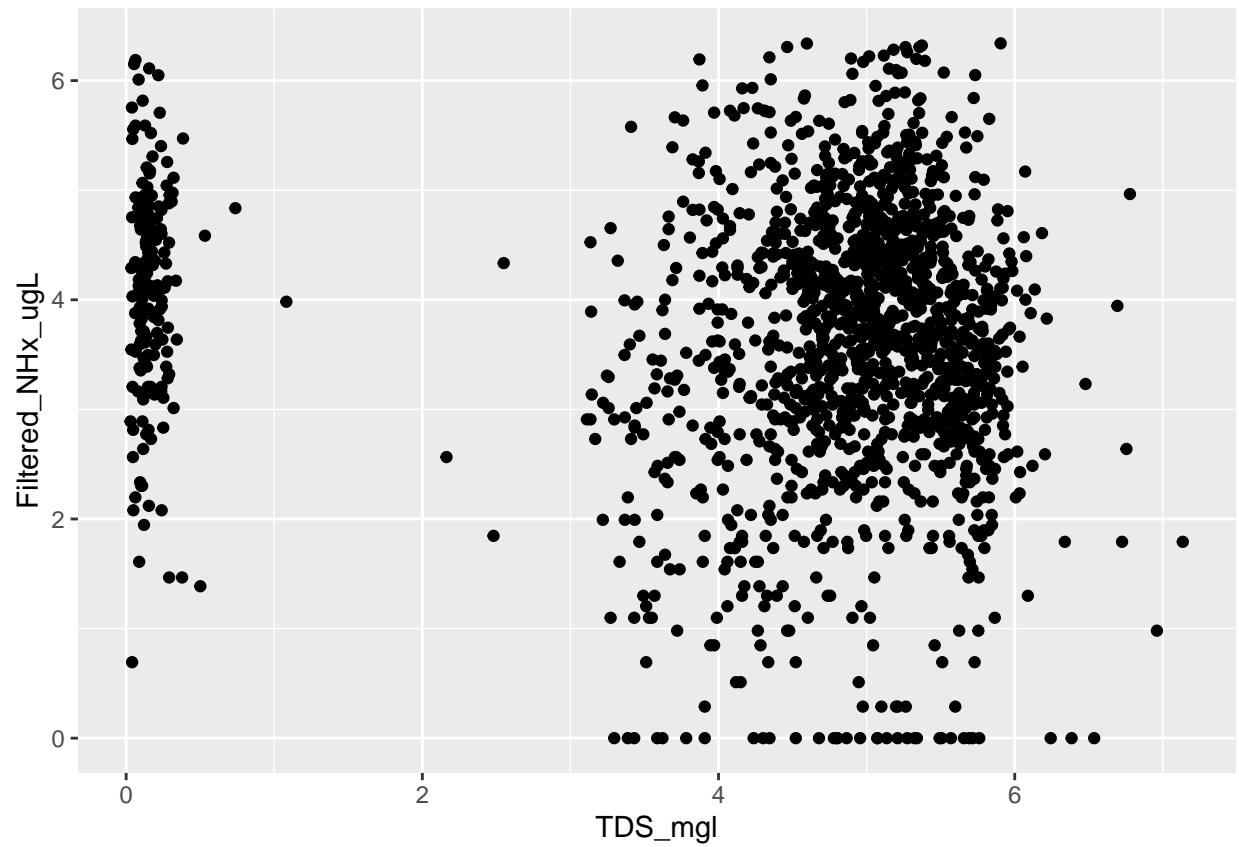
```
ggplot(log_wetland, aes(x = SpCond_mScm, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 23 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



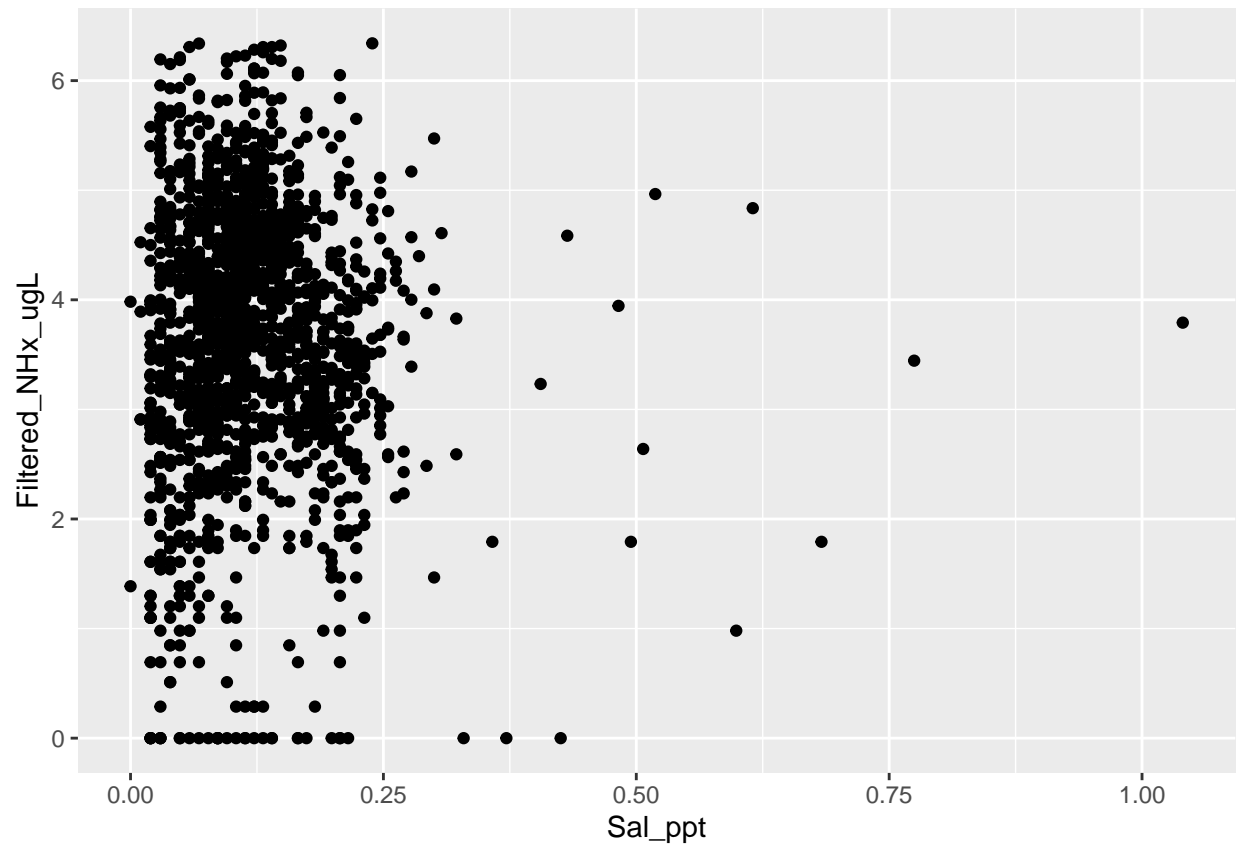
```
ggplot(log_wetland, aes(x = TDS_mgl, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 24 rows containing missing values or values outside the scale range  
## ('geom_point()').
```

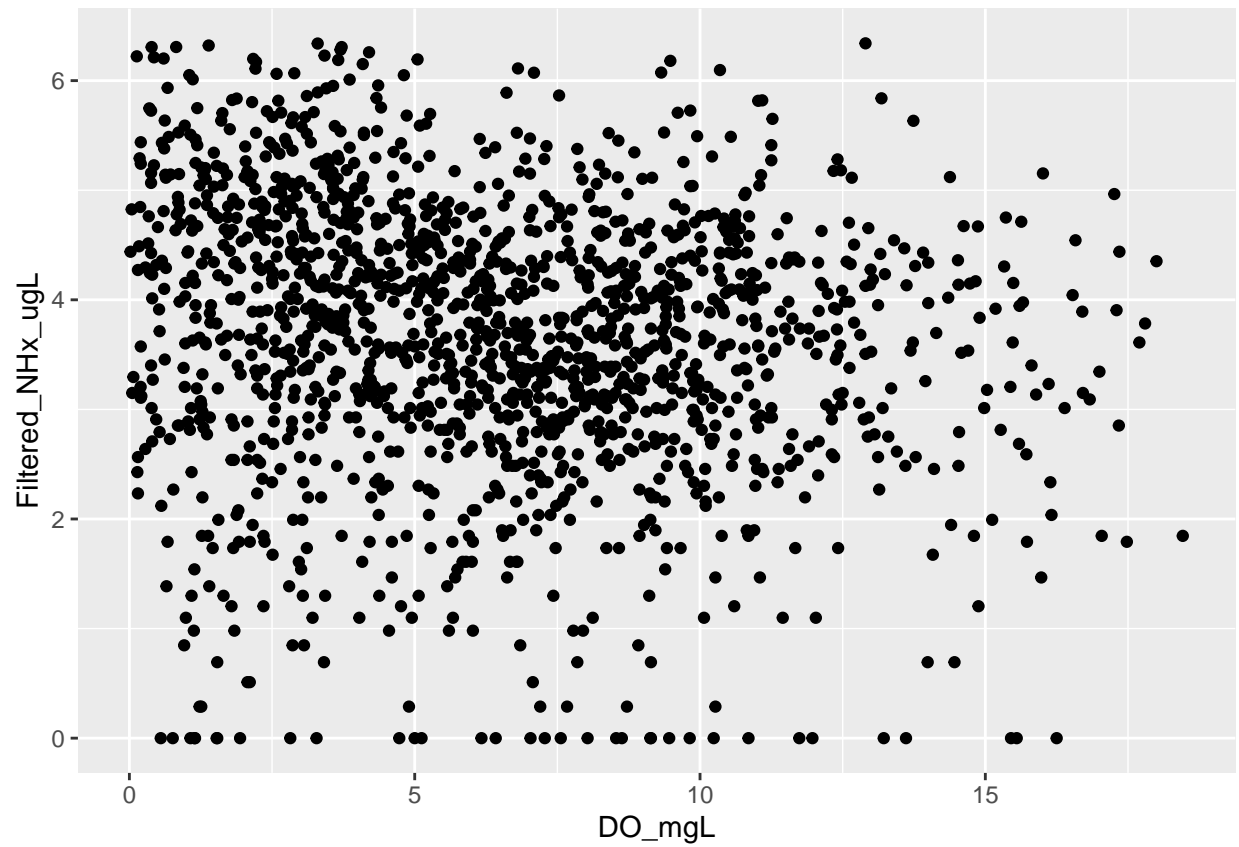
```
ggplot(log_wetland, aes(x = Sal_ppt, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 23 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



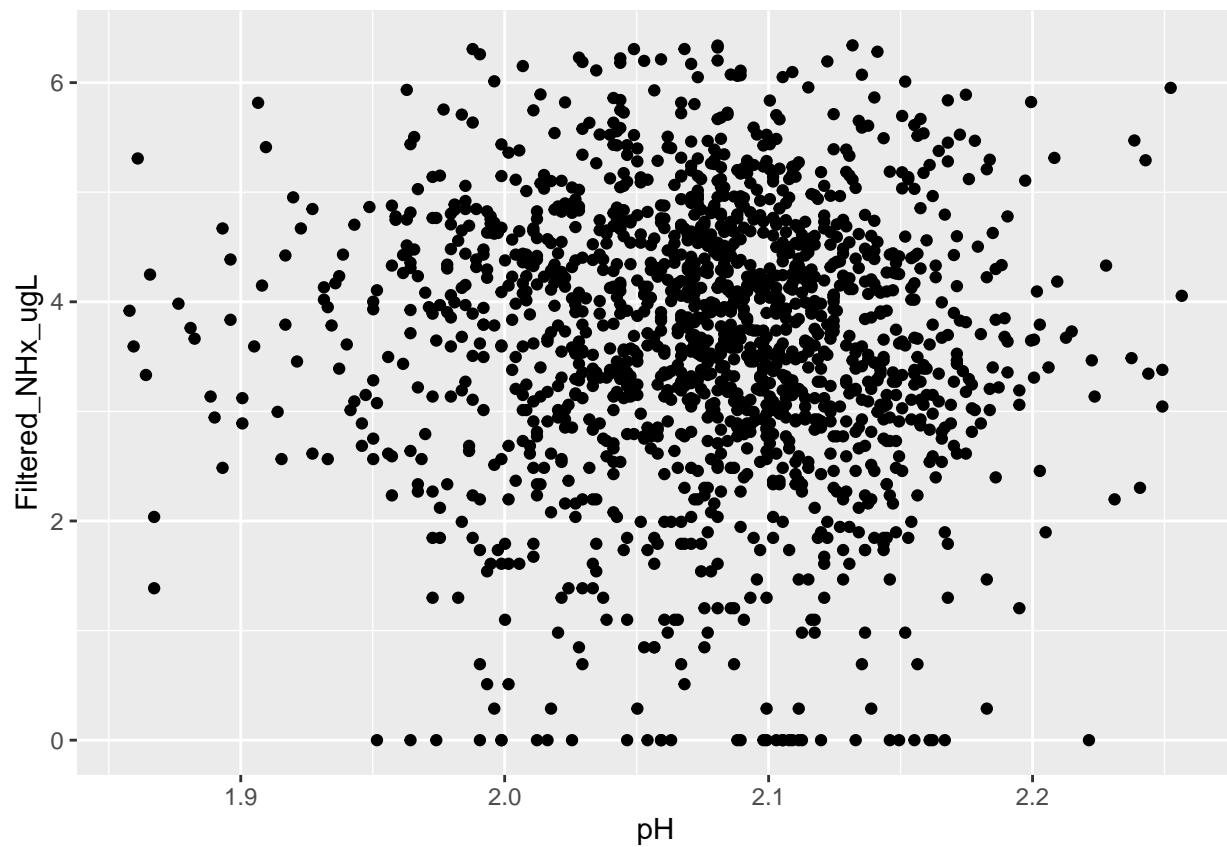
```
ggplot(log_wetland, aes(x = DO_mgL, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 31 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



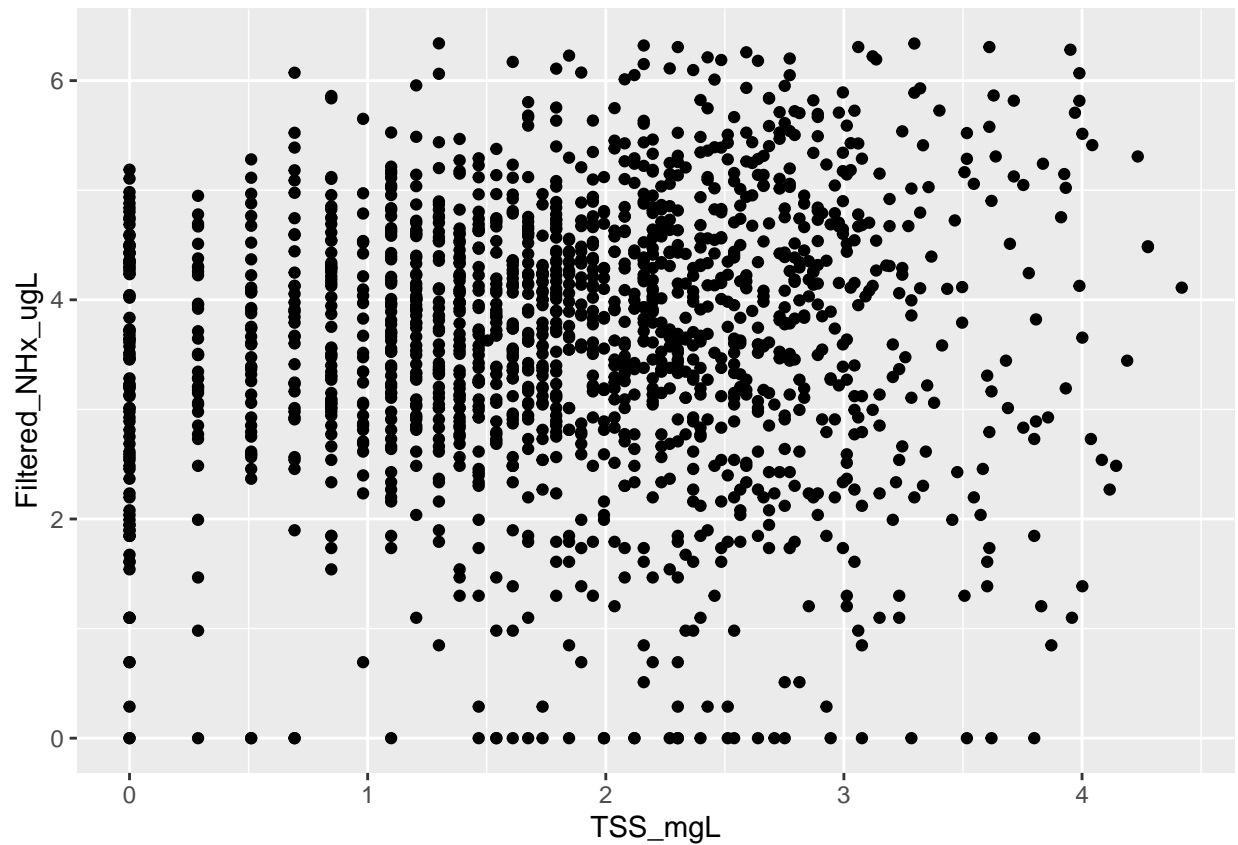
```
ggplot(log_wetland, aes(x = pH, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 39 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



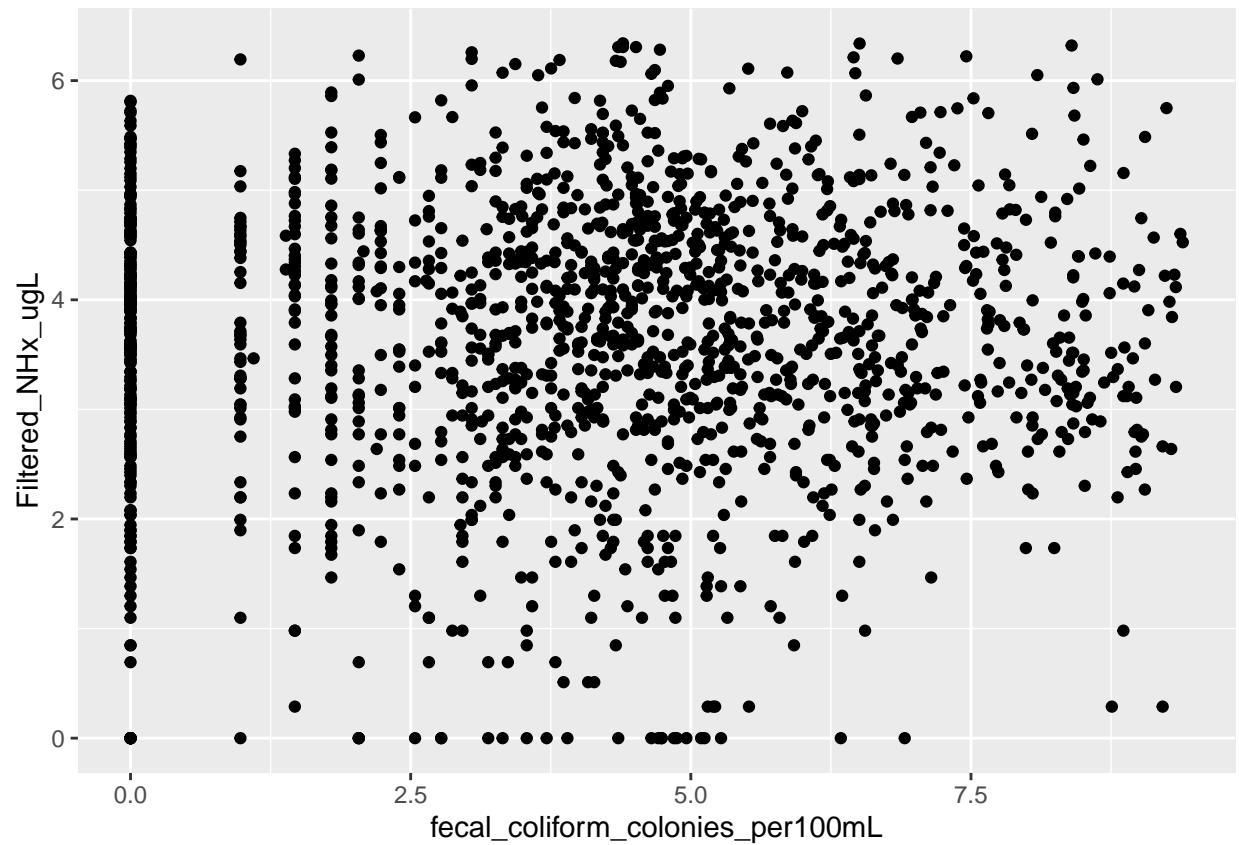
```
ggplot(log_wetland, aes(x = TSS_mgL, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 33 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



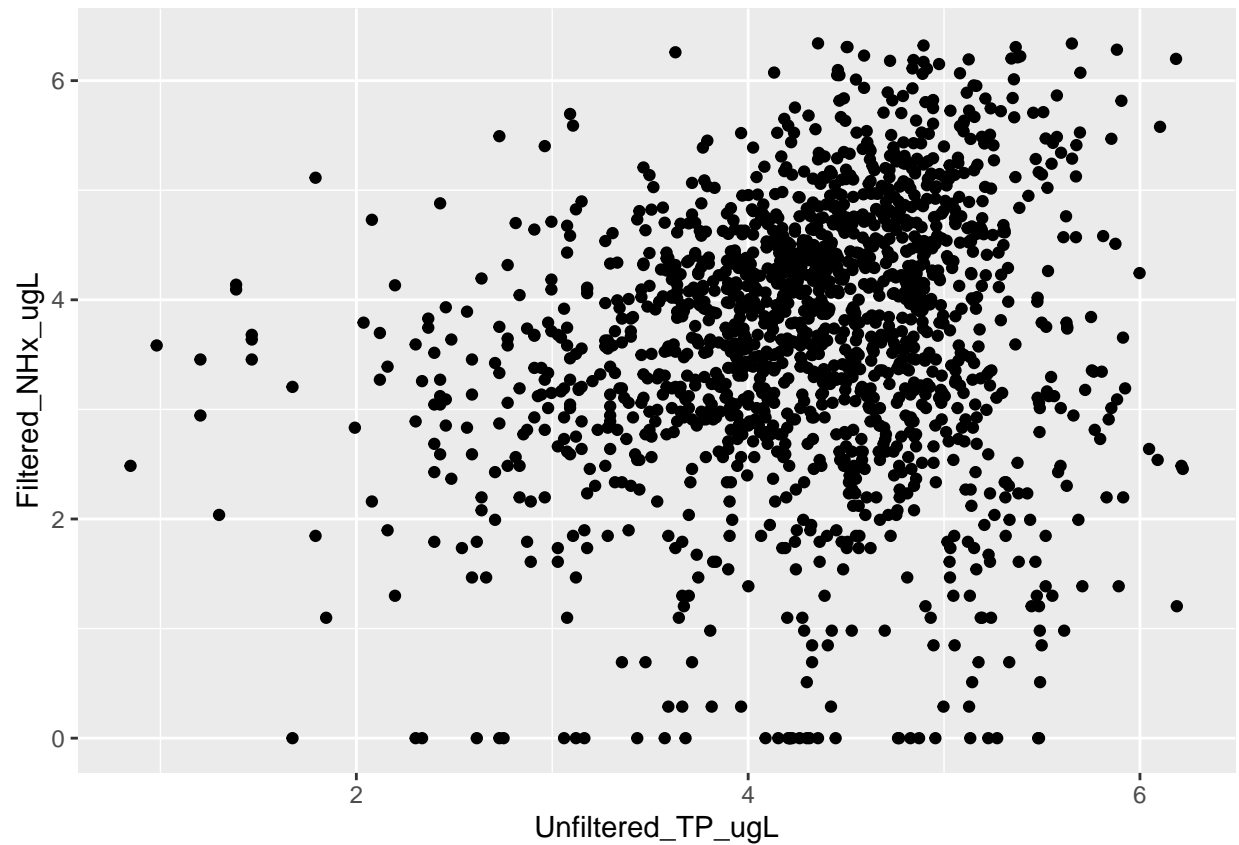
```
ggplot(log_wetland, aes(x = fecal_coliform_colonies_per100mL, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 51 rows containing missing values or values outside the scale range  
## ('geom_point()').
```



```
ggplot(log_wetland, aes(x = Unfiltered_TP_ugL, y = Filtered_NHx_ugL)) +  
geom_point()
```

```
## Warning: Removed 26 rows containing missing values or values outside the scale range  
## ('geom_point()').
```

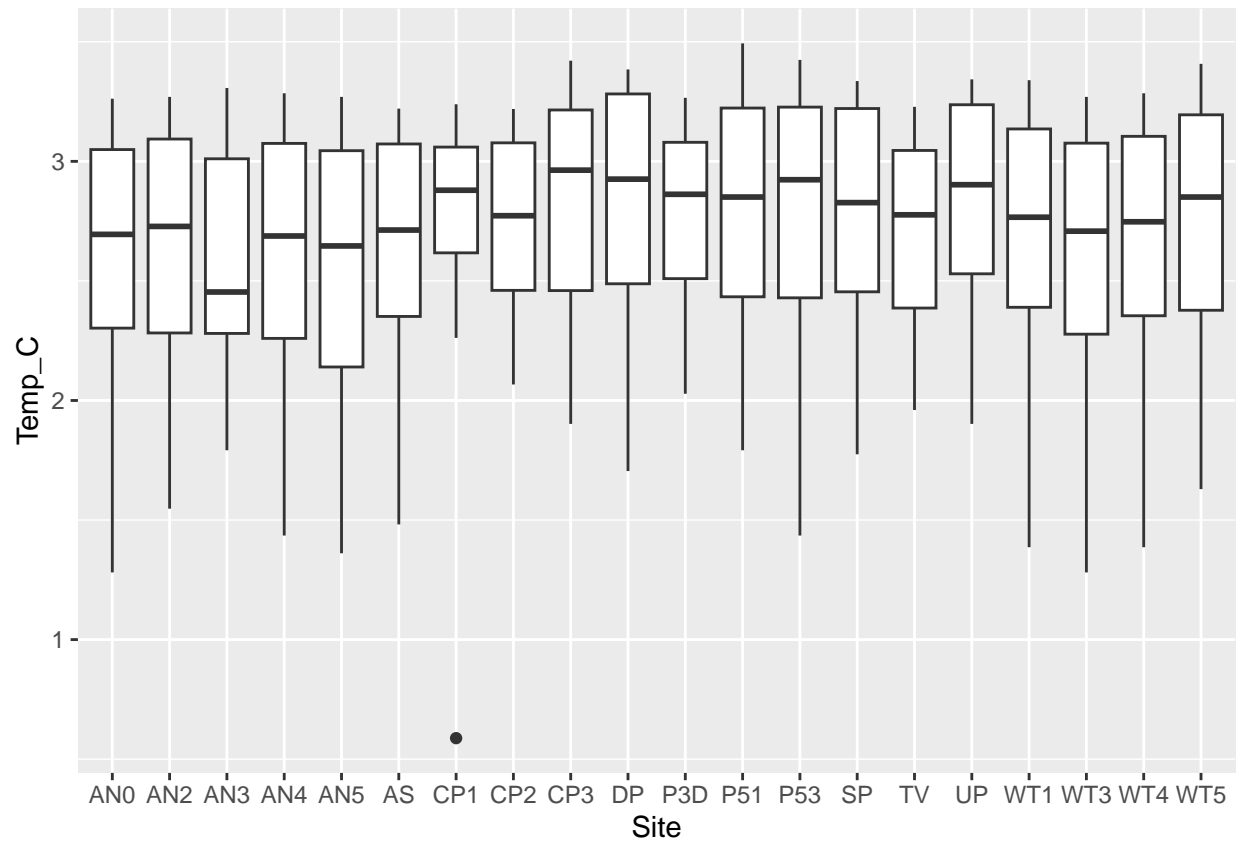


Display fixed effect variables across random effect variable

```
#create boxplots of each fixed effect variable
```

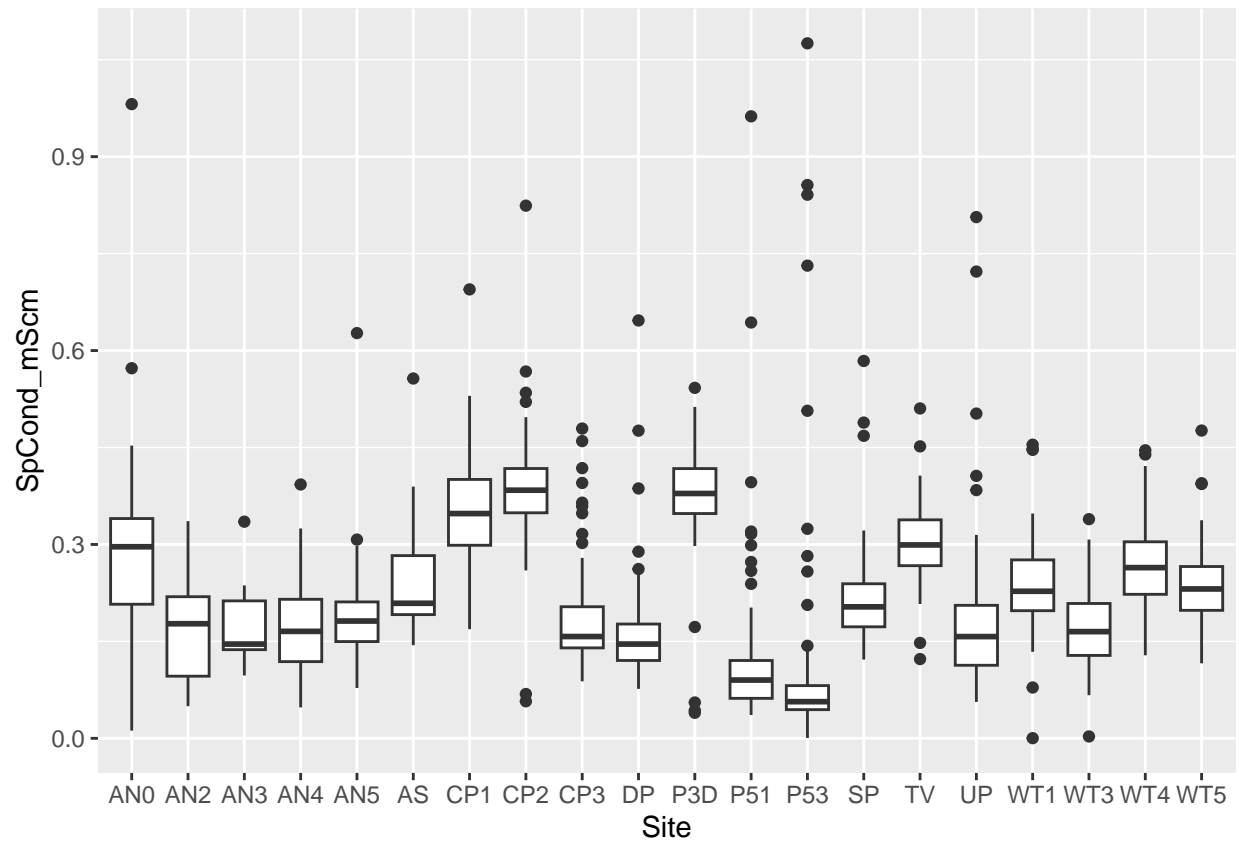
```
ggplot(log_wetland, aes(x = Site, y = Temp_C)) +  
geom_boxplot()
```

```
## Warning: Removed 1 row containing non-finite outside the scale range  
## ('stat_boxplot()').
```



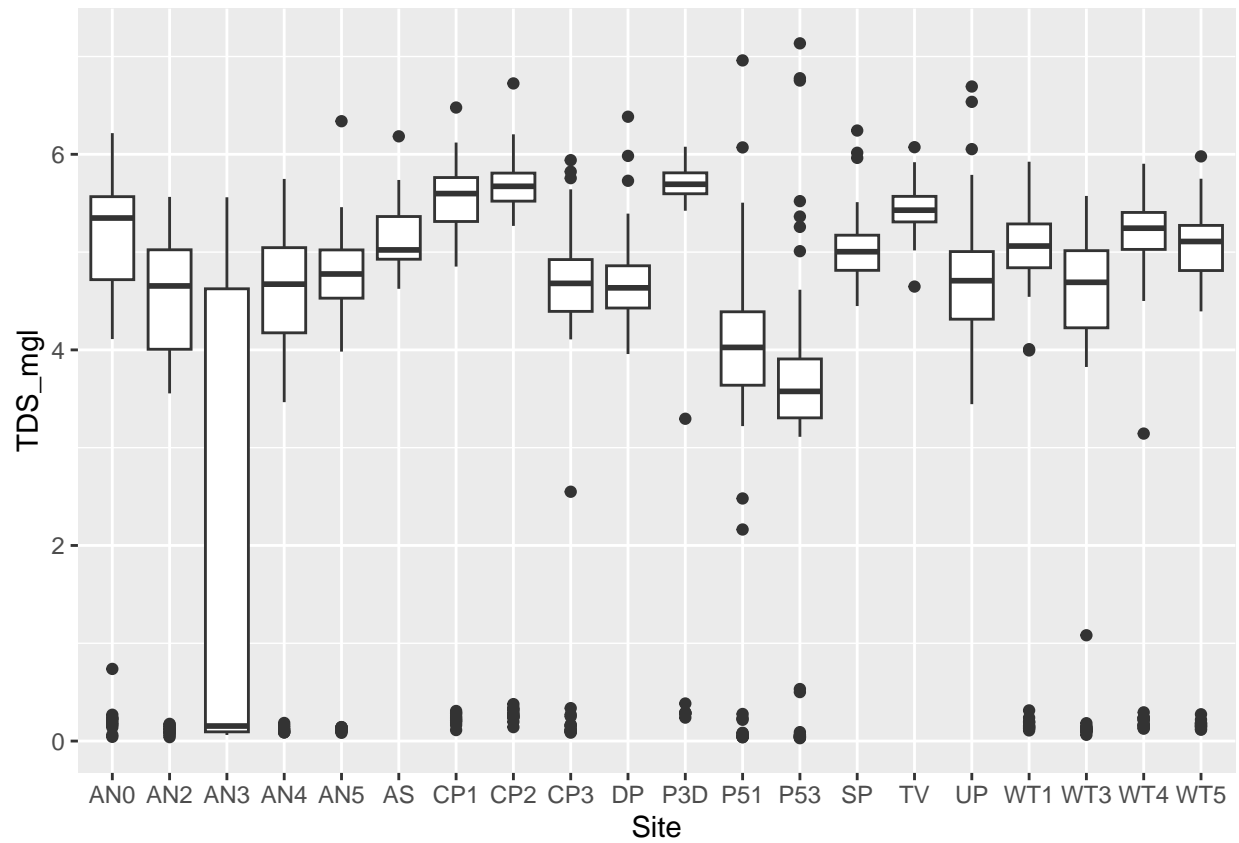
```
ggplot(log_wetland, aes(x = Site, y = SpCond_mScm)) +  
geom_boxplot()
```

```
## Warning: Removed 1 row containing non-finite outside the scale range  
## ('stat_boxplot()').
```

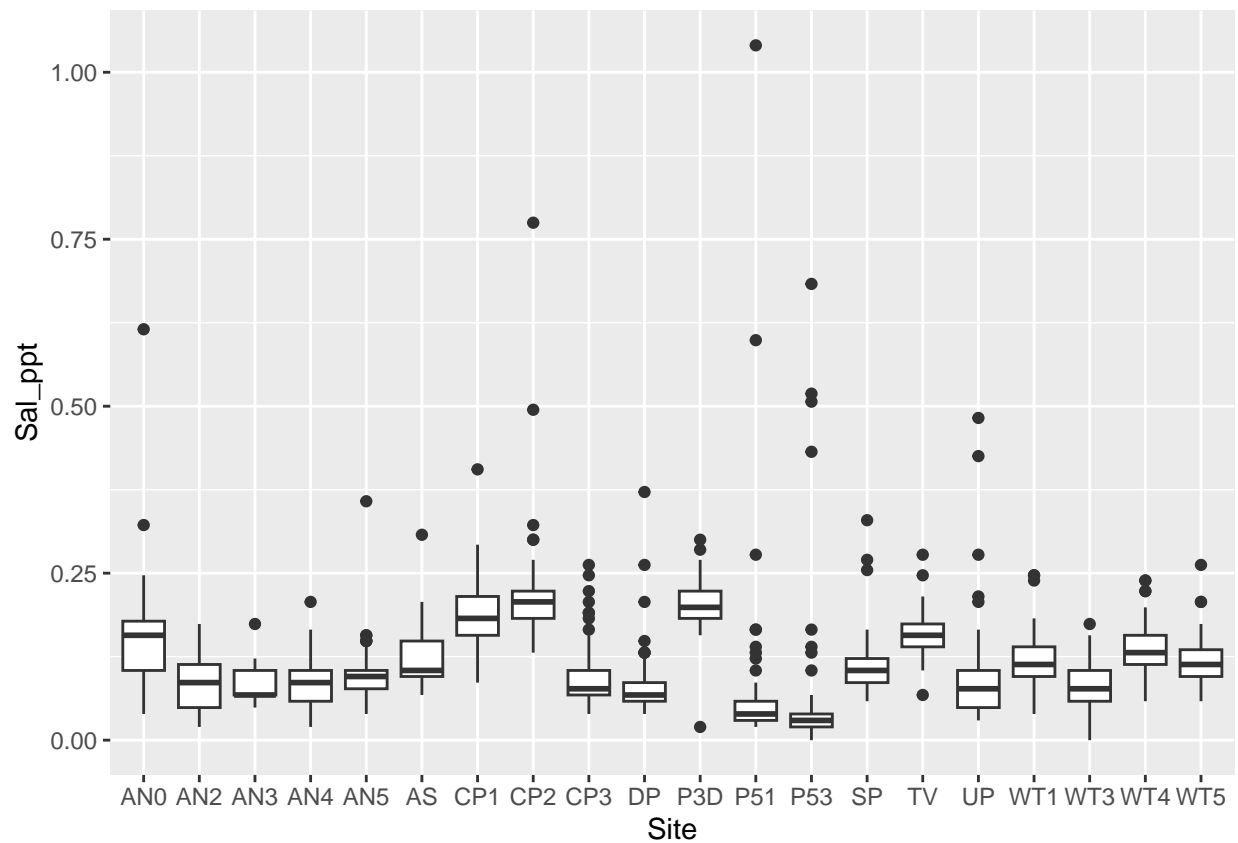
```
ggplot(log_wetland, aes(x = Site, y = TDS_mgl)) +  
geom_boxplot()
```

```
## Warning: Removed 2 rows containing non-finite outside the scale range  
## ('stat_boxplot()').
```



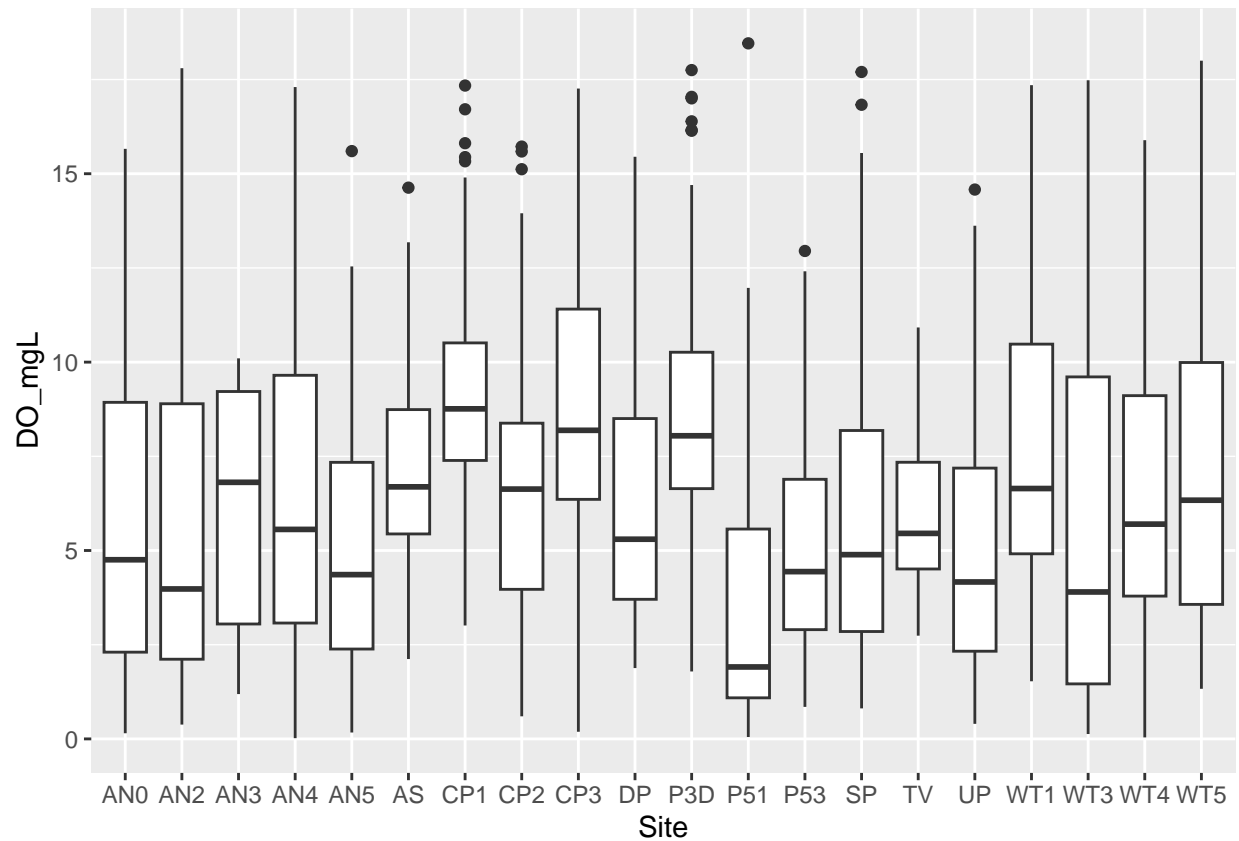
```
ggplot(log_wetland, aes(x = Site, y = Sal_ppt)) +  
geom_boxplot()
```

```
## Warning: Removed 1 row containing non-finite outside the scale range  
## ('stat_boxplot()').
```



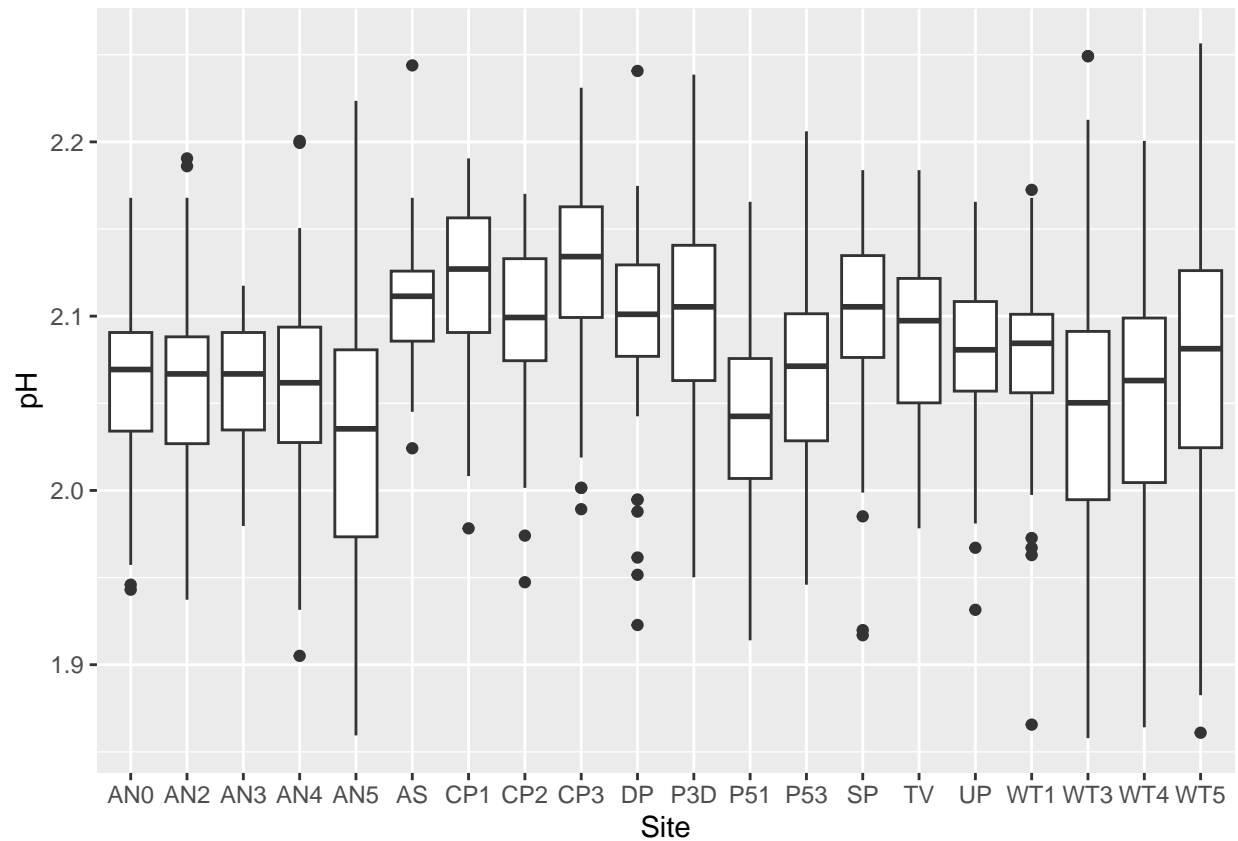
```
ggplot(log_wetland, aes(x = Site, y = DO_mgL)) +  
geom_boxplot()
```

```
## Warning: Removed 8 rows containing non-finite outside the scale range  
## ('stat_boxplot()').
```



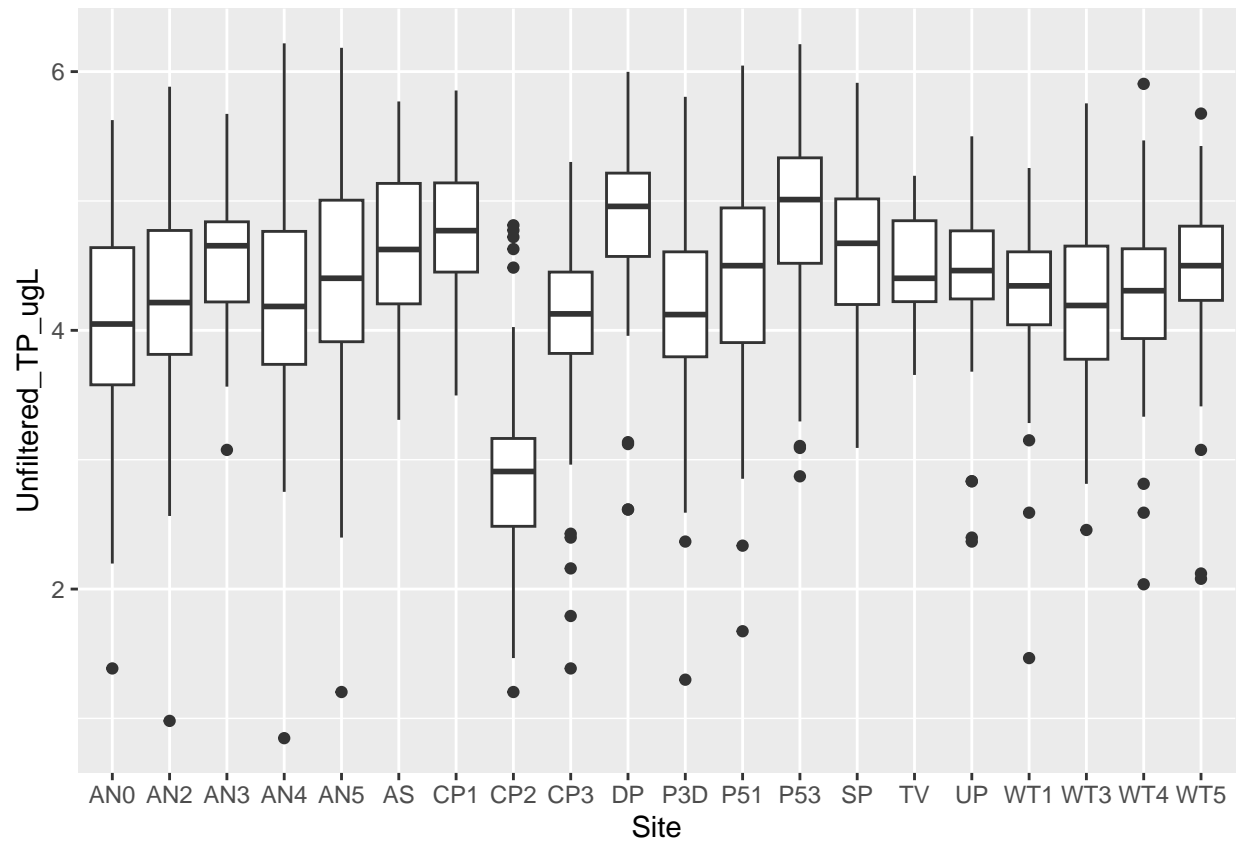
```
ggplot(log_wetland, aes(x = Site, y = pH)) +  
geom_boxplot()
```

```
## Warning: Removed 16 rows containing non-finite outside the scale range  
## ('stat_boxplot()').
```



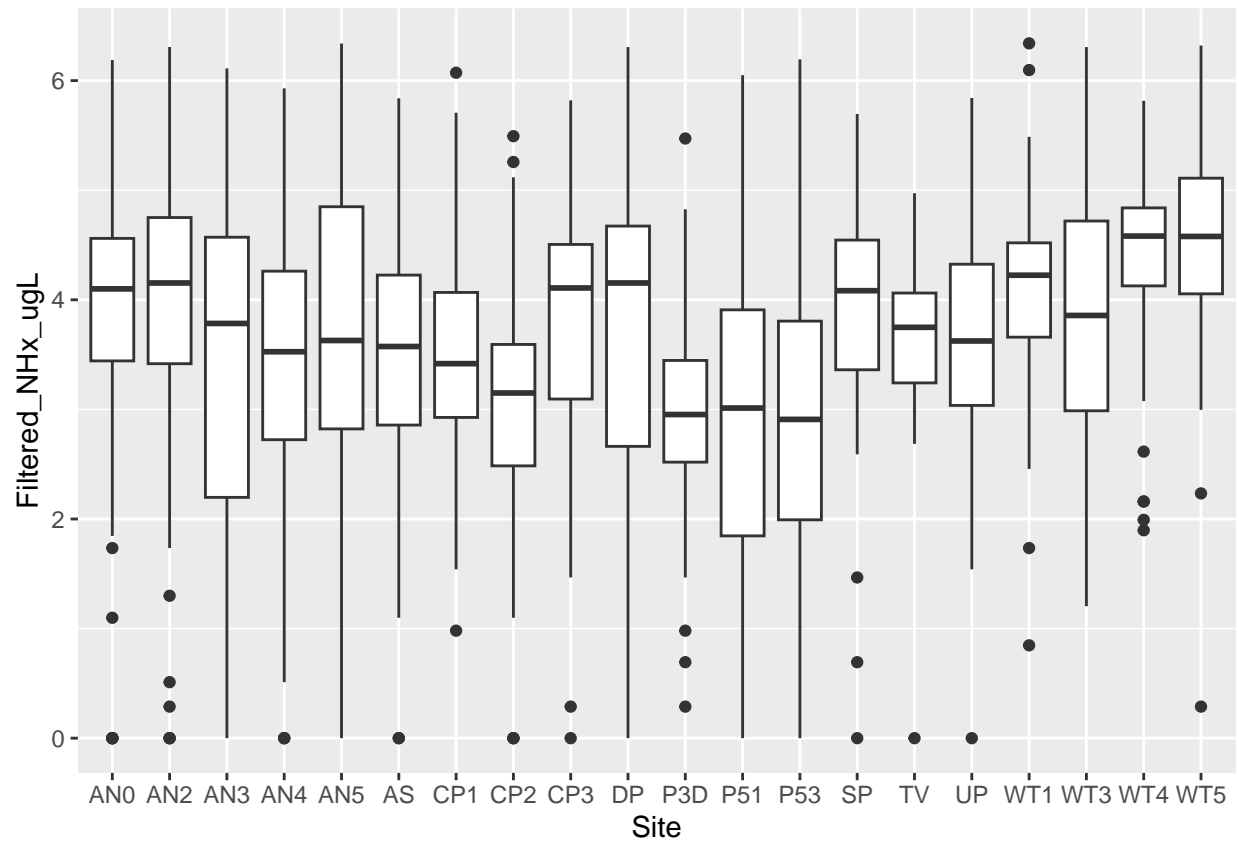
```
ggplot(log_wetland, aes(x = Site, y = Unfiltered_TP_ugL)) +  
geom_boxplot()
```

```
## Warning: Removed 7 rows containing non-finite outside the scale range  
## ('stat_boxplot()').
```



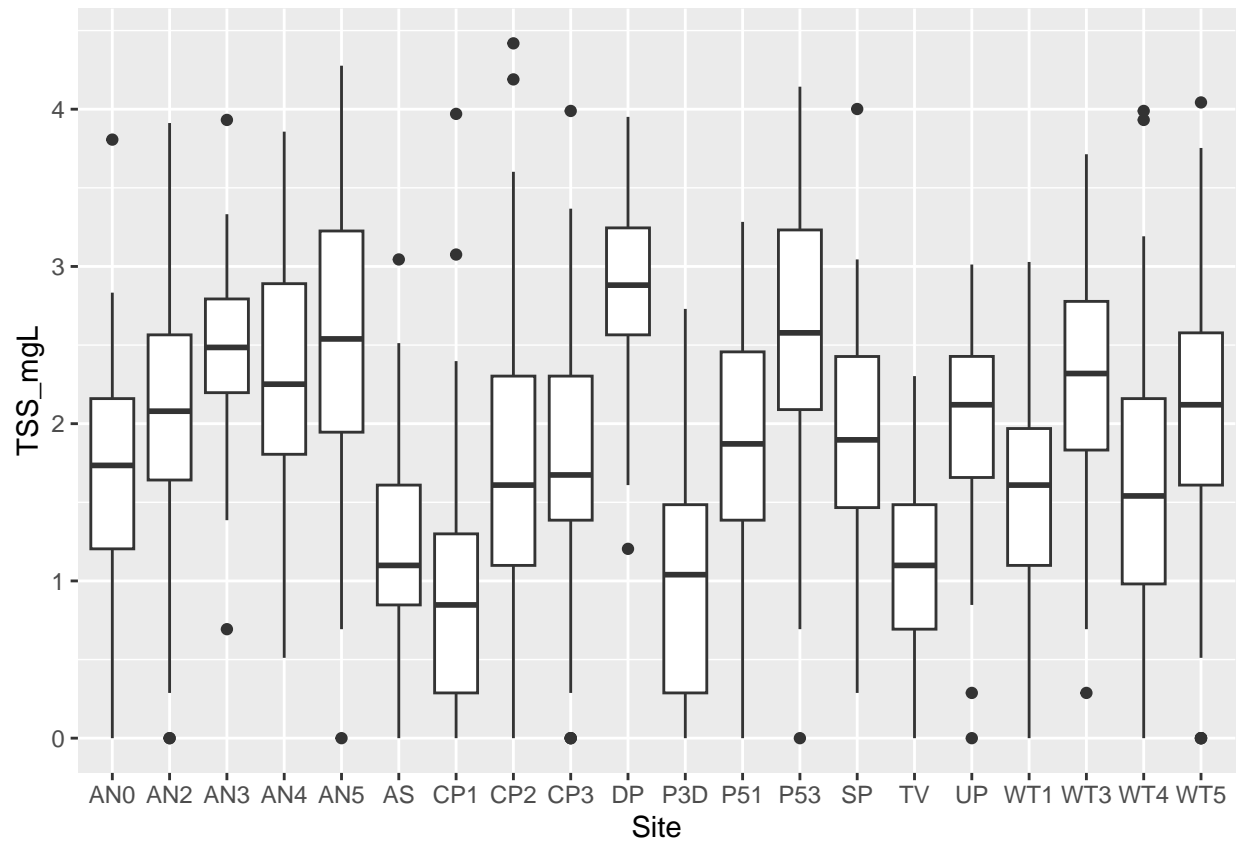
```
ggplot(log_wetland, aes(x = Site, y = Filtered_NHx_ugL)) +  
geom_boxplot()
```

```
## Warning: Removed 23 rows containing non-finite outside the scale range  
## ('stat_boxplot()').
```



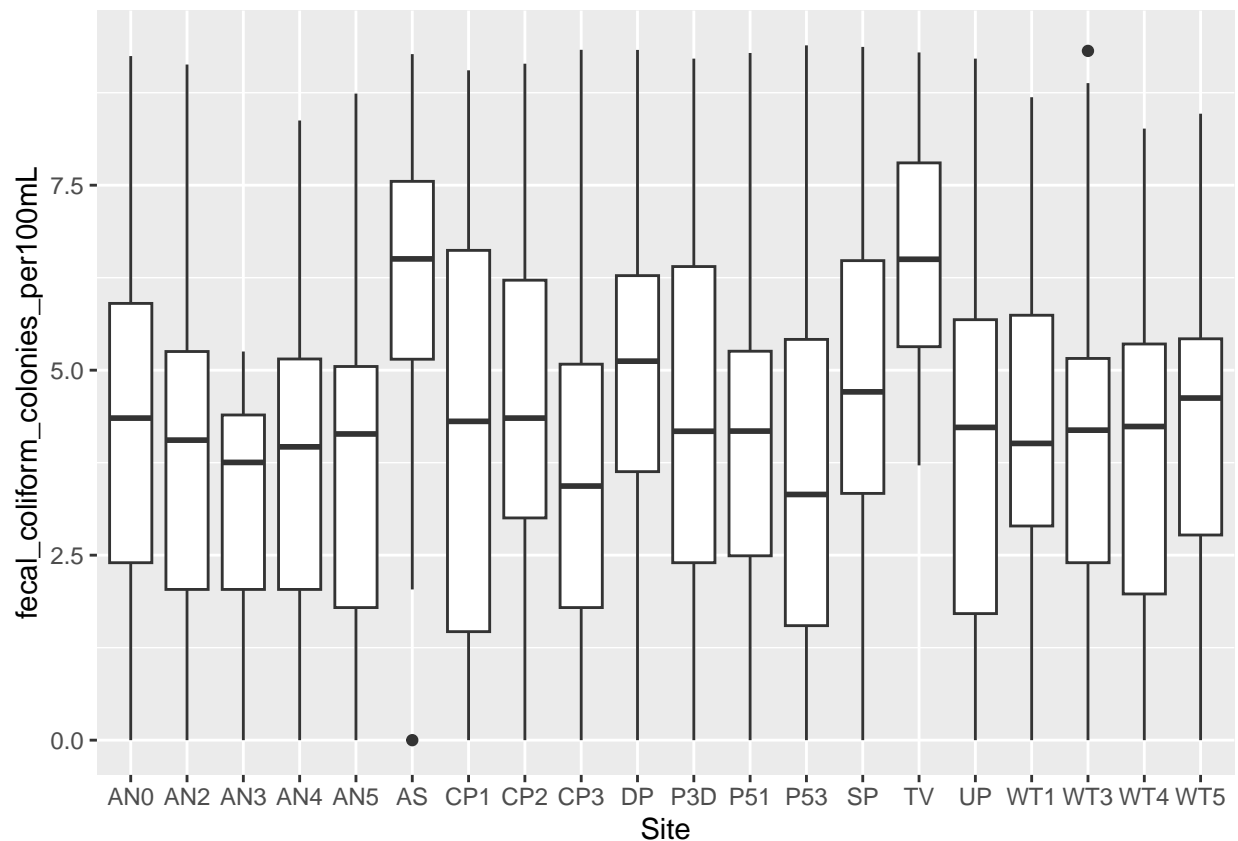
```
ggplot(log_wetland, aes(x = Site, y = TSS_mgL)) +  
geom_boxplot()
```

```
## Warning: Removed 15 rows containing non-finite outside the scale range  
## ('stat_boxplot()').
```



```
ggplot(log_wetland, aes(x = Site, y = fecal_coliform_colonies_per100mL)) +  
geom_boxplot()
```

```
## Warning: Removed 29 rows containing non-finite outside the scale range  
## ('stat_boxplot()').
```

Check for correlation between variables

```
#Temp vs:
cor.test(log_wetland$Temp_C, log_wetland$SpCond_mScm)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Temp_C and log_wetland$SpCond_mScm
## t = -8.2019, df = 1614, p-value = 4.776e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.2463895 -0.1527577
## sample estimates:
## cor
## -0.2000303
```

```
cor.test(log_wetland$Temp_C, log_wetland$TDS_mgl)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Temp_C and log_wetland$TDS_mgl
```

```
## t = -5.3102, df = 1613, p-value = 1.248e-07
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1787132 -0.0828301
## sample estimates:
## cor
## -0.1310782
```

```
cor.test(log_wetland$Temp_C, log_wetland$Sal_ppt)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Temp_C and log_wetland$Sal_ppt
## t = -7.955, df = 1614, p-value = 3.342e-15
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.2407217 -0.1468677
## sample estimates:
## cor
## -0.1942392
```

```
cor.test(log_wetland$Temp_C, log_wetland$DO_mgL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Temp_C and log_wetland$DO_mgL
## t = -24.027, df = 1607, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.5491685 -0.4772175
## sample estimates:
## cor
## -0.5140968
```

```
cor.test(log_wetland$Temp_C, log_wetland$pH)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Temp_C and log_wetland$pH
## t = 5.6194, df = 1599, p-value = 2.256e-08
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.09079065 0.18687861
## sample estimates:
## cor
## 0.1391622
```

```
cor.test(log_wetland$Temp_C, log_wetland$Unfiltered_TP_ugL)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: log_wetland$Temp_C and log_wetland$Unfiltered_TP_ugL  
## t = 10.889, df = 1608, p-value < 2.2e-16  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## 0.2159583 0.3069705  
## sample estimates:  
## cor  
## 0.262047
```

```
cor.test(log_wetland$Temp_C, log_wetland$TSS_mgL)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: log_wetland$Temp_C and log_wetland$TSS_mgL  
## t = 6.0434, df = 1600, p-value = 1.873e-09  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## 0.1011553 0.1969248  
## sample estimates:  
## cor  
## 0.1493904
```

```
cor.test(log_wetland$Temp_C, log_wetland$fecal_coliform_colonies_per100mL)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: log_wetland$Temp_C and log_wetland$fecal_coliform_colonies_per100mL  
## t = 8.3893, df = 1586, p-value < 2.2e-16  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## 0.1585493 0.2527600  
## sample estimates:  
## cor  
## 0.2061323
```

```
#SpCond vs:
```

```
cor.test(log_wetland$SpCond_mScm, log_wetland$TDS_mgl)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: log_wetland$SpCond_mScm and log_wetland$TDS_mgl  
## t = 13.405, df = 1614, p-value < 2.2e-16  
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
## 0.2719393 0.3597157
## sample estimates:
##      cor
## 0.3165049
```

```
cor.test(log_wetland$SpCond_mScm, log_wetland$Sal_ppt)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$SpCond_mScm and log_wetland$Sal_ppt
## t = 84.681, df = 1615, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.8940542 0.9120104
## sample estimates:
##      cor
## 0.9034277
```

```
cor.test(log_wetland$SpCond_mScm, log_wetland$DO_mgL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$SpCond_mScm and log_wetland$DO_mgL
## t = 12.706, df = 1607, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2570739 0.3459077
## sample estimates:
##      cor
## 0.3021467
```

```
cor.test(log_wetland$SpCond_mScm, log_wetland$pH)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$SpCond_mScm and log_wetland$pH
## t = 6.0105, df = 1599, p-value = 2.287e-09
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1003790 0.1962003
## sample estimates:
##      cor
## 0.1486386
```

```
cor.test(log_wetland$SpCond_mScm, log_wetland$Unfiltered_TP_ugL)
```

```
##
```

```
## Pearson's product-moment correlation
##
## data: log_wetland$SpCond_mScm and log_wetland$Unfiltered_TP_ugL
## t = -13.457, df = 1608, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.3613849 -0.2735467
## sample estimates:
## cor
## -0.3181484
```

```
cor.test(log_wetland$SpCond_mScm, log_wetland$TSS_mgL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$SpCond_mScm and log_wetland$TSS_mgL
## t = -16.346, df = 1600, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.4194939 -0.3355318
## sample estimates:
## cor
## -0.3782906
```

```
cor.test(log_wetland$SpCond_mScm, log_wetland$fecal_coliform_colonies_per100mL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$SpCond_mScm and log_wetland$fecal_coliform_colonies_per100mL
## t = -1.7784, df = 1586, p-value = 0.07553
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.093597148 0.004588878
## sample estimates:
## cor
## -0.04461187
```

```
#TDS vs:
cor.test(log_wetland$TDS_mgl, log_wetland$Sal_ppt)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$TDS_mgl and log_wetland$Sal_ppt
## t = 13.18, df = 1614, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2670273 0.3550956
## sample estimates:
## cor
## 0.3117308
```

```
cor.test(log_wetland$TDS_mgl, log_wetland$DO_mgL)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: log_wetland$TDS_mgl and log_wetland$DO_mgL  
## t = 5.6897, df = 1606, p-value = 1.51e-08  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## 0.09231743 0.18815762  
## sample estimates:  
## cor  
## 0.1405668
```

```
cor.test(log_wetland$TDS_mgl, log_wetland$pH)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: log_wetland$TDS_mgl and log_wetland$pH  
## t = 2.7512, df = 1598, p-value = 0.006004  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## 0.01972164 0.11727231  
## sample estimates:  
## cor  
## 0.0686611
```

```
cor.test(log_wetland$TDS_mgl, log_wetland$Unfiltered_TP_ugL)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: log_wetland$TDS_mgl and log_wetland$Unfiltered_TP_ugL  
## t = 1.9267, df = 1607, p-value = 0.05419  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.0008626319 0.0966496975  
## sample estimates:  
## cor  
## 0.04800792
```

```
cor.test(log_wetland$TDS_mgl, log_wetland$TSS_mgL)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: log_wetland$TDS_mgl and log_wetland$TSS_mgL  
## t = -6.0674, df = 1599, p-value = 1.62e-09  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:
```

```
## -0.1975541 -0.1017729
## sample estimates:
##      cor
## -0.1500155
```

```
cor.test(log_wetland$TDS_mgl, log_wetland$fecal_coliform_colonies_per100mL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$TDS_mgl and log_wetland$fecal_coliform_colonies_per100mL
## t = 1.8886, df = 1585, p-value = 0.05912
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.001824798 0.096367114
## sample estimates:
##      cor
## 0.04738563
```

```
#Sal vs
cor.test(log_wetland$Sal_ppt, log_wetland$DO_mgL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Sal_ppt and log_wetland$DO_mgL
## t = 11.111, df = 1607, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2211275 0.3119067
## sample estimates:
##      cor
## 0.2671096
```

```
cor.test(log_wetland$Sal_ppt, log_wetland$pH)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Sal_ppt and log_wetland$pH
## t = 6.0863, df = 1599, p-value = 1.444e-09
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1022353 0.1980030
## sample estimates:
##      cor
## 0.1504721
```

```
cor.test(log_wetland$Sal_ppt, log_wetland$Unfiltered_TP_ugL)
```

```
##
```

```
## Pearson's product-moment correlation
##
## data: log_wetland$Sal_ppt and log_wetland$Unfiltered_TP_ugL
## t = -12.333, df = 1608, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.3379744 -0.2486932
## sample estimates:
##      cor
## -0.2939749
```

```
cor.test(log_wetland$Sal_ppt, log_wetland$TSS_mgL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Sal_ppt and log_wetland$TSS_mgL
## t = -14.28, df = 1600, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.378944 -0.292042
## sample estimates:
##      cor
## -0.3362084
```

```
cor.test(log_wetland$Sal_ppt, log_wetland$fecal_coliform_colonies_per100mL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Sal_ppt and log_wetland$fecal_coliform_colonies_per100mL
## t = -1.5357, df = 1586, p-value = 0.1248
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.08755749 0.01067814
## sample estimates:
##      cor
## -0.03853277
```

```
#DO vs
cor.test(log_wetland$DO_mgL, log_wetland$pH)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$DO_mgL and log_wetland$pH
## t = 3.2221, df = 1592, p-value = 0.001298
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.03151886 0.12908014
## sample estimates:
##      cor
## 0.08049228
```



```
cor.test(log_wetland$DO_mgL, log_wetland$Unfiltered_TP_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$DO_mgL and log_wetland$Unfiltered_TP_ugL
## t = -13.143, df = 1601, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.3556007 -0.2671967
## sample estimates:
## cor
## -0.3120741
```

```
cor.test(log_wetland$DO_mgL, log_wetland$TSS_mgL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$DO_mgL and log_wetland$TSS_mgL
## t = -12.225, df = 1593, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.3371099 -0.2473462
## sample estimates:
## cor
## -0.2928732
```

```
cor.test(log_wetland$DO_mgL, log_wetland$fecal_coliform_colonies_per100mL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$DO_mgL and log_wetland$fecal_coliform_colonies_per100mL
## t = -12.178, df = 1579, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.3374361 -0.2472836
## sample estimates:
## cor
## -0.293011
```

```
#pH vs
```

```
cor.test(log_wetland$pH, log_wetland$Unfiltered_TP_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$pH and log_wetland$Unfiltered_TP_ugL
## t = -1.009, df = 1593, p-value = 0.3131
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
## -0.07426395 0.02383867
## sample estimates:
##      cor
## -0.02527349
```

```
cor.test(log_wetland$pH, log_wetland$TSS_mgL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$pH and log_wetland$TSS_mgL
## t = -5.518, df = 1585, p-value = 3.998e-08
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.18524460 -0.08868277
## sample estimates:
##      cor
## -0.1372898
```

```
cor.test(log_wetland$pH, log_wetland$fecal_coliform_colonies_per100mL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$pH and log_wetland$fecal_coliform_colonies_per100mL
## t = 3.6854, df = 1571, p-value = 0.0002361
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.04335689 0.14136109
## sample estimates:
##      cor
## 0.09258322
```

```
#TP vs
```

```
cor.test(log_wetland$Unfiltered_TP_ugL, log_wetland$TSS_mgL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Unfiltered_TP_ugL and log_wetland$TSS_mgL
## t = 13.204, df = 1600, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2686032 0.3569504
## sample estimates:
##      cor
## 0.3134549
```

```
cor.test(log_wetland$Unfiltered_TP_ugL, log_wetland$fecal_coliform_colonies_per100mL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Unfiltered_TP_ugL and log_wetland$fecal_coliform_colonies_per100mL
## t = 9.1415, df = 1580, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1767985 0.2704263
## sample estimates:
## cor
## 0.2241295
```

```
#TSS vs
cor.test(log_wetland$TSS_mgL, log_wetland$fecal_coliform_colonies_per100mL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$TSS_mgL and log_wetland$fecal_coliform_colonies_per100mL
## t = 6.2136, df = 1572, p-value = 6.617e-10
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1062316 0.2026864
## sample estimates:
## cor
## 0.1548279
```

```
#Predictor and Outcome Variable correlations
cor.test(log_wetland$Temp_C, log_wetland$Filtered_NHx_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Temp_C and log_wetland$Filtered_NHx_ugL
## t = 6.0746, df = 1592, p-value = 1.552e-09
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1021680 0.1981447
## sample estimates:
## cor
## 0.1505109
```

```
cor.test(log_wetland$SpCond_mScm, log_wetland$Filtered_NHx_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$SpCond_mScm and log_wetland$Filtered_NHx_ugL
## t = -0.95093, df = 1593, p-value = 0.3418
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.07281603 0.02529358
```

```
## sample estimates:
##      cor
## -0.02381858
```

```
cor.test(log_wetland$TDS_mgl, log_wetland$Filtered_NHx_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$TDS_mgl and log_wetland$Filtered_NHx_ugL
## t = -3.2848, df = 1592, p-value = 0.001043
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.13062002 -0.03308351
## sample estimates:
##      cor
## -0.08204823
```

```
cor.test(log_wetland$Sal_ppt, log_wetland$Filtered_NHx_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Sal_ppt and log_wetland$Filtered_NHx_ugL
## t = -0.78141, df = 1593, p-value = 0.4347
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.06859105 0.02953660
## sample estimates:
##      cor
## -0.01957436
```

```
cor.test(log_wetland$DO_mgL, log_wetland$Filtered_NHx_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$DO_mgL and log_wetland$Filtered_NHx_ugL
## t = -6.1243, df = 1585, p-value = 1.146e-09
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1997543 -0.1036115
## sample estimates:
##      cor
## -0.1520425
```

```
cor.test(log_wetland$pH, log_wetland$Filtered_NHx_ugL)
```

```
##
## Pearson's product-moment correlation
##
```

```
## data: log_wetland$pH and log_wetland$Filtered_NHx_ugL
## t = -1.4505, df = 1577, p-value = 0.1471
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.08567824 0.01285204
## sample estimates:
## cor
## -0.03650181
```

```
cor.test(log_wetland$Unfiltered_TP_ugL, log_wetland$Filtered_NHx_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$Unfiltered_TP_ugL and log_wetland$Filtered_NHx_ugL
## t = 7.1518, df = 1590, p-value = 1.302e-12
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1285240 0.2237266
## sample estimates:
## cor
## 0.1765381
```

```
cor.test(log_wetland$TSS_mgL, log_wetland$Filtered_NHx_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$TSS_mgL and log_wetland$Filtered_NHx_ugL
## t = 3.2923, df = 1583, p-value = 0.001016
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.03336349 0.13116986
## sample estimates:
## cor
## 0.08246524
```

```
cor.test(log_wetland$fecal_coliform_colonies_per100mL, log_wetland$Filtered_NHx_ugL)
```

```
##
## Pearson's product-moment correlation
##
## data: log_wetland$fecal_coliform_colonies_per100mL and log_wetland$Filtered_NHx_ugL
## t = 1.9234, df = 1565, p-value = 0.05461
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.0009589719 0.0978466011
## sample estimates:
## cor
## 0.04856262
```

SpCond and Sal are too correlated to use together - makes sense. Also all the predictor variables have very low correlations with the outcome variable :(

Step 3 - Fit regular regression model

I think I'm going to try three models.

```
#first convert Season to a factor
log_wetland$Season <- factor(log_wetland$Season,
                             levels = c('Winter', 'Spring', 'Summer', 'Fall'))

# fit regression models
mod1 <- lm(Filtered_NHx_ugL ~ Temp_C + pH + Season,
           data = log_wetland)

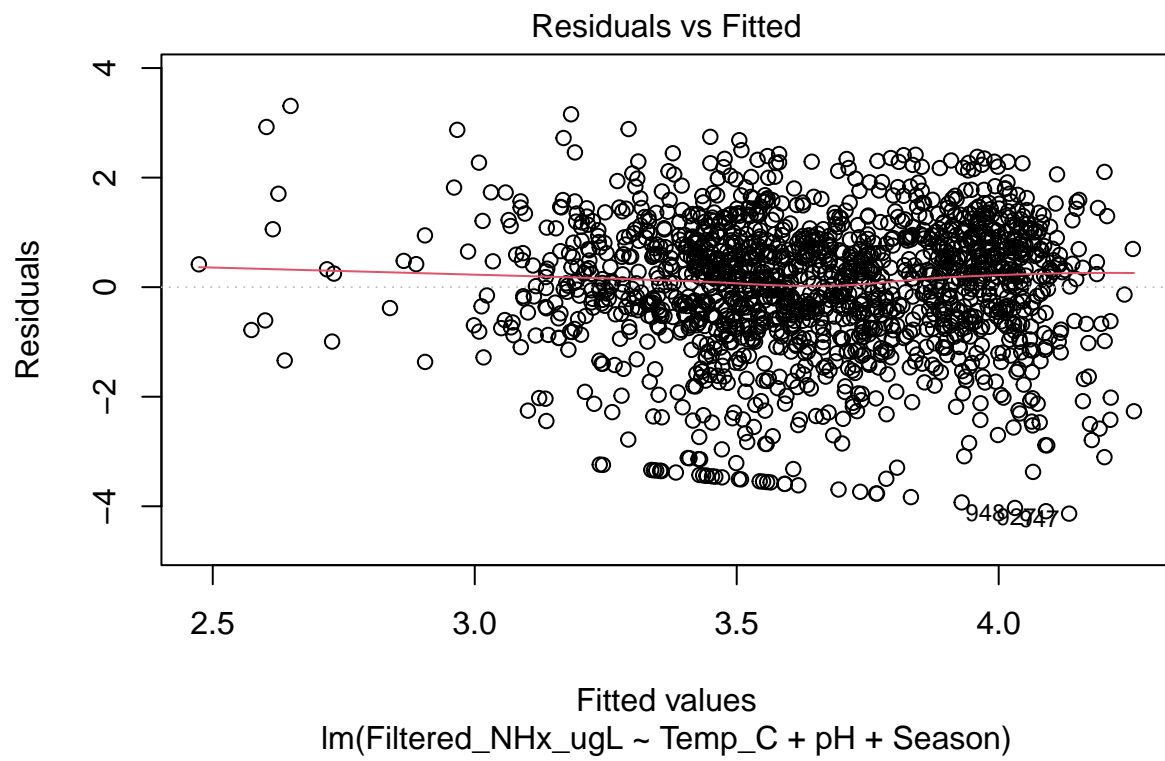
mod2 <- lm(Filtered_NHx_ugL ~ Temp_C + DO_mgL + Season,
           data = log_wetland)

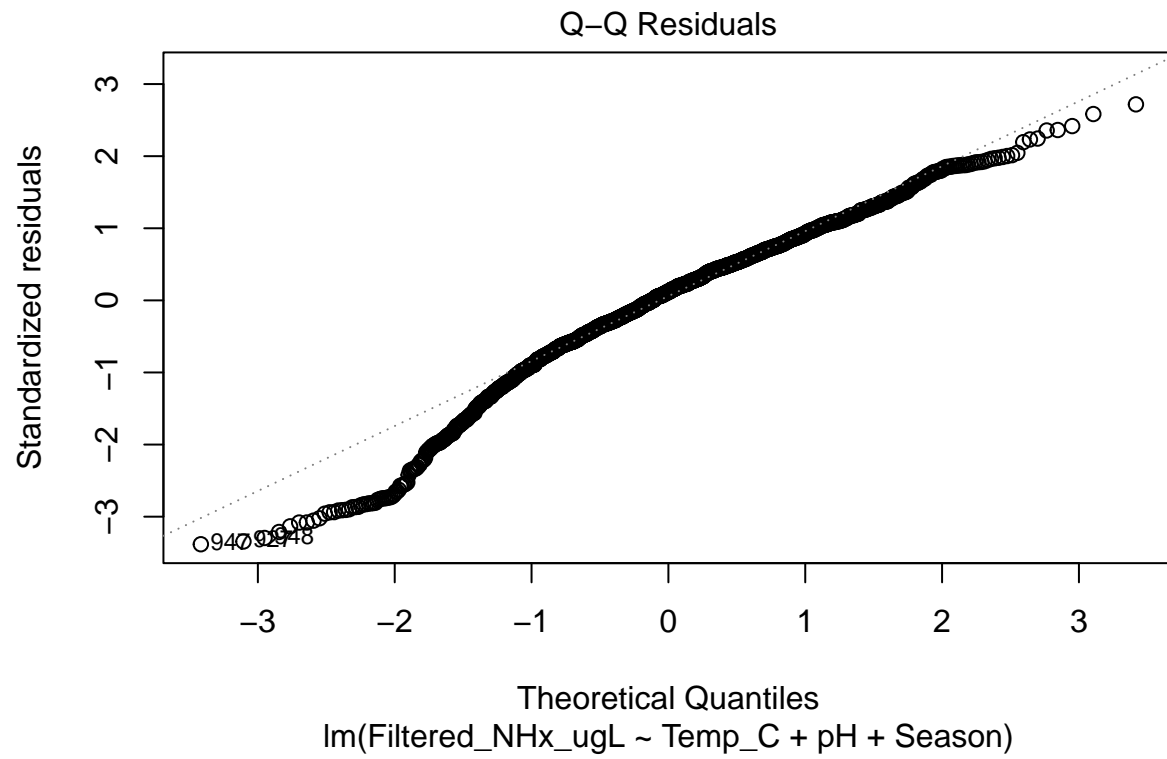
mod3 <- lm(Filtered_NHx_ugL ~ Unfiltered_TP_ugL + DO_mgL + Temp_C + pH + Season,
           data = log_wetland)

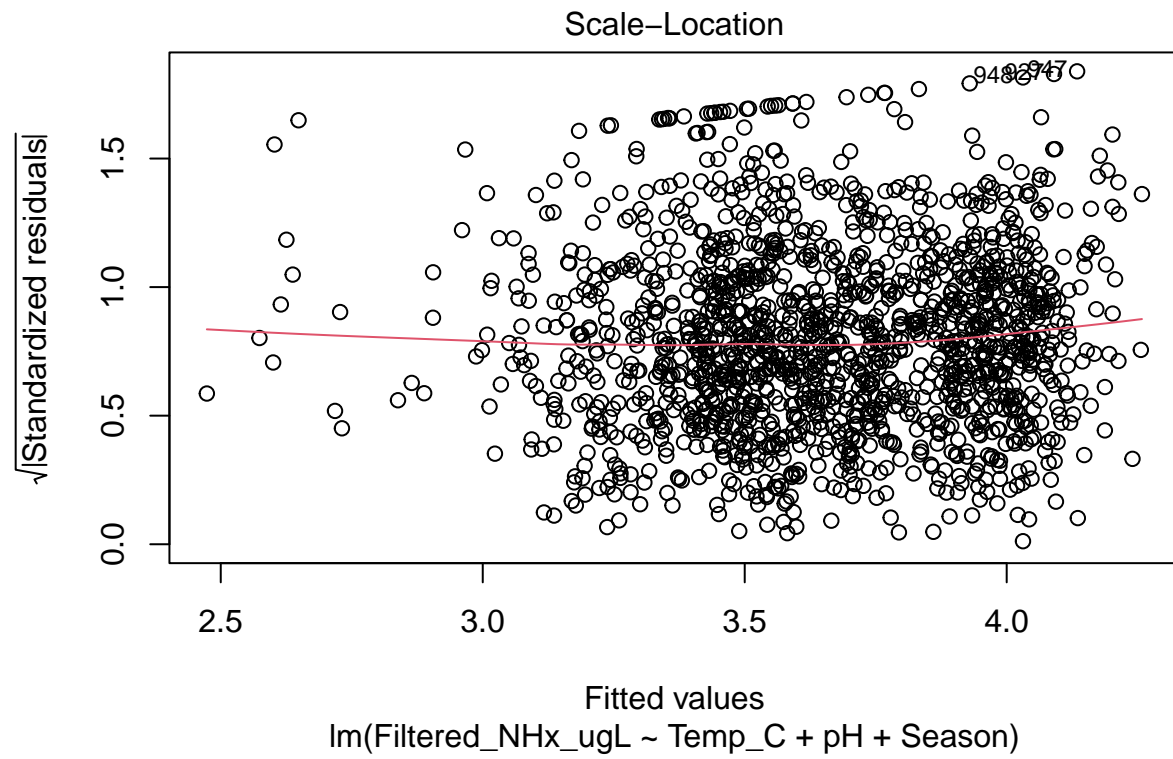
#examine model outputs and residuals
summary(mod1)
```

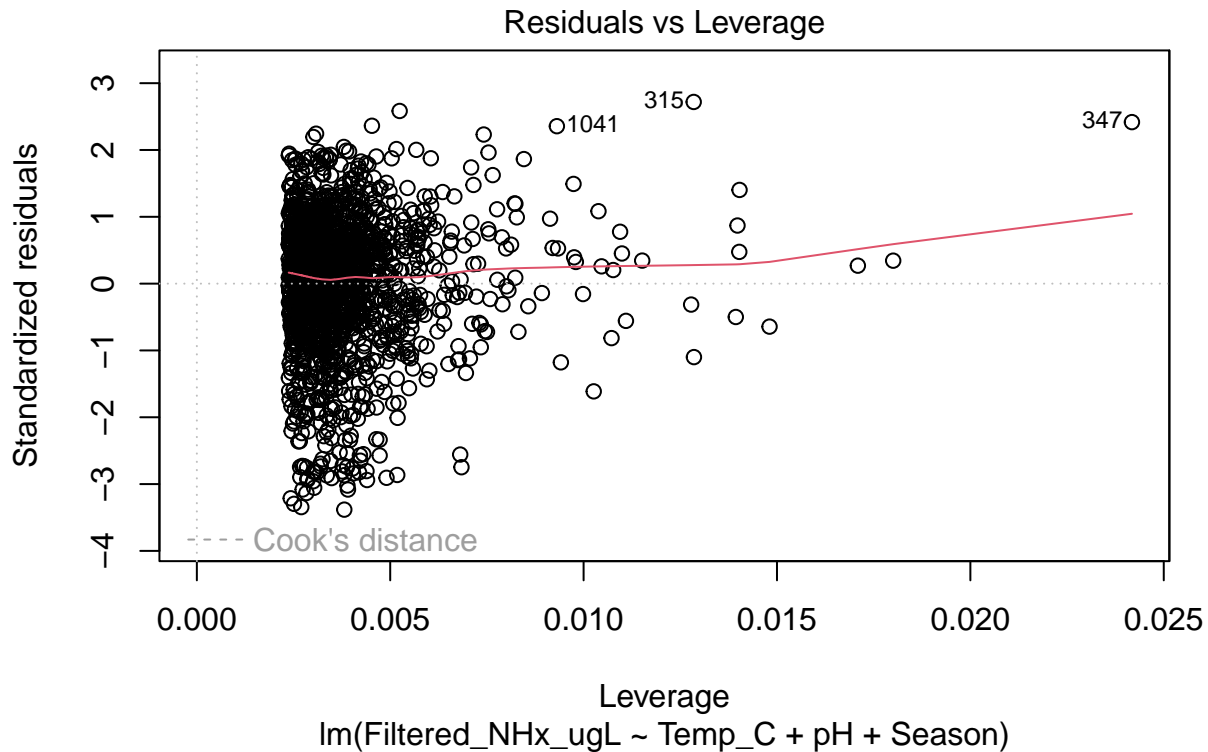
```
##
## Call:
## lm(formula = Filtered_NHx_ugL ~ Temp_C + pH + Season, data = log_wetland)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.1344 -0.6704  0.1464  0.8149  3.3082
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.2959     1.0247   5.168 2.67e-07 ***
## Temp_C         0.6293     0.1147   5.484 4.83e-08 ***
## pH            -1.5045     0.5010  -3.003  0.00272 **
## SeasonSpring  -0.1424     0.1045  -1.363  0.17314
## SeasonSummer  -0.1794     0.1429  -1.255  0.20956
## SeasonFall    -0.6032     0.1165  -5.177 2.55e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.225 on 1572 degrees of freedom
## (40 observations deleted due to missingness)
## Multiple R-squared:  0.05399,    Adjusted R-squared:  0.05098
## F-statistic: 17.94 on 5 and 1572 DF,  p-value: < 2.2e-16
```

```
plot(mod1)
```





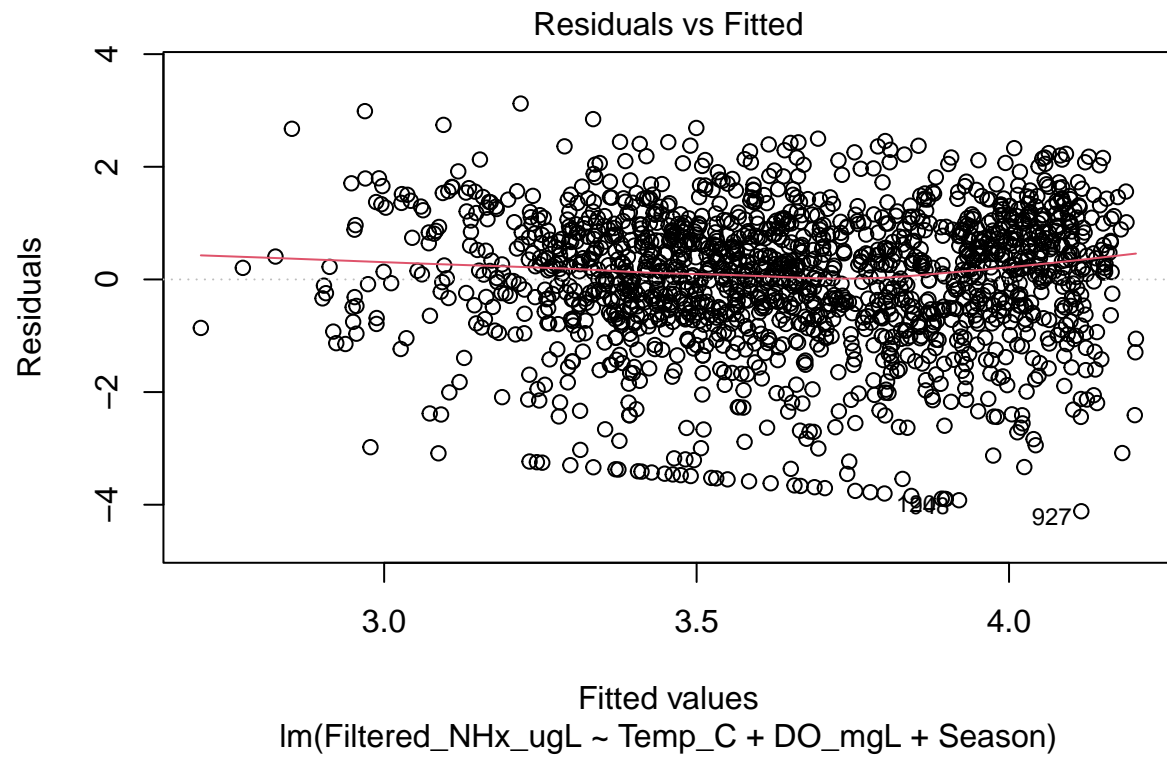


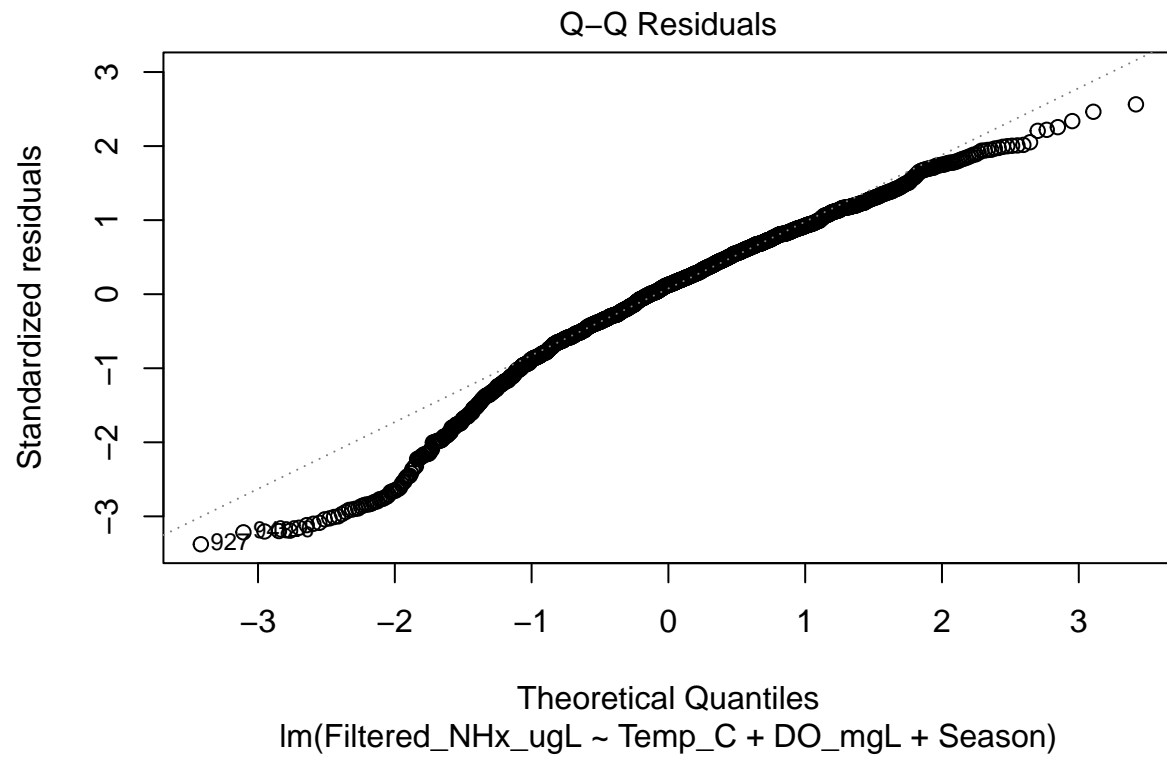


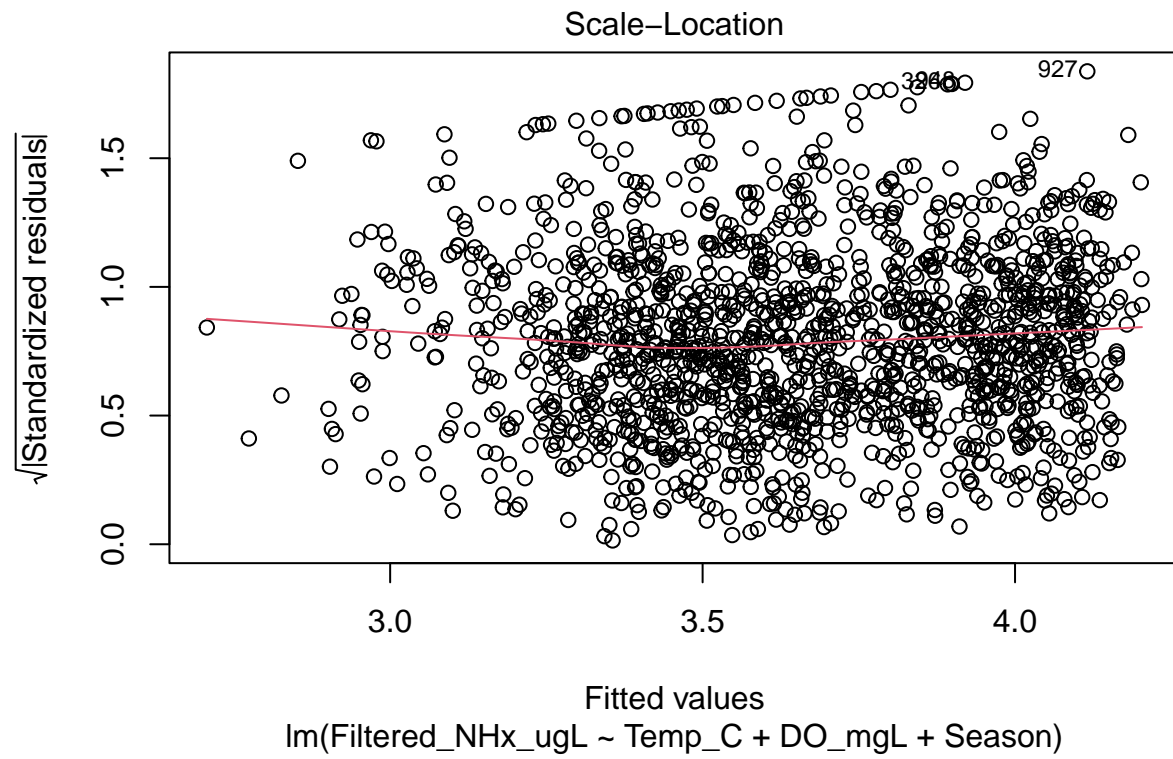
```
summary(mod2)
```

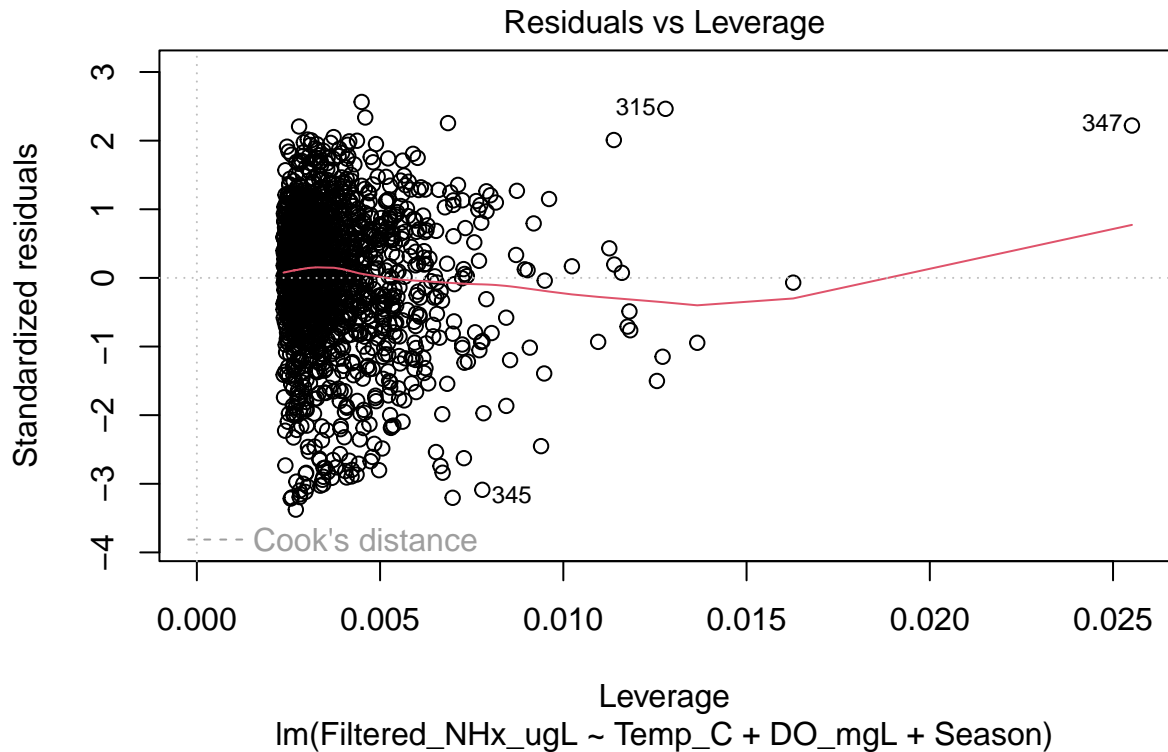
```
##
## Call:
## lm(formula = Filtered_NHx_ugL ~ Temp_C + DO_mgL + Season, data = log_wetland)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.1156 -0.6474  0.1531  0.8343  3.1220
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.956882   0.294948  10.025 < 2e-16 ***
## Temp_C        0.435346   0.116481   3.737 0.000192 ***
## DO_mgL       -0.038464   0.009327  -4.124 3.92e-05 ***
## SeasonSpring -0.157680   0.103794  -1.519 0.128923
## SeasonSummer -0.186690   0.142355  -1.311 0.189900
## SeasonFall   -0.607237   0.116167  -5.227 1.95e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.221 on 1580 degrees of freedom
## (32 observations deleted due to missingness)
## Multiple R-squared:  0.05771,    Adjusted R-squared:  0.05472
## F-statistic: 19.35 on 5 and 1580 DF,  p-value: < 2.2e-16
```

```
plot(mod2)
```







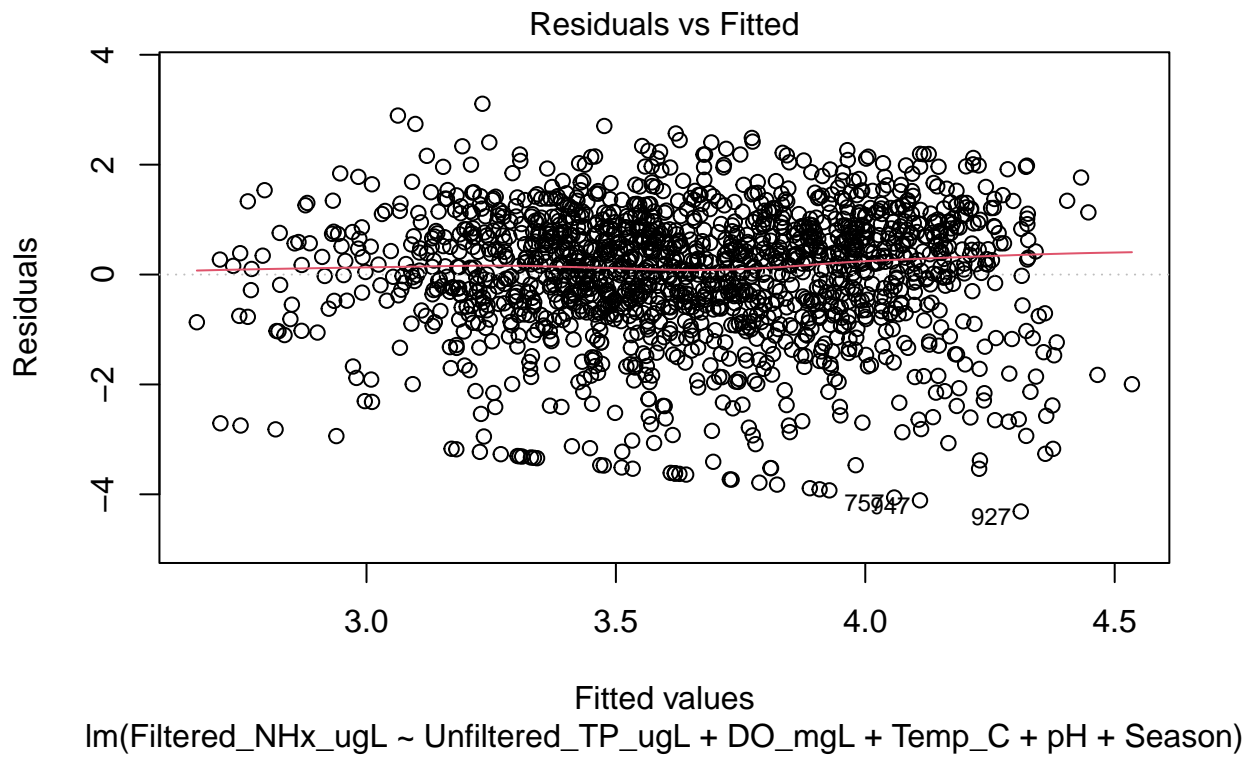


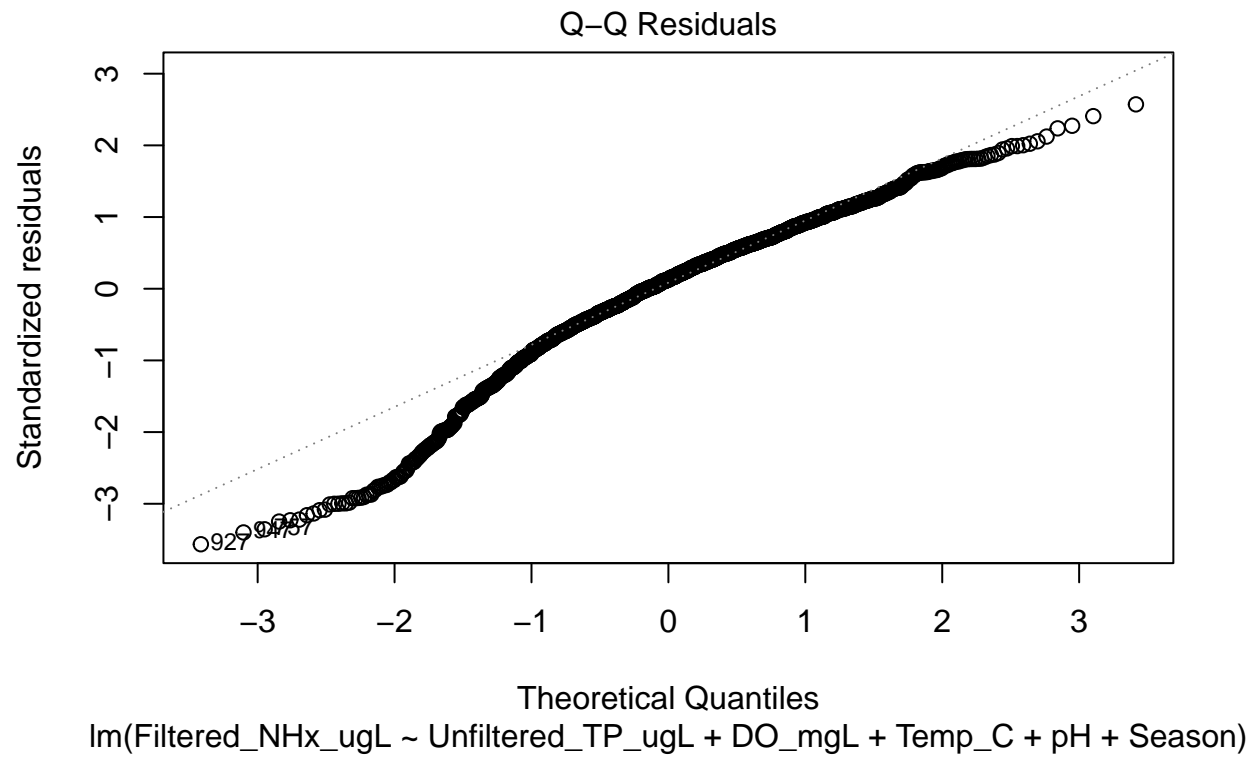
```
summary(mod3)
```

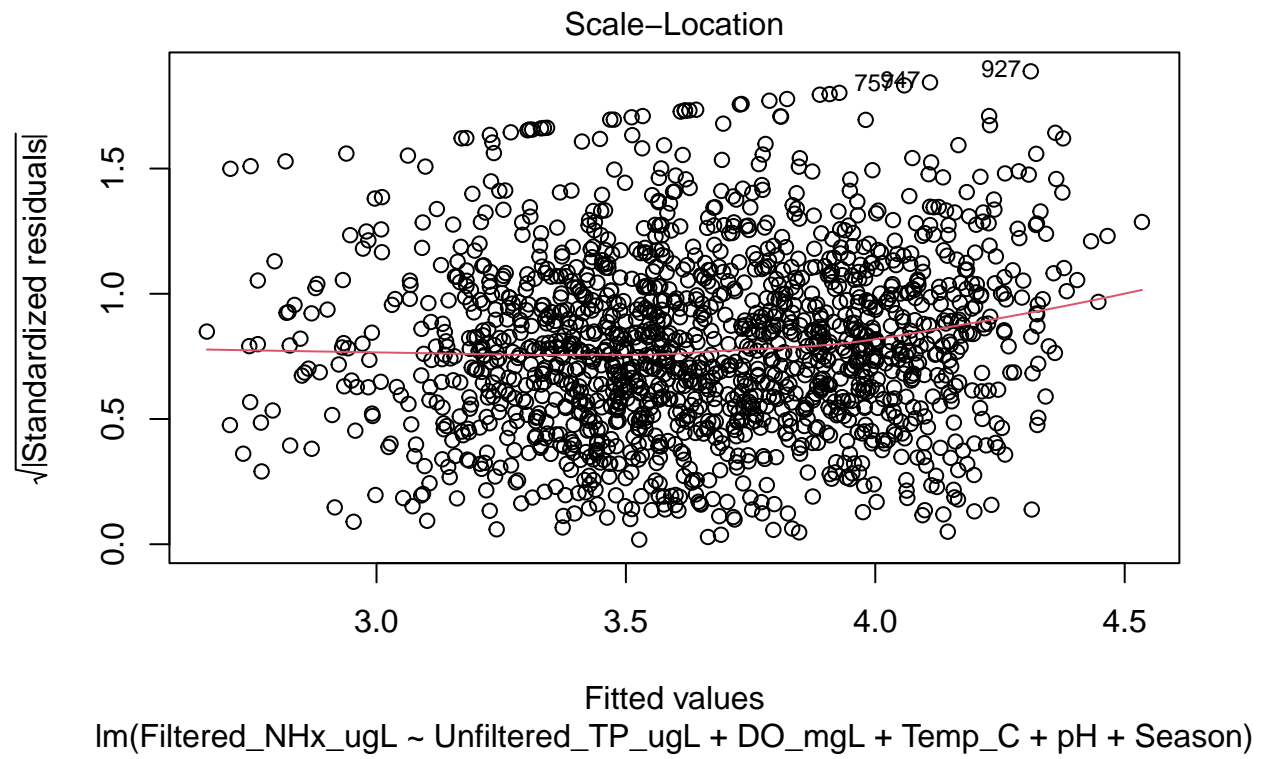
```
##
## Call:
## lm(formula = Filtered_NHx_ugL ~ Unfiltered_TP_ugL + DO_mgL +
##     Temp_C + pH + Season, data = log_wetland)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.3117 -0.6043  0.1580  0.8099  3.1079
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.329500    1.036961   4.175 3.14e-05 ***
## Unfiltered_TP_ugL  0.196591    0.041557   4.731 2.44e-06 ***
## DO_mgL         -0.026211    0.009653  -2.715 0.006696 **
## Temp_C          0.435711    0.119744   3.639 0.000283 ***
## pH             -1.113516    0.503705  -2.211 0.027205 *
## SeasonSpring    -0.108727    0.104773  -1.038 0.299552
## SeasonSummer    -0.186950    0.142830  -1.309 0.190763
## SeasonFall      -0.597691    0.117142  -5.102 3.77e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.212 on 1559 degrees of freedom
```

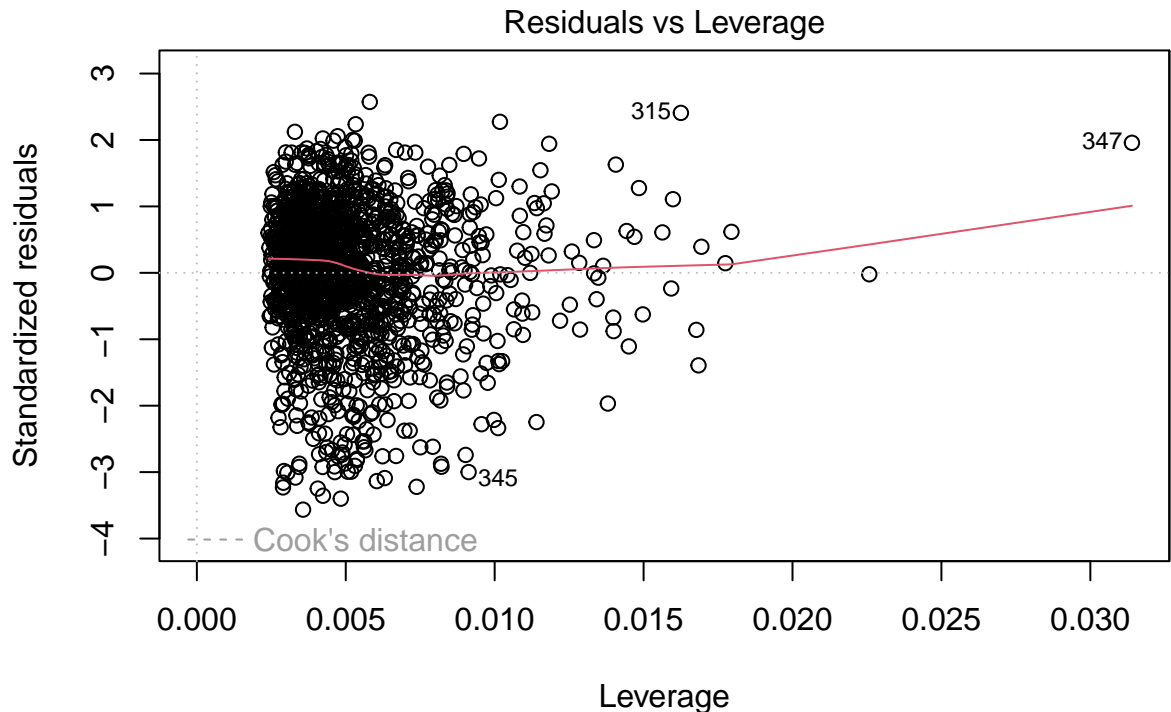
```
## (51 observations deleted due to missingness)
## Multiple R-squared:  0.07715,    Adjusted R-squared:  0.07301
## F-statistic: 18.62 on 7 and 1559 DF,  p-value: < 2.2e-16
```

```
plot(mod3)
```









lm(Filtered_NHx_ugL ~ Unfiltered_TP_ugL + DO_mgL + Temp_C + pH + Season)

Step 4 - Fit Mixed Effects Model

use gls model first

```
#remove NA's
log_wetland <- na.omit(log_wetland)

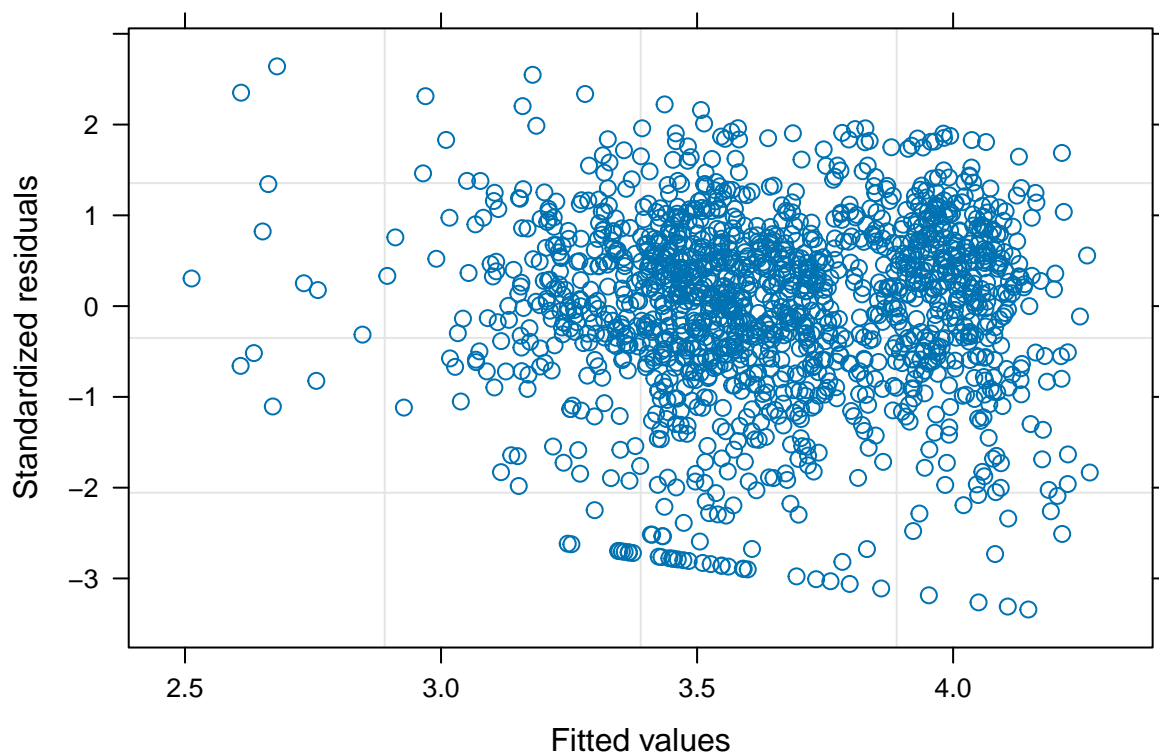
#first refit models using generalized least squares
GLS1 <- gls(Filtered_NHx_ugL ~ Temp_C + pH + Season,
            data = log_wetland)
GLS2 <- gls(Filtered_NHx_ugL ~ Temp_C + DO_mgL + Season,
            data = log_wetland)
GLS3 <- gls(Filtered_NHx_ugL ~ Temp_C + DO_mgL + Unfiltered_TP_ugL + pH + Season,
            data = log_wetland)

#look at model outputs
summary(GLS1)

## Generalized least squares fit by REML
## Model: Filtered_NHx_ugL ~ Temp_C + pH + Season
## Data: log_wetland
##      AIC      BIC    logLik
## 4840.145 4877.182 -2413.072
```

```
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept)  5.126820 1.0756002   4.766474  0.0000
## Temp_C       0.611359 0.1186534   5.152480  0.0000
## pH          -1.412880 0.5259019  -2.686585  0.0073
## SeasonSpring -0.120458 0.1080358  -1.114984  0.2650
## SeasonSummer -0.122891 0.1495183  -0.821915  0.4113
## SeasonFall   -0.564272 0.1214785  -4.645040  0.0000
##
## Correlation:
##              (Intr) Temp_C pH      SsnSpr SsnSmm
## Temp_C      -0.056
## pH          -0.970 -0.181
## SeasonSpring 0.019 -0.530  0.071
## SeasonSummer 0.042 -0.792  0.120  0.678
## SeasonFall  -0.004 -0.659  0.128  0.667  0.751
##
## Standardized residuals:
##              Min      Q1      Med      Q3      Max
## -3.3423242 -0.5500804  0.1361659  0.6730571  2.6411153
##
## Residual standard error: 1.240745
## Degrees of freedom: 1473 total; 1467 residual
```

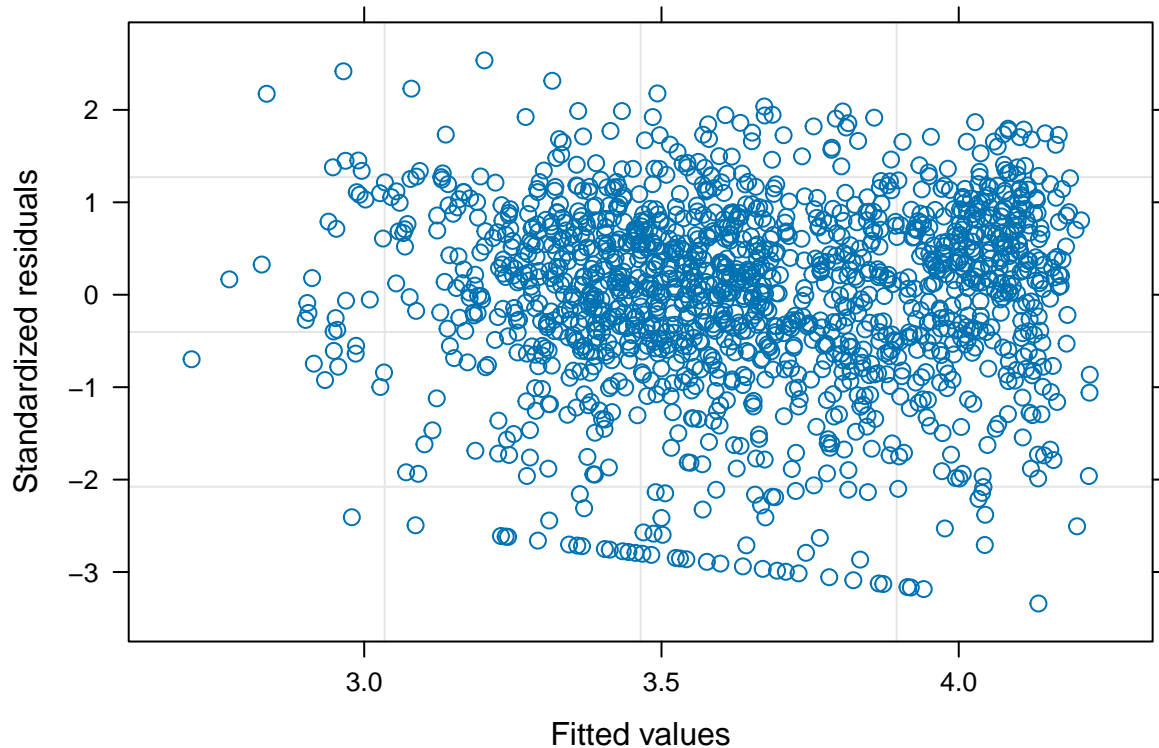
```
plot(GLS1)
```



```
summary(GLS2)
```

```
## Generalized least squares fit by REML
## Model: Filtered_NHx_ugL ~ Temp_C + DO_mgL + Season
## Data: log_wetland
##      AIC      BIC    logLik
## 4840.585 4877.622 -2413.292
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept)  2.9359811 0.3055417  9.609102  0.0000
## Temp_C       0.4337784 0.1205153  3.599365  0.0003
## DO_mgL      -0.0378829 0.0098527 -3.844922  0.0001
## SeasonSpring -0.1319048 0.1078101 -1.223492  0.2213
## SeasonSummer -0.1433860 0.1491303 -0.961481  0.3365
## SeasonFall   -0.5901672 0.1214520 -4.859264  0.0000
##
## Correlation:
##              (Intr) Temp_C DO_mgL SsnSpr SsnSmm
## Temp_C      -0.934
## DO_mgL      -0.521  0.259
## SeasonSpring 0.268 -0.487  0.077
## SeasonSummer 0.494 -0.725  0.120  0.679
## SeasonFall   0.346 -0.585  0.145  0.667  0.752
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -3.3404551 -0.5378194  0.1342968  0.6847263  2.5356795
##
## Residual standard error: 1.237574
## Degrees of freedom: 1473 total; 1467 residual
```

```
plot(GLS2)
```



```
summary(GLS3)
```

```
## Generalized least squares fit by REML
## Model: Filtered_NHx_ugL ~ Temp_C + DO_mgL + Unfiltered_TP_ugL + pH + Season
## Data: log_wetland
##      AIC      BIC    logLik
## 4822.34 4869.946 -2402.17
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept)   4.107441 1.0893839   3.770426  0.0002
## Temp_C         0.418140 0.1232538   3.392510  0.0007
## DO_mgL        -0.023774 0.0101541  -2.341363  0.0193
## Unfiltered_TP_ugL 0.206228 0.0445620   4.627883  0.0000
## pH            -1.022281 0.5260554  -1.943295  0.0522
## SeasonSpring  -0.078643 0.1081220  -0.727350  0.4671
## SeasonSummer  -0.137587 0.1489750  -0.923560  0.3559
## SeasonFall    -0.557091 0.1219153  -4.569495  0.0000
##
## Correlation:
##              (Intr) Temp_C DO_mgL U_TP_L pH      SsnSpr SsnSmm
## Temp_C      -0.030
## DO_mgL      -0.065  0.240
## Unfiltered_TP_ugL -0.214 -0.127  0.237
## pH          -0.947 -0.215 -0.120  0.056
```

```
## SeasonSpring      -0.012 -0.497  0.098  0.135  0.068
## SeasonSummer       0.026 -0.727  0.115  0.058  0.107  0.681
## SeasonFall        -0.029 -0.597  0.150  0.110  0.114  0.673  0.755
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -3.5243055 -0.5007331  0.1487491  0.6738212  2.5195716
##
## Residual standard error: 1.227459
## Degrees of freedom: 1473 total; 1465 residual
```

```
plot(GLS3)
```

