Vermont Watersheds: Regressions and Trend Analyses

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Part 1: Analysis of New Haven River and Little Otter Creek

My team and I are interested in analysing hydrological data collected from Vermont watersheds. This data set contains mean Turbidity values (in NTUs) and mean Total Phosphorus (TP) concentrations (in ug/L) measured at five water quality monitoring stations in the Little Otter Creek watershed and six stations in the New Haven River watershed.

Also included are the percentages of agricultural land use (Perc_Ag) and percentages of glaciolacustrine soils (Perc_GL) contained in the immediate river corridor of the incremental watershed areas draining to each station. Glaciolacustrine soils are silt- and clay-rich sediments deposited in fresh-water of marine-water lakes by glacial meltwater.

Let's begin. First, we will read in and view the data set:

```
library(readr)
library(ggplot2)
```

```
## Registered S3 methods overwritten by 'ggplot2':
##   method         from
##   [.quosures     rlang
##   c.quosures     rlang
##   print.quosures rlang
```

```
library(ggpmisc)
```

```
## For news about 'ggpmisc', please, see https://www.r4photobiology.info/
```

```
library(Kendall)
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
```

```
df <- read_csv("WQ_LOC_NHR.csv")
```

```
## Parsed with column specification:
## cols(
##   Watershed = col_character(),
##   WQ_Subwatershed = col_character(),
##   Incr_Area_sqmi = col_double(),
##   Perc_GL = col_double(),
##   Perc_Ag = col_double(),
##   Turb_mn = col_double(),
##   TP_mn = col_double()
## )
```

```
df
```

```
## # A tibble: 11 x 7
##    Watershed WQ_Subwatershed Incr_Area_sqmi Perc_GL Perc_Ag Turb_mn TP_mn
##    <chr>     <chr>                    <dbl>   <dbl>   <dbl>   <dbl> <dbl>
##  1 LOC       LOC4.3                   1.03   92.3     71.5    59.9  136.
##  2 LOC       LOC7.8                   1.14   80.2     52.8    74.9  168.
##  3 LOC       LOC10                    3.06   73.2     58.5    50.6  156.
##  4 LOC       LOC14.4                  1.18   55.5     49.9    40.2  154.
##  5 LOC       MDC1.2                   1.17   91.4     69.8    25.9  205.
##  6 NHR       NHR0.5                   0.37   50.2     60.8     6.05  28.7
##  7 NHR       NHR2                     3.97   38.3     34.4     7.05  30.4
##  8 NHR       NHR6                     0.729  24.3     41.9     2.09  16.7
##  9 NHR       NHR9                     1.87    0.825    7.44    2.14  21.8
## 10 NHR       NHR11.5                  2.74    0.323    6.25    1.13  12.5
## 11 NHR       NHR15                    2.73    0.325    4.31    1.17  11.3
```

Before conducting a regression analysis, we must investigate whether or not these variables (TP_mn, Turb_mn, Perc_GL, and Perc_Ag) are normally distributed. We can run the Shapiro-Wilks Test for Normality at the 95% confidence level. The null hypothesis of this test states that the data are normally distributed. As the output shows below, this test indicates that the variables TP_mn and Turb_mn are not normally distributed:

```
shapiro.test(df$TP_mn) # p-value = 0.01027, alpha = 0.05, reject null
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df$TP_mn
## W = 0.8029, p-value = 0.01027
```

```
shapiro.test(df$Turb_mn) # p-value = 0.02182, reject null
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df$Turb_mn
## W = 0.82776, p-value = 0.02182
```

```
shapiro.test(df$Perc_GL) # p-value = 0.1698, fail to reject null
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df$Perc_GL
## W = 0.89699, p-value = 0.1698
```

```
shapiro.test(df$Perc_Ag) # p-value = 0.09962, fail to reject null
```

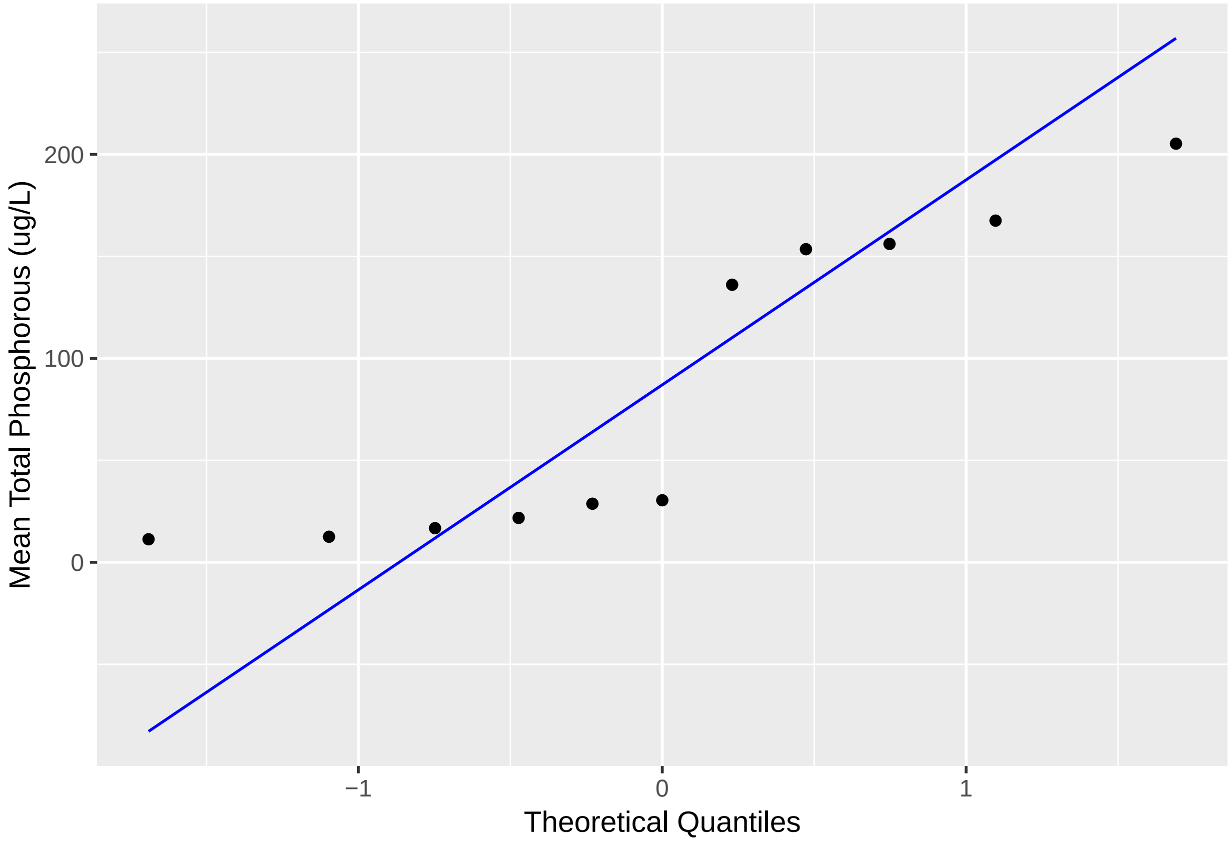
```
##
##  Shapiro-Wilk normality test
##
## data:  df$Perc_Ag
## W = 0.87851, p-value = 0.09962
```

The output of these tests suggest the following:

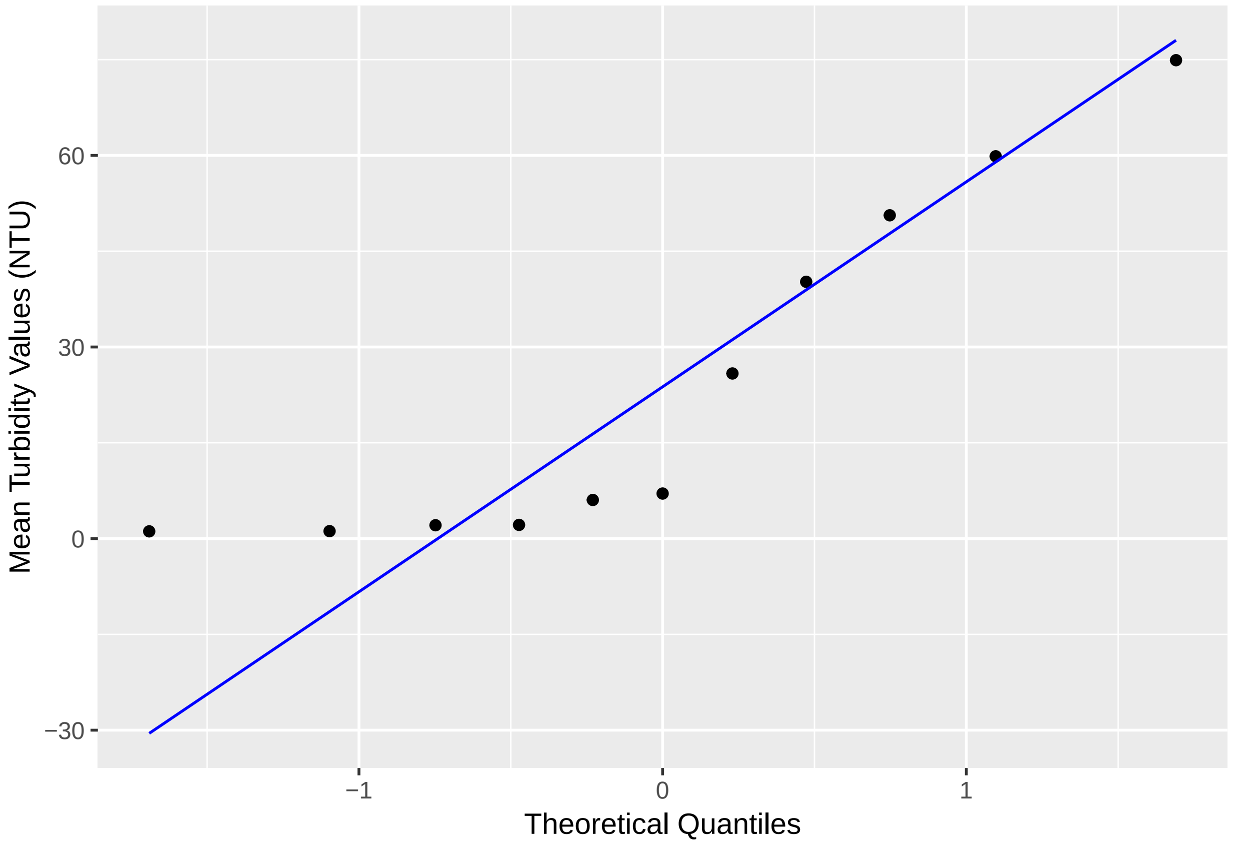
1. TP_mn: we reject the null in favor of the alternate (p = 0.01). This variable is not likely to be normally distributed.
2. Turb_mn: we reject the null in favor of the alternate (p = 0.02). This variable is not likely to be normally distributed.
3. Perc_GL: we accept the null hypothesis that this variable is normally distributed (p = 0.17).
4. Perc_Ag: we accept the null hypothesis that this variable is normally distributed (p = 0.10).

We can further investigate this by creating quantile-quantile plots, also known as Q-Q plots. On a Q-Q plot, normally distributed data appears as roughly a straight line (although the ends of the Q-Q plot may start to deviate from the straight line).

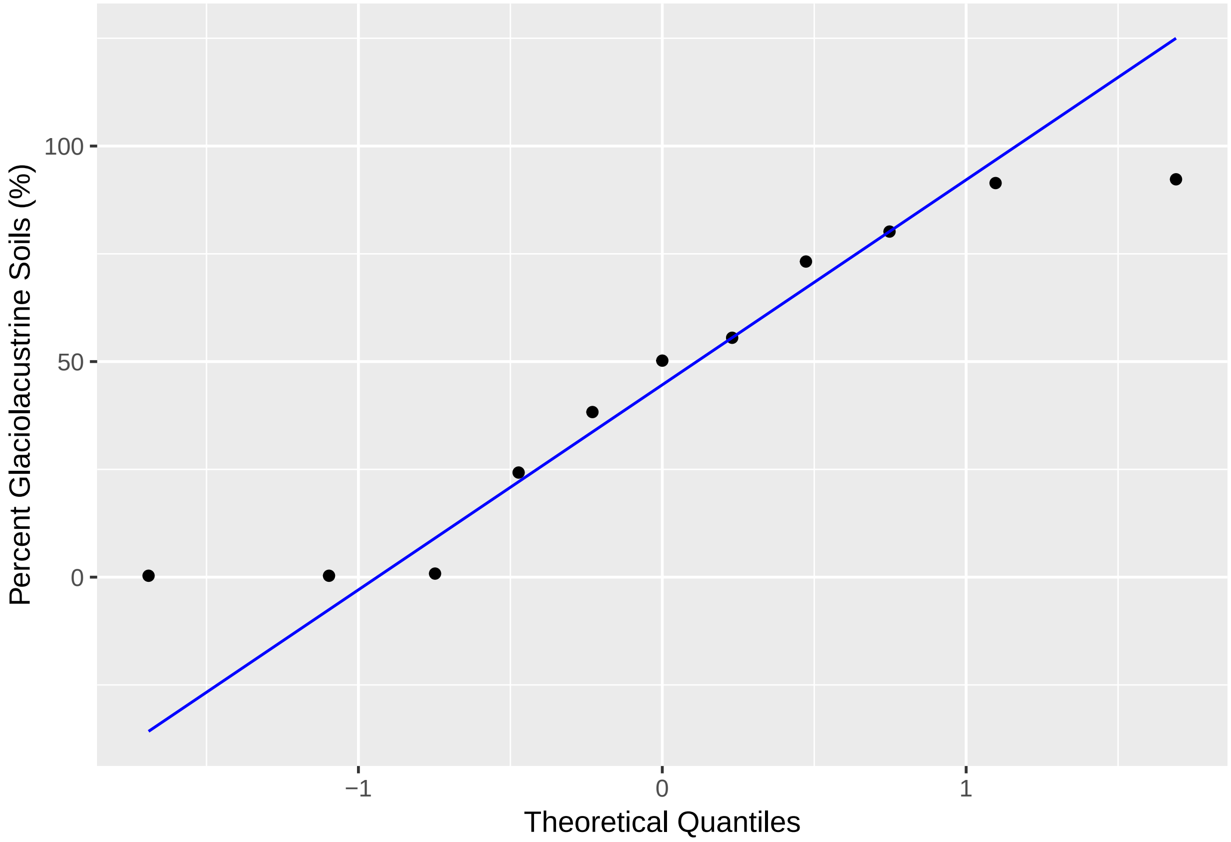
```
ggplot(df, aes(sample = TP_mn)) +
  stat_qq() +
  geom_qq_line(col = "blue") +
  labs(x = "Theoretical Quantiles",
       y = "Mean Total Phosphorous (ug/L)")
```



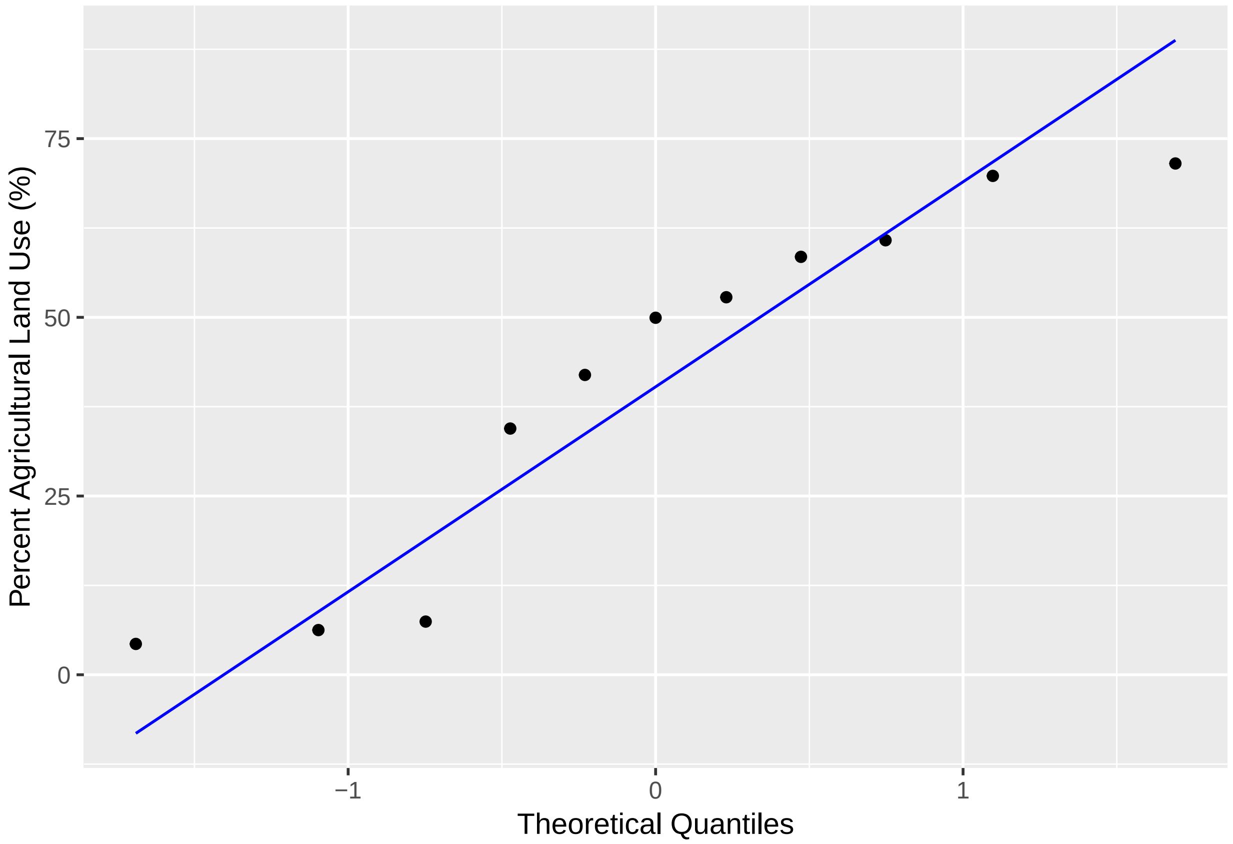
```r
ggplot(df, aes(sample = Turb_mn)) +
  stat_qq() +
  geom_qq_line(col = "blue") +
  labs(x = "Theoretical Quantiles",
       y = "Mean Turbidity Values (NTU)")
```



```
ggplot(df, aes(sample = Perc_GL)) +
  stat_qq() +
  geom_qq_line(col = "blue") +
  labs(x = "Theoretical Quantiles",
       y = "Percent Glaciolacustrine Soils (%)")
```



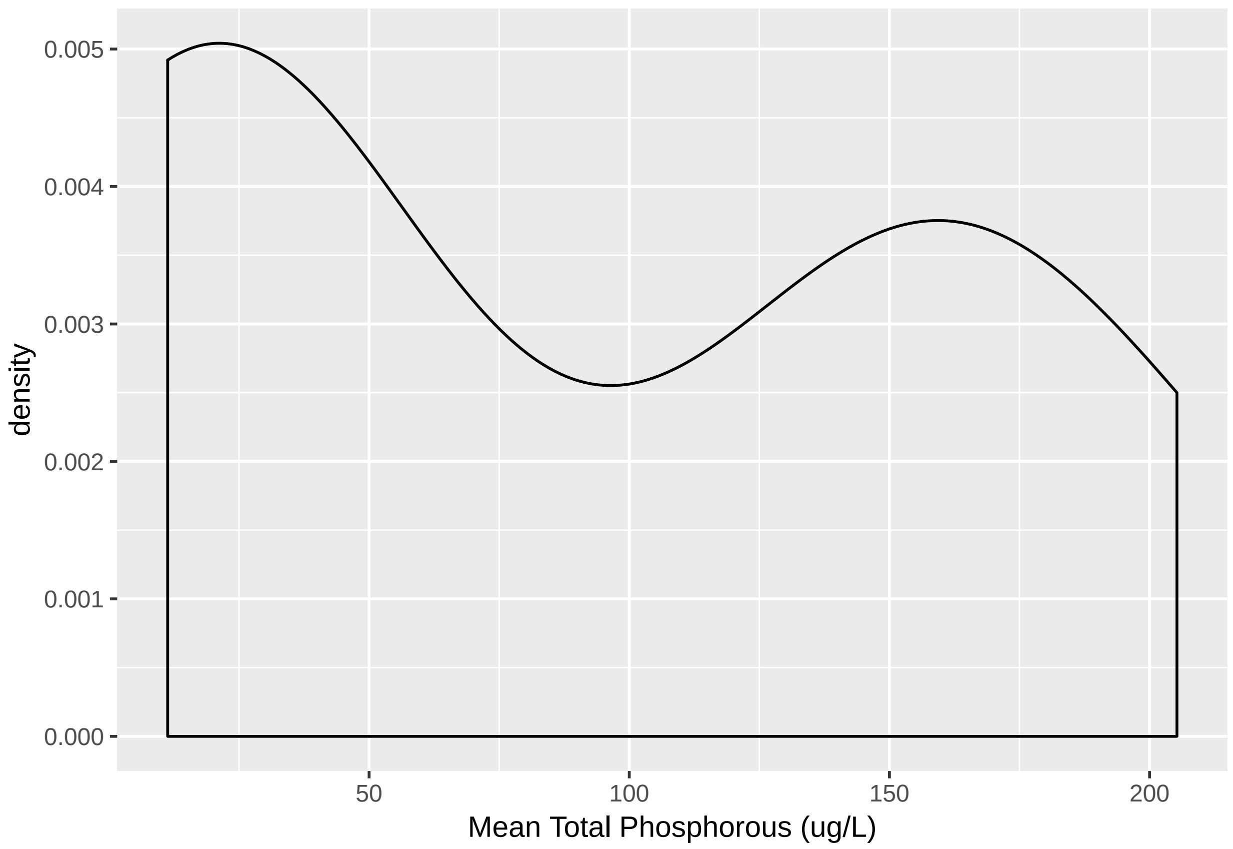
```
ggplot(df, aes(sample = Perc_Ag)) +
  stat_qq() +
  geom_qq_line(col = "blue") +
  labs(x = "Theoretical Quantiles",
       y = "Percent Agricultural Land Use (%)")
```



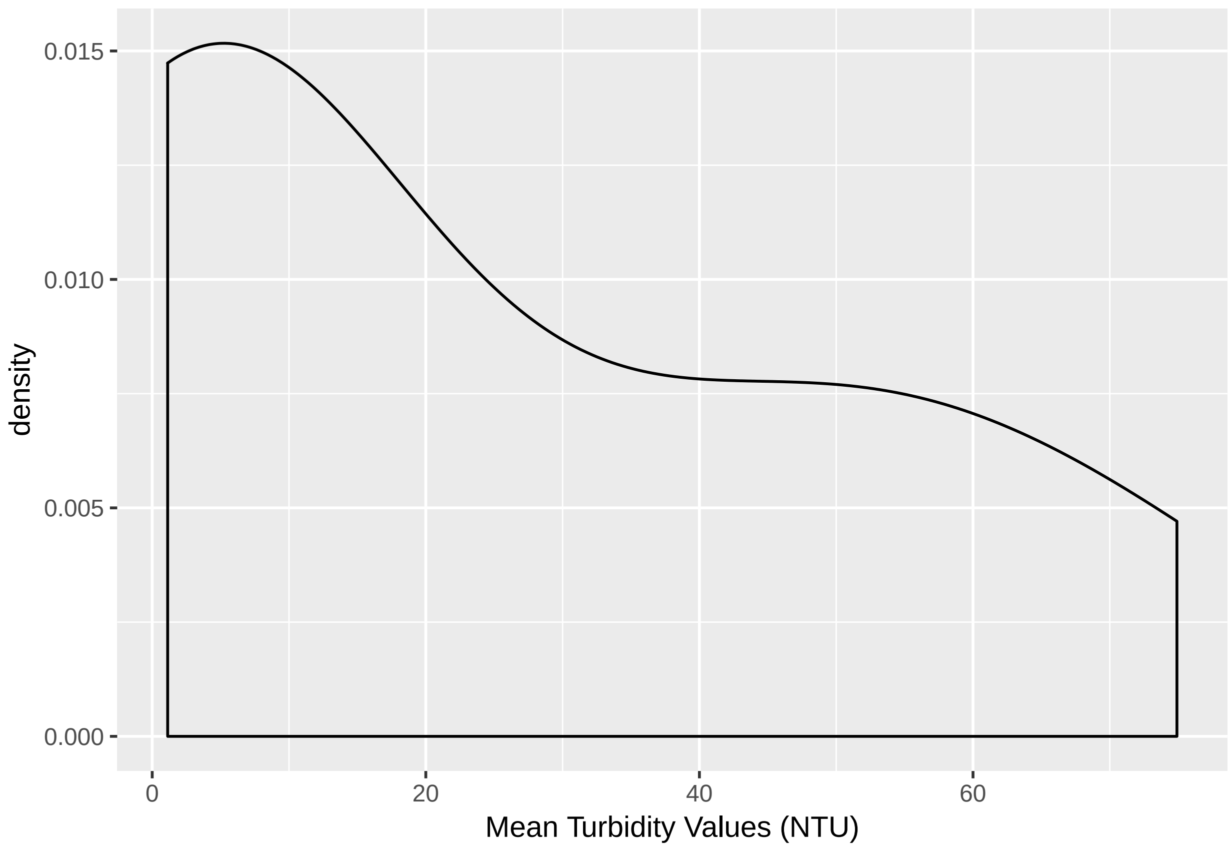
From visual inspection of these Q-Q plots, the variables TP_mn and Turb_mn do not appear to be normally distributed.

But what do the density distributions of these variables look like? Do they further confirm our suspicions?

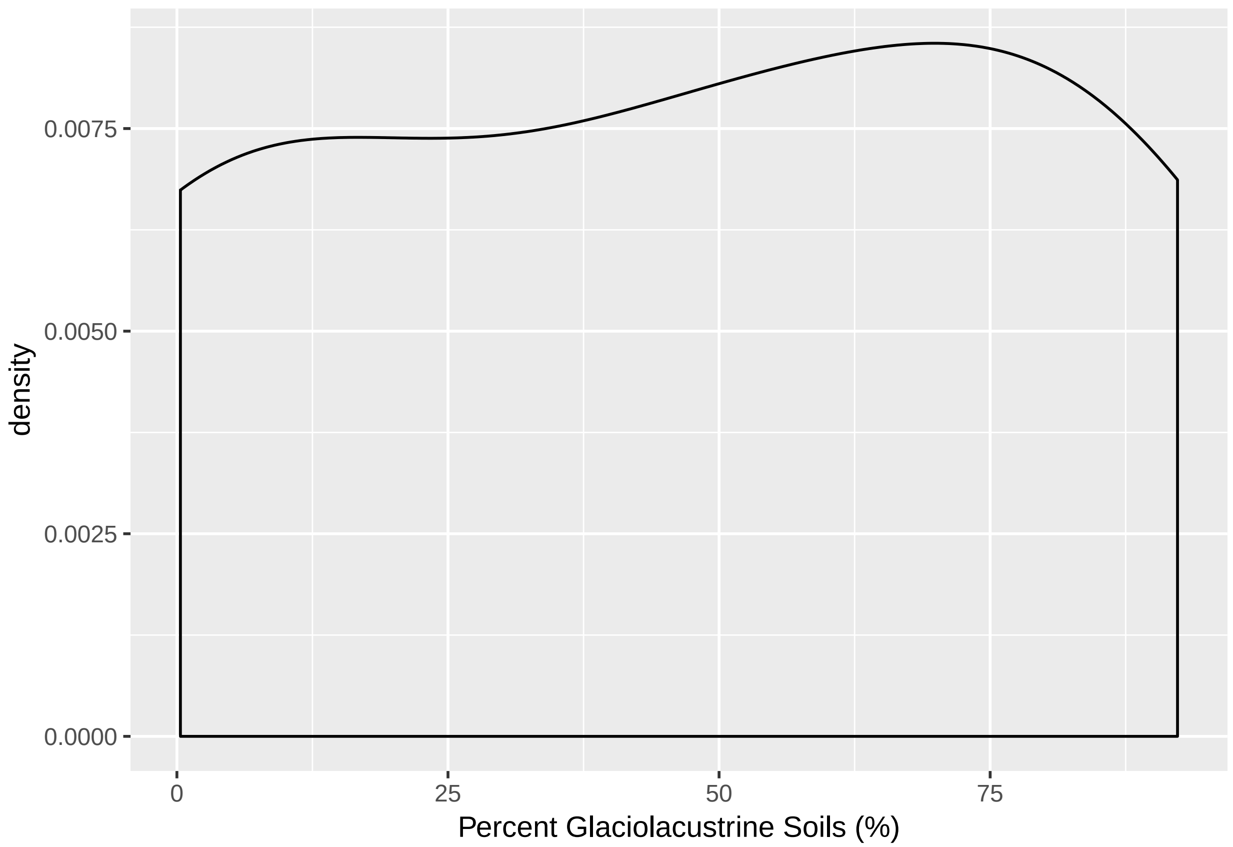
```r
ggplot(df, aes(x = TP_mn)) +
  geom_density() +
  xlab("Mean Total Phosphorous (ug/L)")
```



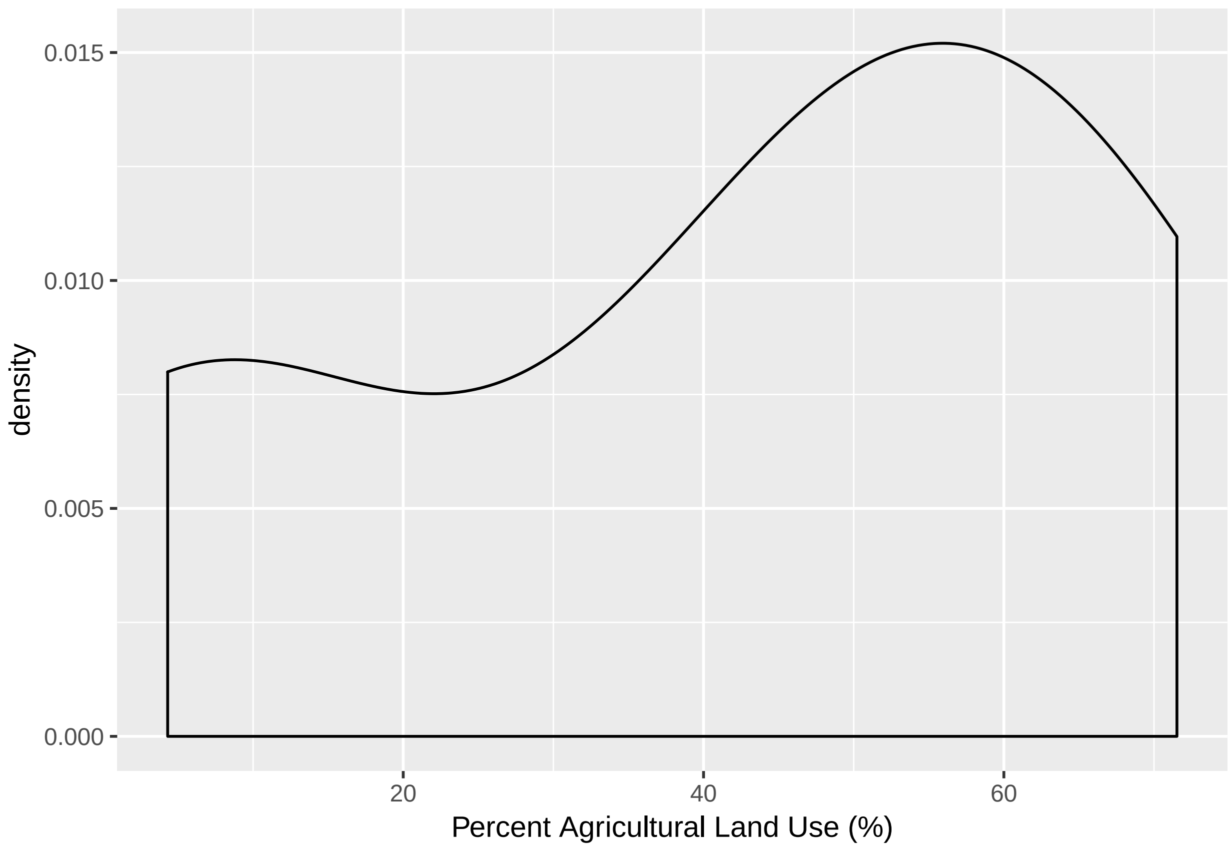
```
ggplot(df, aes(x = Turb_mn)) +
  geom_density() +
  xlab("Mean Turbidity Values (NTU)")
```



```r
ggplot(df, aes(x = Perc_GL)) +
  geom_density() +
  xlab("Percent Glaciolacustrine Soils (%)")
```



```r
ggplot(df, aes(x = Perc_Ag)) +
  geom_density() +
  xlab("Percent Agricultural Land Use (%)")
```



Yes, they do. We are confident that Perc_GL and Perc_Ag are normally distributed variables, while TP_mn and Turb_mn are not.

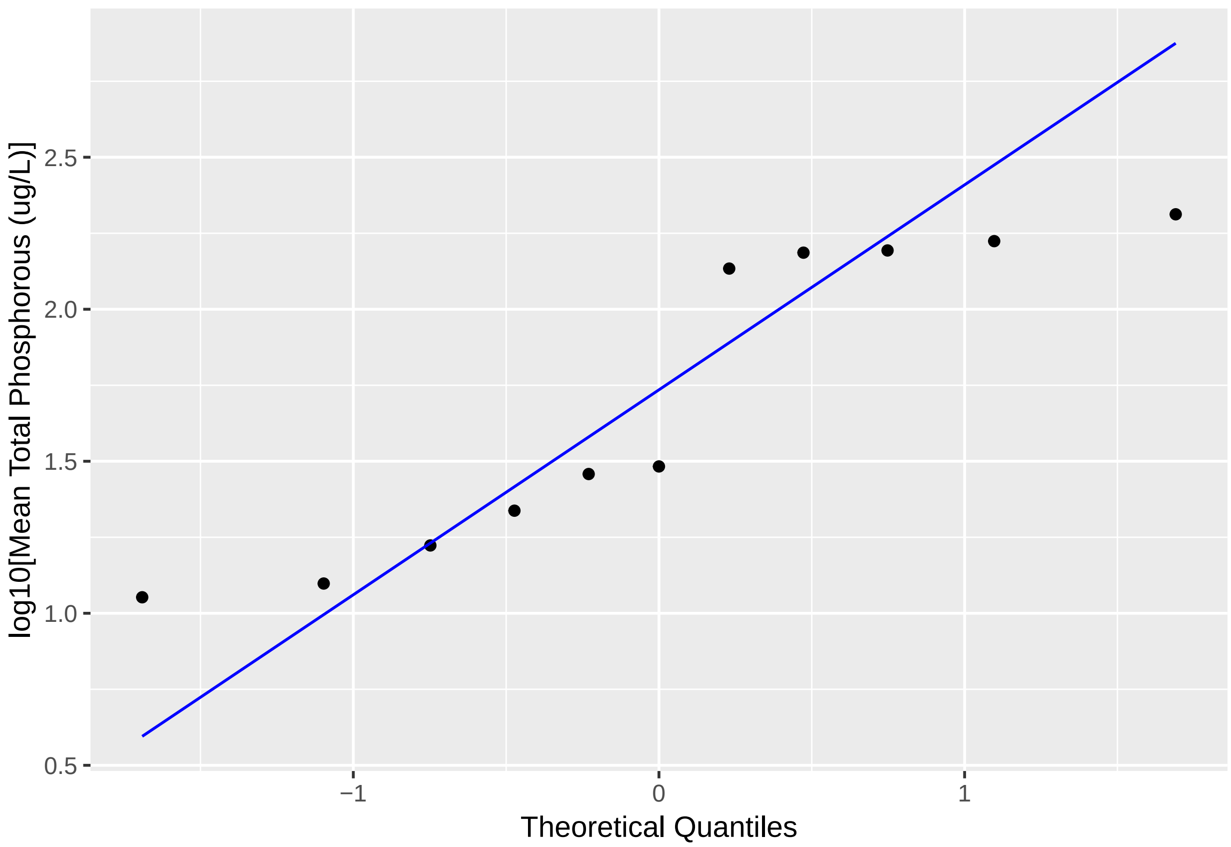
Because this is raw data from a real-world example, we cannot expect perfect bell curves. However, the bimodal distribution curves for the variables TP_mn and Turb_mn further build our case that they are not normally distributed.

Therefore, we shall transform these water quality variables using a log10 tranformation:

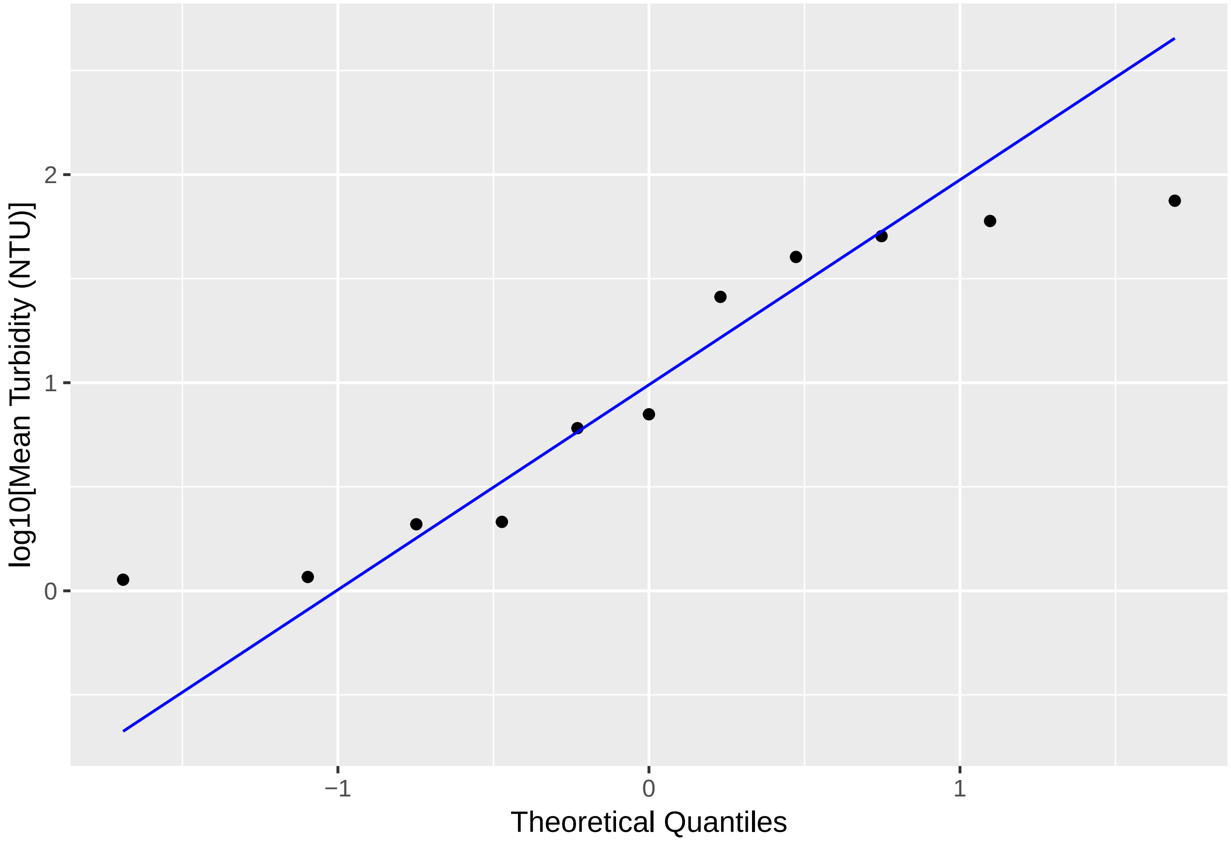
```
df$log10_TP_mn <- log10(df$TP_mn)
df$log10_Turb_mn <- log10(df$Turb_mn)
```

Did this work to transform the data to a nearly normal distribution? Let's check the Q-Q plots:

```
ggplot(df, aes(sample = log10_TP_mn)) +
  stat_qq() +
  geom_qq_line(col = "blue") +
  labs(x = "Theoretical Quantiles",
       y = "log10[Mean Total Phosphorous (ug/L)]")
```



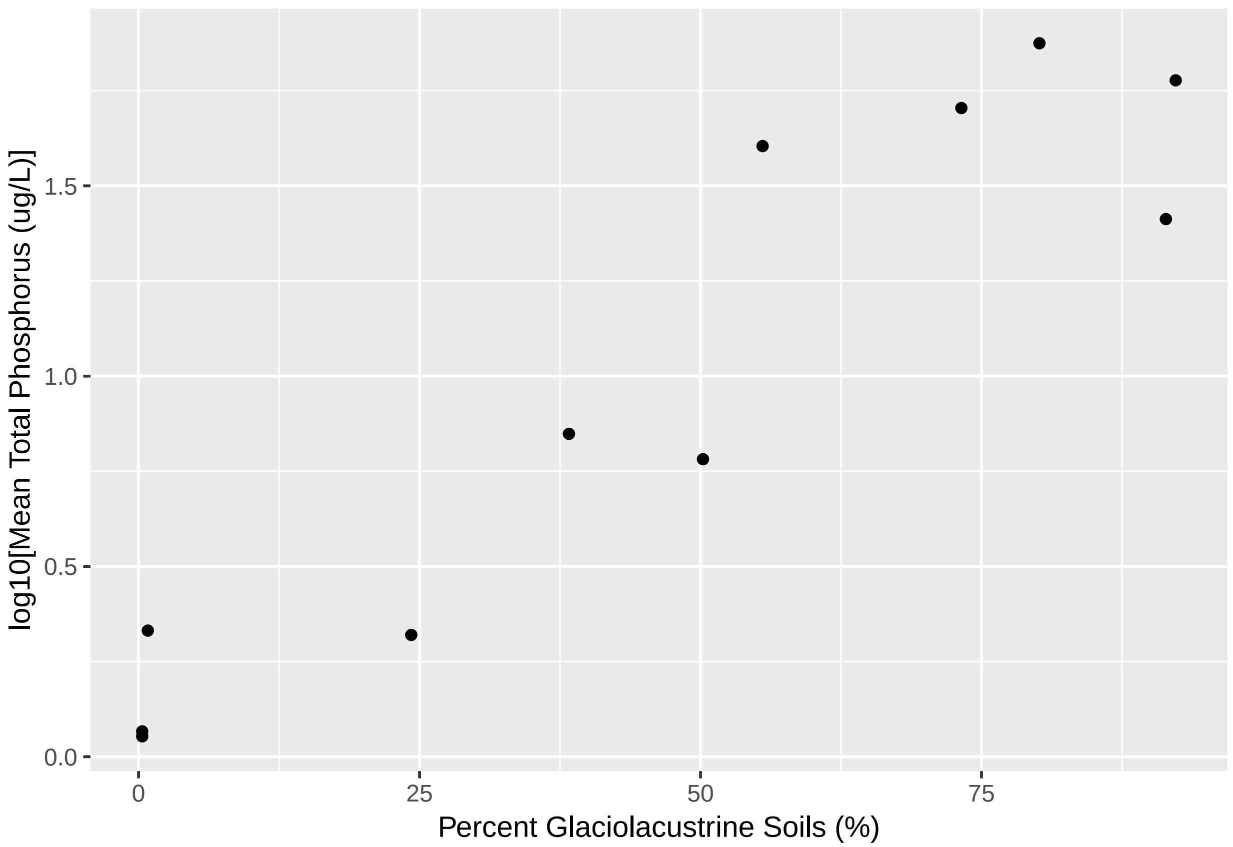
```
ggplot(df, aes(sample = log10_Turb_mn)) +
  stat_qq() +
  geom_qq_line(col = "blue") +
  labs(x = "Theoretical Quantiles",
       y = "log10[Mean Turbidity (NTU)]")
```



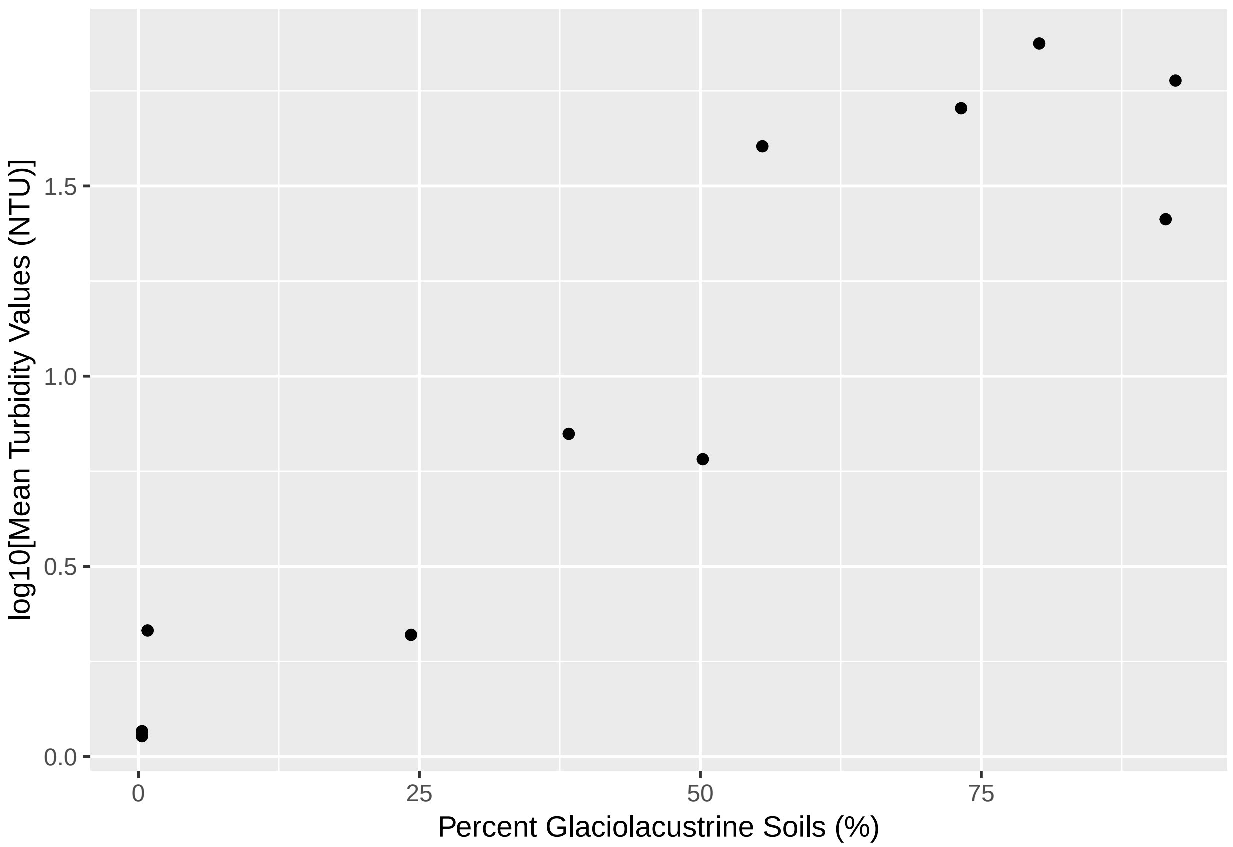
Turb_mn seems to have improved much more from this transformation than TP_mn. We can see that in this transformed Turb-mn Q-Q plot, the deviations from the straight line are minimal when compared to the non-transformed plot above. Visual inspection shows us that there is slight improvement to the TP_mn variable.

Next, let's visualize the data:

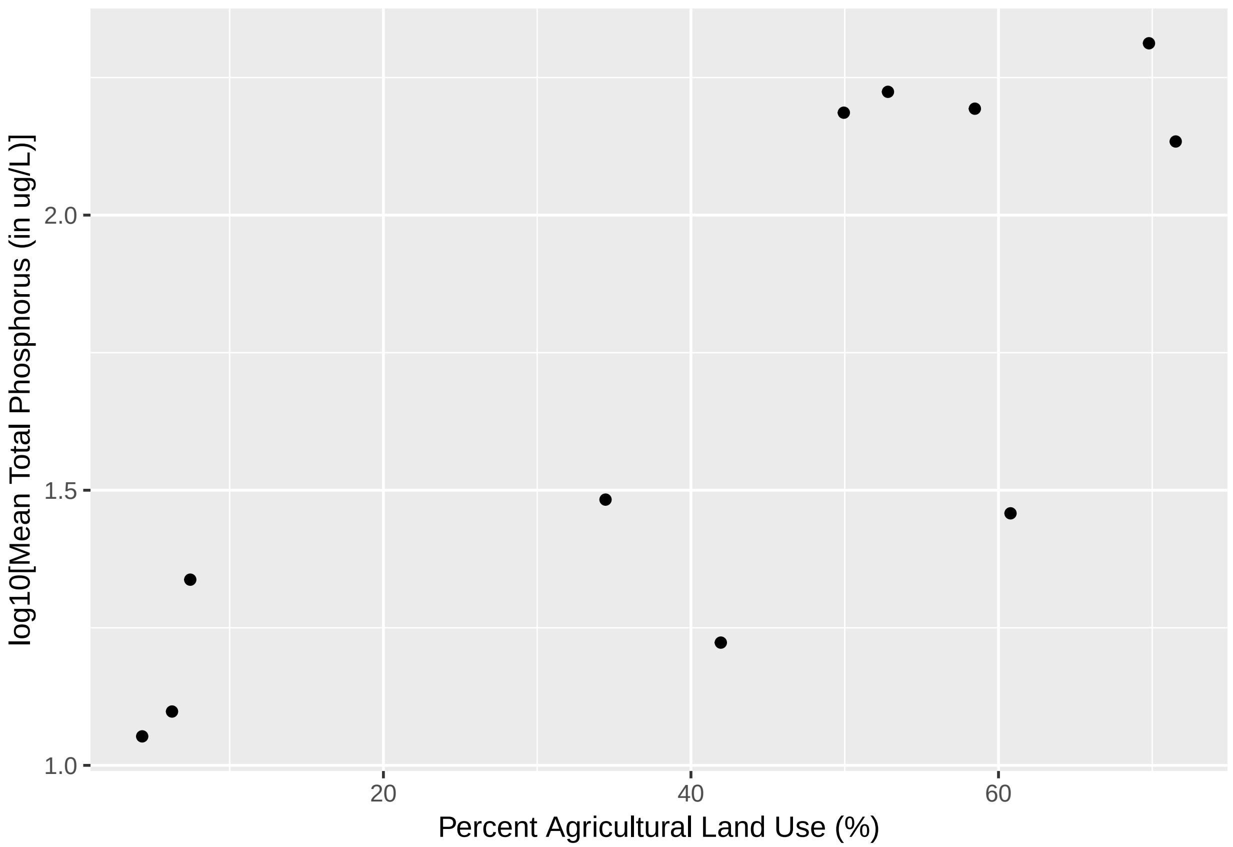
```
ggplot(df, aes(x = Perc_GL, y = log10_Turb_mn)) +
  geom_point() +
  labs(x = "Percent Glaciolacustrine Soils (%)",
       y = "log10[Mean Total Phosphorus (ug/L)]")
```



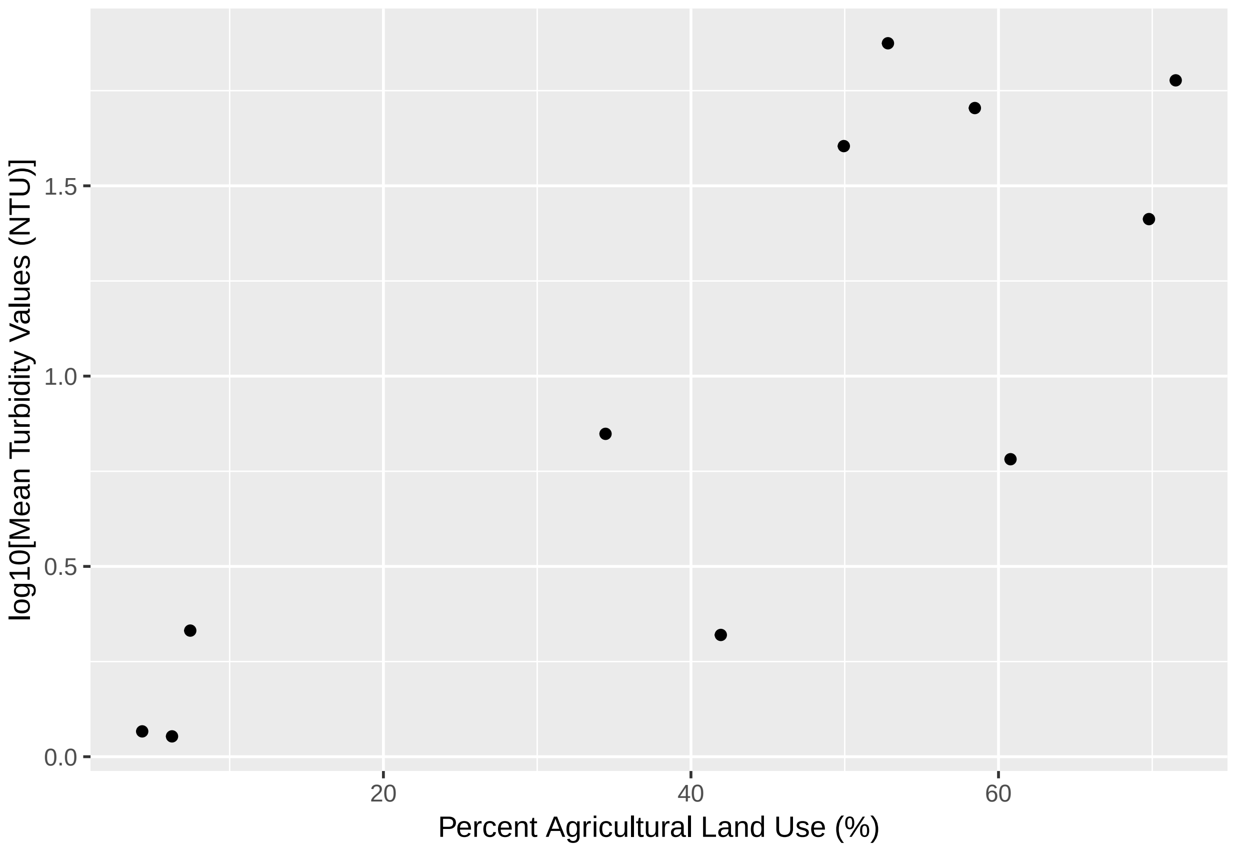
```
ggplot(df, aes(x = Perc_GL, y = log10_Turb_mn)) +
  geom_point() +
  labs(x = "Percent Glaciolacustrine Soils (%)",
       y = "log10[Mean Turbidity Values (NTU)]")
```



```r
ggplot(df, aes(x = Perc_Ag, y = log10_TP_mn)) +
  geom_point() +
  labs(x = "Percent Agricultural Land Use (%)",
       y = "log10[Mean Total Phosphorus (in ug/L)]")
```



```r
ggplot(df, aes(x = Perc_Ag, y = log10_Turb_mn)) +
  geom_point() +
  labs(x = "Percent Agricultural Land Use (%)",
       y = "log10[Mean Turbidity Values (NTU)]")
```



We will now calculate Pearson correlation coefficients to assess the strength of these linear relationships:

```
cor(df$Perc_GL, df$log10_TP_mn, method = c("pearson"))
```

```
## [1] 0.9231598
```

```
cor(df$Perc_GL, df$log10_Turb_mn, method = c("pearson"))
```

```
## [1] 0.9318165
```

```
cor(df$Perc_Ag, df$log10_TP_mn, method = c("pearson"))
```

```
## [1] 0.8047242
```

```
cor(df$Perc_Ag, df$log10_Turb_mn, method = c("pearson"))
```

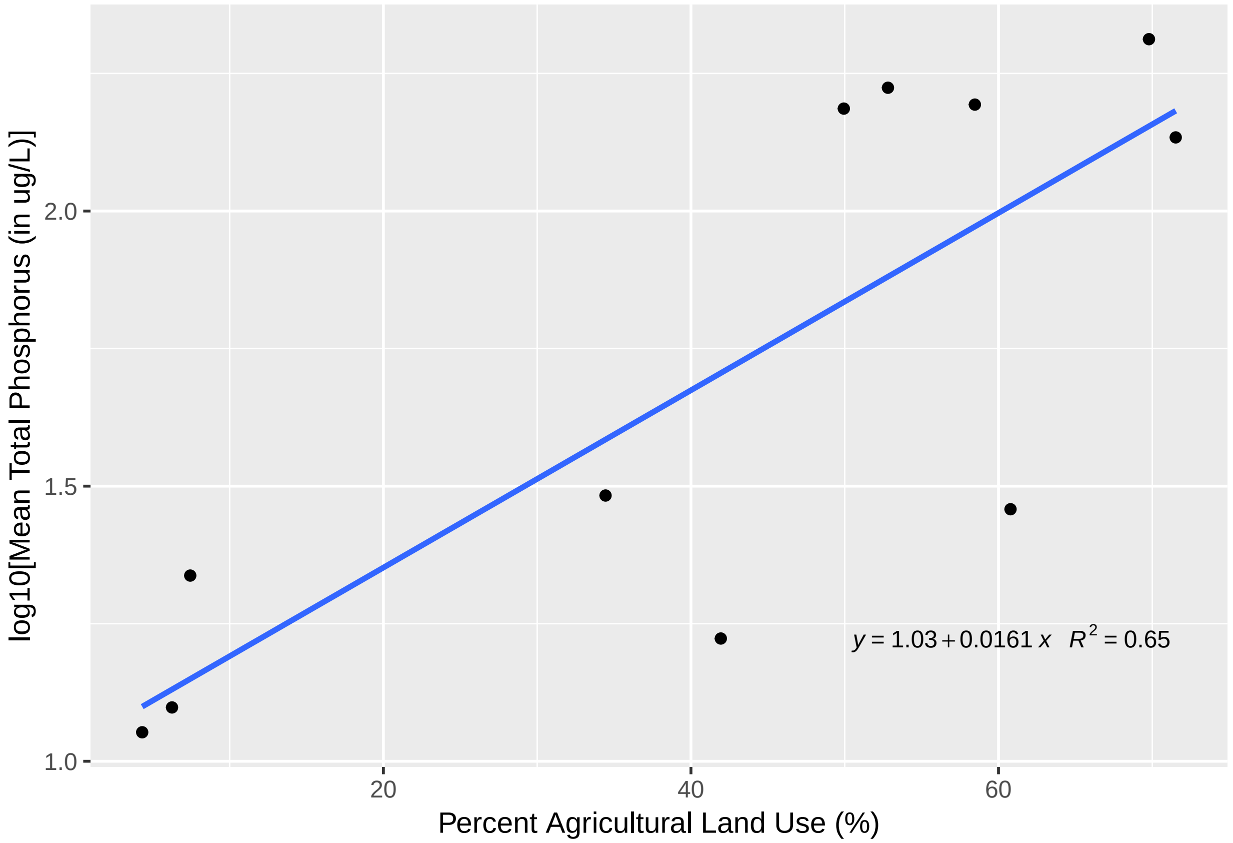
```
## [1] 0.8236255
```

All Pearson correlation coefficients are above 0.80, indicating strong linear relationships between respective variables.

The watershed group believes that total phosphorus concentrations in these rivers are caused by agricultural land use. To investigate this, we will construct a simple linear regression model that relates total phospohorous to agricultural land use:

```r
x = df$Perc_Ag
y = df$log10_TP_mn
formula <- y ~ x

ggplot(df, aes(x = Perc_Ag, y = log10_TP_mn)) +
  geom_point() +
  stat_smooth(method = "lm", formula = y ~ x, se = FALSE) +
  labs(x = "Percent Agricultural Land Use (%)",
       y = "log10[Mean Total Phosphorus (in ug/L)]") +
  stat_poly_eq(aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~")),
               label.x.npc = "right", label.y.npc = 0.15,
               formula = formula, parse = TRUE, size = 3)
```



```r
model <- lm(y~x)
summary(model)
```

```
##
## Call:
## lm(formula = y ~ x)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.55104 -0.07507 -0.03269  0.20480  0.35174
##
## Coefficients:
```

```
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.029787   0.190525   5.405  0.00043 ***
## x           0.016111   0.003962   4.067  0.00281 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3168 on 9 degrees of freedom
## Multiple R-squared:  0.6476, Adjusted R-squared:  0.6084
## F-statistic: 16.54 on 1 and 9 DF,  p-value: 0.002814
```

The results of our linear regression analysis indicate that there is indeed evidence of a relationship between percent agricultural land use and mean total phosphorous for the Little Otter and New River catchments at the 95% confidence level (F = 16.54, p < 0.0028). The coefficient of determination indicates that this model is a moderate fit for the data (Rˆ2 = 0.65).

The assumptions for a simple linear regression are as follows: linearity of residuals, independence of residuals, normal distribution of residuals, and equal variance of residuals.

Because the scatter plot follows a linear pattern (i.e. not a curvilinear pattern), that shows that the linearity assumption is met. Independence implies that each point is independent from every other point, which we can also assume to be true. Normality was investigates in our trials above and corrected with a log10 transformation. Lastly, comes the equal variance assumption. The scatter plot shows that the data may exhibit heteroscedasticity as the residuals of the scatter plot tend to fan out at the midpoint of the x-axis. In the future, the collection of more data points is recommended to further make this judgement call.

The instream water quality criteria for TP in surface waters is 27 ug/L.
We would like to calculate the percentage of agricultural land use according to this model, so we will perform the following calculation:

```r
PercentALU <- (log10(27)-1.03)/(0.16)
PercentALU
```

```
## [1] 2.508524
```

Our model predicts that 2.51% agricultural land use in the nearby upstream river corridor corresponds to 27 ug/L Total Phosphorous in surface waters.

Since phosphorus likes to sorb to fine silts and clays, TP may also be a function of Turbidity levels. Let's construct a multiple linear regression model that relates TP to both agricultural land use and Turb_mn:

```r
multi_model <- lm(df$log10_TP_mn ~ df$Perc_Ag + df$Turb_mn)
summary(multi_model)
```

```
##
## Call:
## lm(formula = df$log10_TP_mn ~ df$Perc_Ag + df$Turb_mn)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.23371 -0.16115 -0.04492  0.11996  0.35923
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.077224   0.132623   8.122 3.91e-05 ***
## df$Perc_Ag  0.008506   0.003588   2.371   0.0452 *
## df$Turb_mn  0.010917   0.003322   3.286   0.0111 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2192 on 8 degrees of freedom
## Multiple R-squared:   0.85,  Adjusted R-squared:  0.8125
## F-statistic: 22.67 on 2 and 8 DF,  p-value: 0.0005061
```

The results of our multiple linear regression analysis indicate that there is indeed evidence of a relationship between percent agricultural land use and mean total phosphorous for the Little Otter and New River catchments at the 95% confidence level (F = 22.67, p = 0.0005). The model is as follows:

$$log10[Mean\ Total\ Phosphorous\ in\ ug/L] = 1.077 + (0.0085 * Percent\ Agricultural\ Land\ Use) + (0.0109 * log10[Mean\ Turbidi$$

The model assumptions described above for the previous model are also obeyed in the creation of this model, with the possible heteroscedasticity as a slight concern. The coefficient of determination in the above summary statistics shows us that this model is a strong fit for the data (Rˆ2 = 0.85). In comparision to our previous model, using a multiple regression with both the percent agricultural land use and and the mean turbidity values give us a better fit to the available data. This tells us that this multiple regression model is a better representation of our Earth system (i.e., the Little Otter and New River catchments).

Part 2: New Haven River and Little Otter Creek Watershed Data Analysis

For the second part of our investigation, we will be investigating daily mean flow data for the Mad River, which is a tributary to the Winooski River in Vermont. It has its headwaters in Granville Gulf, then flows north through the towns of Warren, Waitsfield, and Moretown before entering the Winooski River just downstream from Middlesex.

This set contains flow data from 1929 to 2015.

```r
df_mad <- read_csv("Mad.csv")
```

```
## Parsed with column specification:
## cols(
##   Date = col_character(),
##   Discharge = col_double()
## )
```

```r
head(df_mad)
```

```
## # A tibble: 6 x 2
##   Date     Discharge
##   <chr>        <dbl>
## 1 1/1/1929        56
## 2 1/2/1929        52
## 3 1/3/1929        50
## 4 1/4/1929        56
## 5 1/5/1929       111
## 6 1/6/1929       144
```

We would like to create a plot of the frequency by year (from year 1990 through 2015) when discharge exceeded the 95Th percentile (940 cfs).

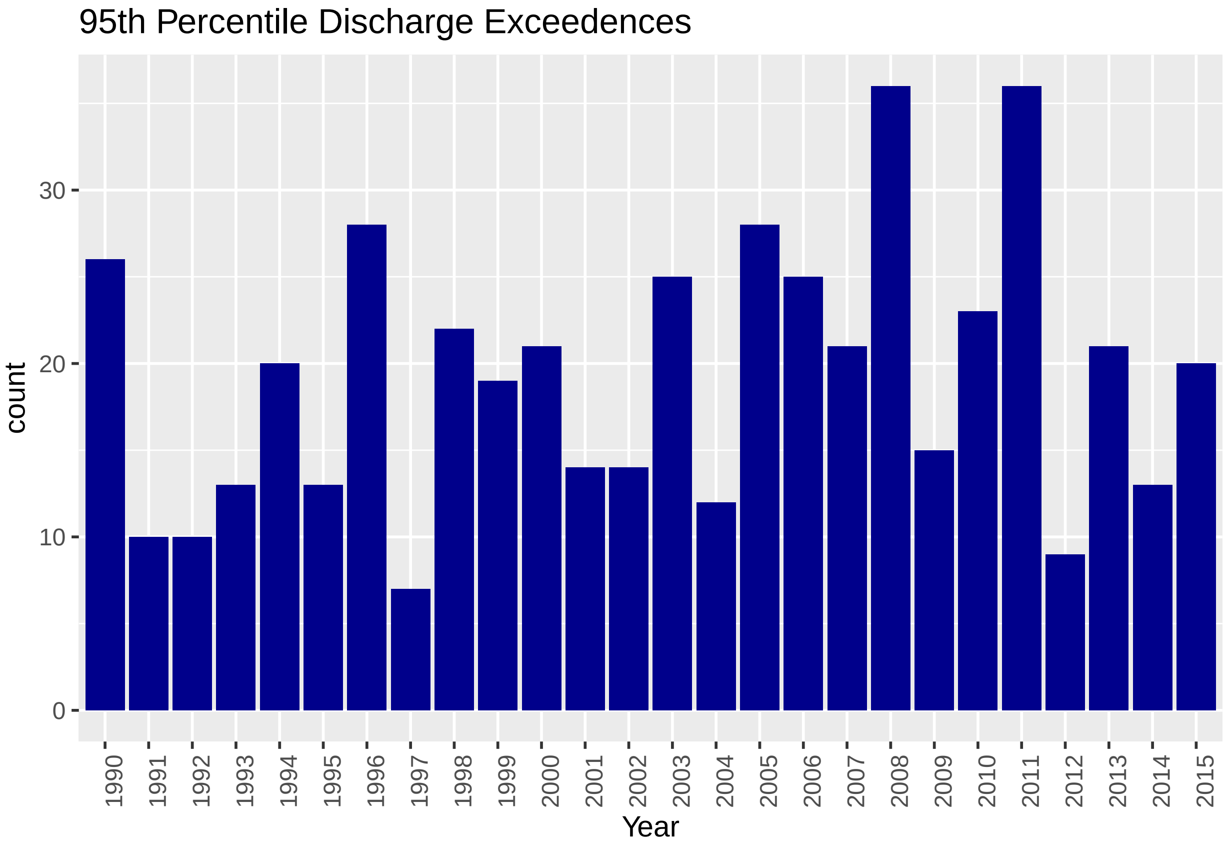
We must select only rows with discharge value > 940 cfs and subset the data for the years 1990 to 2015:

```r
df_mad$Date <- format(as.Date(df_mad$Date, format="%m/%d/%Y"),"%Y") # we are only interested in indexin

df_exceed <- df_mad %>%
  filter(Discharge > 940) %>%
  filter(Date >= 1990 & Date <= 2015)
```

Finally, we can create our barplot:

```r
ggplot(data = df_exceed, aes(x = factor(Date))) +
  geom_bar(fill = "darkblue") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  labs(x = "Year", title = "95th Percentile Discharge Exceedences")
```



Next, we would like to fit a linear regression model to the record of days per year. First, we will create new data frame to contain only the year column and the frequencies (instead of the year column and actual discharge values that are greater than the 95th percentile as we have before):

```r
df_freq <- as.data.frame(table(df_exceed$Date))
```

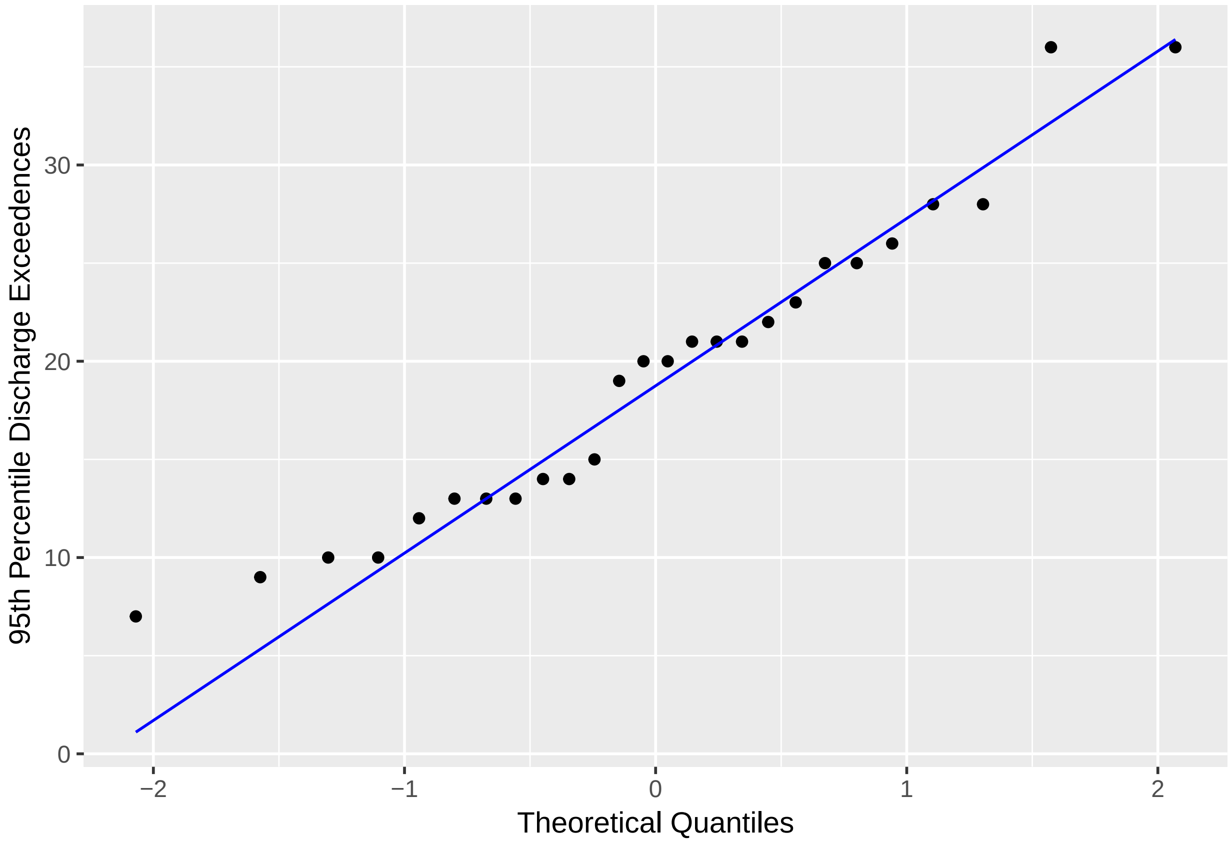
Is this data normally distributed? Let's conduct the Shapiro-Wilks Test for Normality:

```
shapiro.test(df_freq$Freq)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df_freq$Freq
## W = 0.95042, p-value = 0.2372
```

Because the p-value = 0.2372 and alpha = 0.05, we fail to reject null. Let's check the Q-Q plot to further ensure that the data is normally distributed:

```
ggplot(df_freq, aes(sample = Freq)) +
  stat_qq() +
  geom_qq_line(col = "blue") +
  labs(x = "Theoretical Quantiles",
       y = "95th Percentile Discharge Exceedences")
```

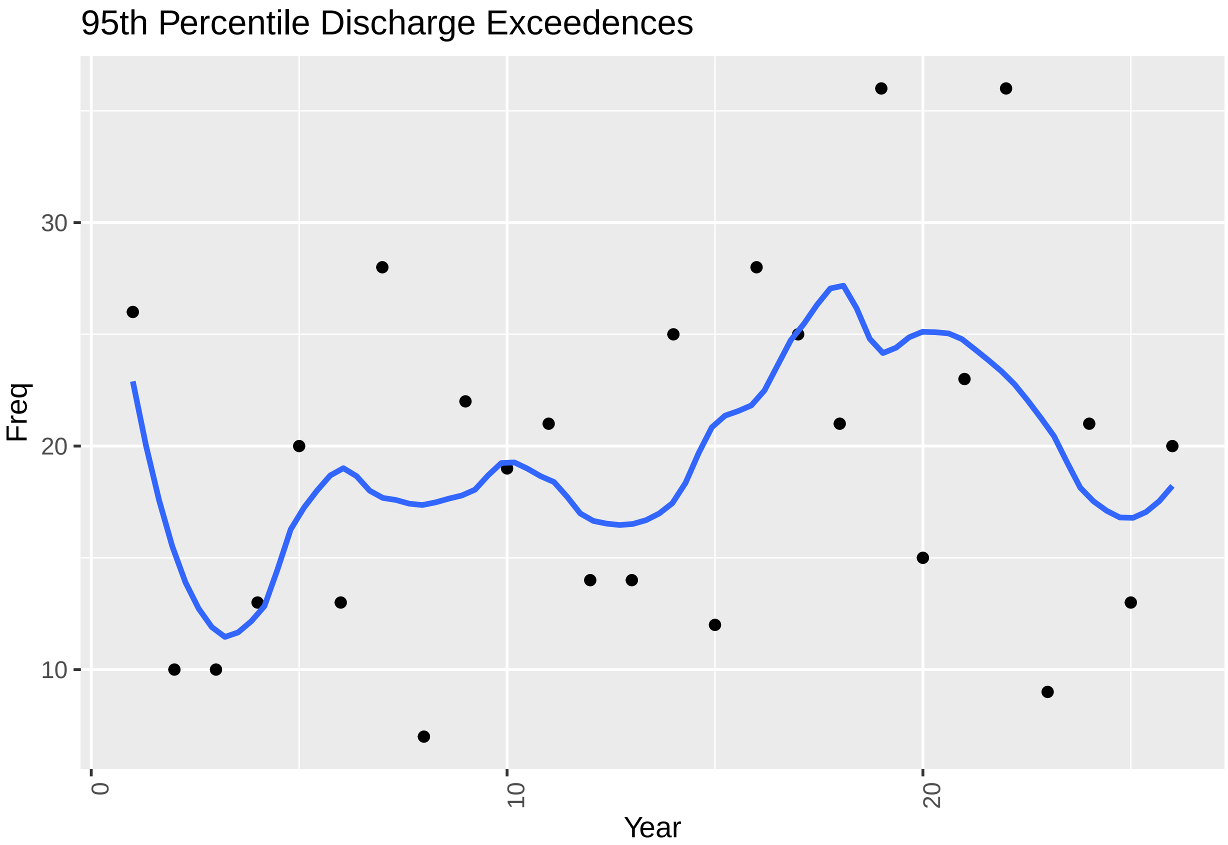


Yes, the data seems to pass the visual inspection from a Q-Q plot. Despite fitting a normal distribution, a parametric model is not valid for interpretation of trend. Why? Because the data is not independent due to temporal dependence.

LOWESS (Locally Weighted Scatterplot Smoothing) Models are a great tool in regression analyses for creating line through timeplots to visualize relationships between variables and foresee trends. Let's fit a LOWESS model to the frequency of days per year:

```
ggplot(data = df_freq, aes(x = as.numeric(Var1), y = Freq)) +
  geom_point() +
  geom_smooth(span=1/3, se = FALSE) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  labs(x = "Year", title = "95th Percentile Discharge Exceedences")
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



Is a trend evident? It is not too clear. From visual inspection, it appears as though the frequency of flow exceedences above the 95th percentile might be increasing. We choose the Mann-Kendall statistical test to characterize significance of the trend. This test is a non-parametric test used to identify a trend in a series:

```
MannKendall(df_freq$Freq)
```

```
## tau = 0.154, 2-sided pvalue =0.28849
```

Because the null hypothesis of the Mann-Kendall test states that there is no trend in the series, the results show that we must fail to reject the null (tau = 0.15, p = 0.29). At the 95% confidence level, there is not enough evidence to suggest that there is a trend in the series.