Tomato nutrient study correlations

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## Load library

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

## Start script

script\_path <- "C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018"  
in\_dir <- "C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018"  
out\_dir <- "C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/output"  
data <- data.frame(read.csv("C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/TomatoHT\_Data\_CHARTS\_10.31.18\_nutrientlevels.csv"))

## Create dataframe w/variables of interest, omit rows with NA

tomatofun\_nitrate <- subset(data, select = c("Nitrate.N..ppm..SME", "Nitrate.N..ppm..MM", "TN.....Leaf.Analysis"))  
tomatofun\_nitrateNONA <- na.omit(tomatofun\_nitrate)

## Check distribution - all are non normal

shapiro.test(tomatofun\_nitrateNONA$Nitrate.N..ppm..SME)

##   
## Shapiro-Wilk normality test  
##   
## data: tomatofun\_nitrateNONA$Nitrate.N..ppm..SME  
## W = 0.82868, p-value = 0.0001196

shapiro.test(tomatofun\_nitrateNONA$Nitrate.N..ppm..MM)

##   
## Shapiro-Wilk normality test  
##   
## data: tomatofun\_nitrateNONA$Nitrate.N..ppm..MM  
## W = 0.85274, p-value = 0.0003914

shapiro.test(tomatofun\_nitrateNONA$TN.....Leaf.Analysis)

##   
## Shapiro-Wilk normality test  
##   
## data: tomatofun\_nitrateNONA$TN.....Leaf.Analysis  
## W = 0.91736, p-value = 0.0155

## Correlation tests

cor(tomatofun\_nitrateNONA, method = "spearman")

## Nitrate.N..ppm..SME Nitrate.N..ppm..MM  
## Nitrate.N..ppm..SME 1.0000000 0.9784389  
## Nitrate.N..ppm..MM 0.9784389 1.0000000  
## TN.....Leaf.Analysis 0.3242791 0.3533640  
## TN.....Leaf.Analysis  
## Nitrate.N..ppm..SME 0.3242791  
## Nitrate.N..ppm..MM 0.3533640  
## TN.....Leaf.Analysis 1.0000000

cor.test(x = tomatofun\_nitrateNONA$Nitrate.N..ppm..SME, y = tomatofun\_nitrateNONA$Nitrate.N..ppm..MM, alternative = "two.sided", method = "spearman", exact = NULL)

## Warning in cor.test.default(x = tomatofun\_nitrateNONA  
## $Nitrate.N..ppm..SME, : Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: tomatofun\_nitrateNONA$Nitrate.N..ppm..SME and tomatofun\_nitrateNONA$Nitrate.N..ppm..MM  
## S = 129.02, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.9784389

cor.test(x = tomatofun\_nitrateNONA$Nitrate.N..ppm..SME, y = tomatofun\_nitrateNONA$TN.....Leaf.Analysis, alternative = "two.sided", method = "spearman", exact = NULL)

## Warning in cor.test.default(x = tomatofun\_nitrateNONA  
## $Nitrate.N..ppm..SME, : Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: tomatofun\_nitrateNONA$Nitrate.N..ppm..SME and tomatofun\_nitrateNONA$TN.....Leaf.Analysis  
## S = 4043.5, p-value = 0.0656  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.3242791

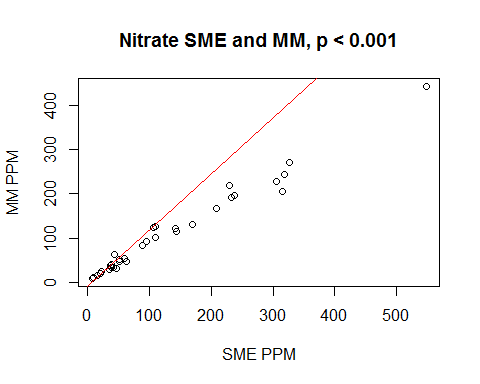
cor.test(x = tomatofun\_nitrateNONA$Nitrate.N..ppm..MM, y = tomatofun\_nitrateNONA$TN.....Leaf.Analysis, alternative = "two.sided", method = "spearman", exact = NULL)

## Warning in cor.test.default(x = tomatofun\_nitrateNONA$Nitrate.N..ppm..MM, :  
## Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: tomatofun\_nitrateNONA$Nitrate.N..ppm..MM and tomatofun\_nitrateNONA$TN.....Leaf.Analysis  
## S = 3869.5, p-value = 0.04367  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.353364

## plot SME and MM correlations

plot(tomatofun\_nitrateNONA$Nitrate.N..ppm..SME, tomatofun\_nitrateNONA$Nitrate.N..ppm..MM, type = "p", main = "Nitrate SME and MM, p < 0.001", xlab = "SME PPM", ylab = "MM PPM")  
abline(lm(tomatofun\_nitrateNONA$Nitrate.N..ppm..SME~tomatofun\_nitrateNONA$Nitrate.N..ppm..MM), col = "red") # regression line

 ## plot MM and TN correlations

plot(tomatofun\_nitrateNONA$Nitrate.N..ppm..MM, tomatofun\_nitrateNONA$TN.....Leaf.Analysis, type = "p", main = "Nitrate MM and TN Leaf, p < 0.05", xlab = "MM PPM", ylab = "TN leaf")  
abline(lm(tomatofun\_nitrateNONA$Nitrate.N..ppm..MM~tomatofun\_nitrateNONA$TN.....Leaf.Analysis), col = "red") # regression line

