Tomato nutrient study correlations, 2nd version

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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

library(ggpubr)

## Loading required package: ggplot2

## Loading required package: magrittr

library(ggplot2)  
library(car)

## Loading required package: carData

##   
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':  
##   
## recode

library(gvlma)  
library(reshape2)

## Questions of interest

1. The effects of cumulative nutrient applications on leaf tissue and soil nutrient levels the month after. (MASS only)
2. The effects of soil test in any given month and the leaf tissue samples of the following month.
3. The effects of diseases on yield (H1: powdery mildew will have the biggest effect)
4. The effect of compaction on yield
5. The effect of plant density on yield
6. The effect of planting date on yield

## Start script

# Data preparation

script\_path <- "C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/CSV"  
in\_dir <- "C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/CSV"  
out\_dir <- "C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/output/CSV"

# read in datasets

FARMS <- data.frame(read.csv("C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/CSV/Farms.csv"))  
NUTADDED <- data.frame(read.csv("C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/CSV/NutAdd.csv"))  
NUTLEVELS <- data.frame(read.csv("C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/CSV/NutLevel.csv"))  
PESTS <- data.frame(read.csv("C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/CSV/Pests.csv"))  
SPACEYIELD <- data.frame(read.csv("C:/Users/rschattman/Documents/Research/Greenhouse\_tomatoes\_2018/CSV/SpaceYield.csv"))

## Merge dataframes

NUTS <-merge(NUTADDED, SPACEYIELD)  
NUTS2 <- merge(NUTS, NUTLEVELS)

# Question 2: The effects of soil test in any given month and the leaf tissue samples of the following month.

## Test variables for normal distribution

### Note to self: figure out this whole batch processing business.

#shapiro.test(NUTLEVELS$TMY) #not normal  
#shapiro.test(NUTLEVELS$MYsqFT)#not normal  
#shapiro.test(NUTLEVELS$NSME) #not normal  
#shapiro.test(NUTLEVELS$ASME) #not normal  
#shapiro.test(NUTLEVELS$PSME) #not normal  
#shapiro.test(NUTLEVELS$KSME) #not normal  
#shapiro.test(NUTLEVELS$MagSME) #NORMAL DIST  
#shapiro.test(NUTLEVELS$CaSME) #not normal  
#shapiro.test(NUTLEVELS$AlSME) #not normal  
#shapiro.test(NUTLEVELS$BoSME) #not normal  
#shapiro.test(NUTLEVELS$CoSME) #not normal  
#shapiro.test(NUTLEVELS$FeSME) #NORMAL DIST  
  
#NUTLEVELS$MangSME <- as.numeric(NUTLEVELS$MangSME) #transform into numberic  
#shapiro.test(NUTLEVELS$MangSME) #NORMAL DIST  
  
#shapiro.test(NUTLEVELS$SoSME) #not normal  
#shapiro.test(NUTLEVELS$SuSME) #not normal  
#shapiro.test(NUTLEVELS$ZSME) #not normal  
#shapiro.test(NUTLEVELS$NMM) #not normal  
#shapiro.test(NUTLEVELS$PMM) #not normal  
#shapiro.test(NUTLEVELS$KMM) #NORMAL DIST  
#shapiro.test(NUTLEVELS$CaMM) #NORMAL DIST  
#shapiro.test(NUTLEVELS$MaMM) #not normal  
#shapiro.test(NUTLEVELS$SuMM) #not normal  
#shapiro.test(NUTLEVELS$BoMM) #not normal  
#shapiro.test(NUTLEVELS$CoMM) #not normal  
#shapiro.test(NUTLEVELS$FeMM) #NORMAL DIST  
#shapiro.test(NUTLEVELS$MangMM)#not normal  
#shapiro.test(NUTLEVELS$ZMM) #not normal  
  
#NUTLEVELS$TNLA <- as.numeric(NUTLEVELS$TNLA)  
#shapiro.test(NUTLEVELS$TNLA) #not normal  
  
#NUTLEVELS$CALA <- as.numeric(NUTLEVELS$CALA)  
#shapiro.test(NUTLEVELS$CALA) #not normal  
  
#NUTLEVELS$KLA <- as.numeric(NUTLEVELS$KLA)  
#shapiro.test(NUTLEVELS$KLA) #not normal  
  
#NUTLEVELS$MgLA <- as.numeric(NUTLEVELS$MgLA)  
#shapiro.test(NUTLEVELS$MgLA) #not normal  
  
#NUTLEVELS$PLA <- as.numeric(NUTLEVELS$PLA)  
#shapiro.test(NUTLEVELS$PLA) #not normal  
  
#NUTLEVELS$AlLA <- as.numeric(NUTLEVELS$AlLA)  
#shapiro.test(NUTLEVELS$AlLA) #not normal  
  
#NUTLEVELS$BLA <- as.numeric(NUTLEVELS$BLA)  
#shapiro.test(NUTLEVELS$BLA) #not normal  
  
#NUTLEVELS$CuLA <- as.numeric(NUTLEVELS$CuLA)  
#shapiro.test(NUTLEVELS$CuLA) #not normal  
  
#NUTLEVELS$FeLA <- as.numeric(NUTLEVELS$FeLA)  
#shapiro.test(NUTLEVELS$FeLA) #not normal  
  
#NUTLEVELS$MnLA <- as.numeric(NUTLEVELS$MnLA)  
#shapiro.test(NUTLEVELS$MnLA) #not normal  
  
#NUTLEVELS$ZLA <- as.numeric(NUTLEVELS$ZLA)  
#shapiro.test(NUTLEVELS$ZLA) #not normal

## Subset modified morgans (MM), saturdated media (SM) and leaf tissue (LT) tests by month after transplan (MX in SampPer). MM and SM are for same month, leaf tissue is for following month.

### First month soil, second month leaf

# subset 1M rows, MM and SM columns  
MM\_SM\_M1 <- NUTLEVELS[which(NUTLEVELS$SampPer == "1M"), names(NUTLEVELS) %in% c("ID", "TMY", "MYsqFT", "NSME", "ASME", "PSME", "KSME", "MagSME", "CaSME", "AlSME", "BoSME", "CoSME", "FeSME", "MangSME", "SoSME", "SuSME", "ZSME", "NMM", "PMM", "KMM", "CaMM", "MaMM", "SuMM", "BoMM", "CoMM", "FeMM", "MangMM", "ZMM")]   
  
# subset 2M rows, LT columns  
LA\_M2 <- NUTLEVELS[which(NUTLEVELS$SampPer == "2M"), names(NUTLEVELS) %in% c("ID", "TNLA", "CALA", "KLA", "MgLA", "PLA", "AlLA", "BLA", "CuLA", "FeLA", "MnLA", "ZLA")]  
  
# merge MM\_SM\_M1 and LA\_M2  
M1\_M2 <- merge(MM\_SM\_M1, LA\_M2)  
  
# some columns need to be tranformed into numberic vectors   
# M1\_M2 <- sapply(M1\_M2, as.numeric)  
# is.numeric(M1\_M2)

### Second month soil, third month leaf

# subset 2M rows, MM and SM columns  
MM\_SM\_M2 <- NUTLEVELS[which(NUTLEVELS$SampPer == "2M"), names(NUTLEVELS) %in% c("ID", "TMY", "MYsqFT", "NSME", "ASME", "PSME", "KSME", "MagSME", "CaSME", "AlSME", "BoSME", "CoSME", "FeSME", "MangSME", "SoSME", "SuSME", "ZSME", "NMM", "PMM", "KMM", "CaMM", "MaMM", "SuMM", "BoMM", "CoMM", "FeMM", "MangMM", "ZMM")]   
  
# subset 3M rows, LT columns  
LA\_M3 <- NUTLEVELS[which(NUTLEVELS$SampPer == "3M"), names(NUTLEVELS) %in% c("ID", "TNLA", "CALA", "KLA", "MgLA", "PLA", "AlLA", "BLA", "CuLA", "FeLA", "MnLA", "ZLA")]  
  
# merge MM\_SM\_M2 and LA\_M3  
M2\_M3 <- merge(MM\_SM\_M2, LA\_M3)

### Third month soil, fourth month leaf

# subset 3M rows, MM and SM columns  
MM\_SM\_M3 <- NUTLEVELS[which(NUTLEVELS$SampPer == "3M"), names(NUTLEVELS) %in% c("ID", "TMY", "MYsqFT", "NSME", "ASME", "PSME", "KSME", "MagSME", "CaSME", "AlSME", "BoSME", "CoSME", "FeSME", "MangSME", "SoSME", "SuSME", "ZSME", "NMM", "PMM", "KMM", "CaMM", "MaMM", "SuMM", "BoMM", "CoMM", "FeMM", "MangMM", "ZMM")]   
  
# subset 4M rows, LT columns  
LA\_M4 <- NUTLEVELS[which(NUTLEVELS$SampPer == "4M"), names(NUTLEVELS) %in% c("ID", "TNLA", "CALA", "KLA", "MgLA", "PLA", "AlLA", "BLA", "CuLA", "FeLA", "MnLA", "ZLA")]  
  
# merge MM\_SM\_M3 and LA\_M4  
M3\_M4 <- merge(MM\_SM\_M3, LA\_M4)

### Fourth month soil, fifth month leaf

# subset 3M rows, MM and SM columns  
MM\_SM\_M4 <- NUTLEVELS[which(NUTLEVELS$SampPer == "4M"), names(NUTLEVELS) %in% c("ID", "TMY", "MYsqFT", "NSME", "ASME", "PSME", "KSME", "MagSME", "CaSME", "AlSME", "BoSME", "CoSME", "FeSME", "MangSME", "SoSME", "SuSME", "ZSME", "NMM", "PMM", "KMM", "CaMM", "MaMM", "SuMM", "BoMM", "CoMM", "FeMM", "MangMM", "ZMM")]   
  
# subset 4M rows, LT columns  
LA\_M5 <- NUTLEVELS[which(NUTLEVELS$SampPer == "5M"), names(NUTLEVELS) %in% c("ID", "TNLA", "CALA", "KLA", "MgLA", "PLA", "AlLA", "BLA", "CuLA", "FeLA", "MnLA", "ZLA")]  
  
# merge MM\_SM\_M4 and LA\_M5  
M4\_M5 <- merge(MM\_SM\_M3, LA\_M4)

## Regress leaf tissue analysis on SME and MM for N

# N  
# 1MAT soil, 2MAT leaf --> No sig correlation  
  
cor.test(x = M1\_M2$NSME, y = M1\_M2$TNLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M1\_M2$TNLA), exact = NULL)

## Warning in cor.test.default(x = M1\_M2$NSME, y = M1\_M2$TNLA, alternative =  
## "two.sided", : Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: M1\_M2$NSME and M1\_M2$TNLA  
## S = 494.8, p-value = 0.118  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.3936236

cor.test(x = M1\_M2$NMM, y = M1\_M2$TNLA, alternative = "two.sided", method = "spearman", exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M1\_M2$NMM and M1\_M2$TNLA  
## S = 140, p-value = 0.6818  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.1515152

# 2MAT soil, 3MAT leaf --> No sig correlation  
  
cor.test(x = M2\_M3$NSME, y = M2\_M3$TNLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M2\_M3$TNLA), exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M2\_M3$NSME and M2\_M3$TNLA  
## S = 548, p-value = 0.47  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.1941176

cor.test(x = M2\_M3$NMM, y = M2\_M3$TNLA, alternative = "two.sided", method = "spearman", exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M2\_M3$NMM and M2\_M3$TNLA  
## S = 200, p-value = 0.7966  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.09090909

# 3MAT soil, 4MAT leaf --> SME not sig correlated. MM is significantly correlated at the 0.05 level. However, linear model is not significant.  
  
cor.test(x = M3\_M4$NSME, y = M3\_M4$TNLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M3\_M4$TNLA), exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M3\_M4$NSME and M3\_M4$TNLA  
## S = 112, p-value = 0.1292  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.4909091

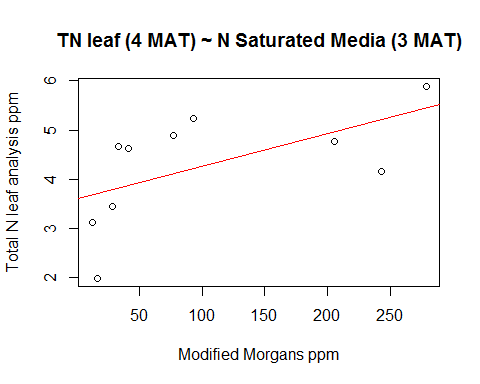
cor.test(x = M3\_M4$NMM, y = M3\_M4$TNLA, alternative = "two.sided", method = "spearman", exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M3\_M4$NMM and M3\_M4$TNLA  
## S = 40, p-value = 0.01592  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.7575758

mod1 <- lm(NSME~TNLA, data=M3\_M4)  
  
summary(mod1)

##   
## Call:  
## lm(formula = NSME ~ TNLA, data = M3\_M4)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -110.23 -77.99 -64.62 99.25 184.59   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)  
## (Intercept) -2.031 151.926 -0.013 0.990  
## TNLA 32.480 35.143 0.924 0.379  
##   
## Residual standard error: 125.3 on 9 degrees of freedom  
## (4 observations deleted due to missingness)  
## Multiple R-squared: 0.08669, Adjusted R-squared: -0.01479   
## F-statistic: 0.8542 on 1 and 9 DF, p-value: 0.3795

plot(M3\_M4$NMM, M3\_M4$TNLA, type = "p", main = "TN leaf (4 MAT) ~ N Saturated Media (3 MAT)", xlab = "Modified Morgans ppm", ylab = "Total N leaf analysis ppm")  
abline(lm(M3\_M4$TNLA~M3\_M4$NMM), col = "red") # regression line



# 4MAT soil, 5MAT leaf --> SME not sig correlated. MM is significantly correlated at the 0.05 level. However, linear model is not significant.  
  
cor.test(x = M4\_M5$NSME, y = M4\_M5$TNLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M4\_M5$TNLA), exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M4\_M5$NSME and M4\_M5$TNLA  
## S = 112, p-value = 0.1292  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.4909091

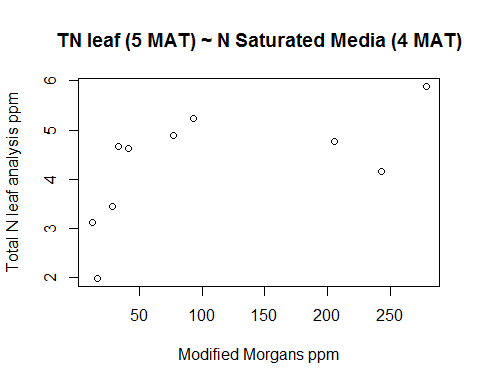
cor.test(x = M4\_M5$NMM, y = M4\_M5$TNLA, alternative = "two.sided", method = "spearman", exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M4\_M5$NMM and M4\_M5$TNLA  
## S = 40, p-value = 0.01592  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.7575758

mod2 <- lm(NSME~TNLA, data=M4\_M5)  
  
summary(mod2)

##   
## Call:  
## lm(formula = NSME ~ TNLA, data = M4\_M5)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -110.23 -77.99 -64.62 99.25 184.59   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)  
## (Intercept) -2.031 151.926 -0.013 0.990  
## TNLA 32.480 35.143 0.924 0.379  
##   
## Residual standard error: 125.3 on 9 degrees of freedom  
## (4 observations deleted due to missingness)  
## Multiple R-squared: 0.08669, Adjusted R-squared: -0.01479   
## F-statistic: 0.8542 on 1 and 9 DF, p-value: 0.3795

plot(M4\_M5$NMM, M4\_M5$TNLA, type = "p", main = "TN leaf (5 MAT) ~ N Saturated Media (4 MAT)", xlab = "Modified Morgans ppm", ylab = "Total N leaf analysis ppm")



## Regress leaf tissue analysis on SME and MM for P

# P  
# 1MAT soil, 2MAT leaf --> No sig correlation  
  
cor.test(x = M1\_M2$PSME, y = M1\_M2$PLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M1\_M2$PLA), exact = NULL)

## Warning in cor.test.default(x = M1\_M2$PSME, y = M1\_M2$PLA, alternative =  
## "two.sided", : Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: M1\_M2$PSME and M1\_M2$PLA  
## S = 735.75, p-value = 0.7073  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.09834052

cor.test(x = M1\_M2$PMM, y = M1\_M2$PLA, alternative = "two.sided", method = "spearman", exact = NULL)

## Warning in cor.test.default(x = M1\_M2$PMM, y = M1\_M2$PLA, alternative =  
## "two.sided", : Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: M1\_M2$PMM and M1\_M2$PLA  
## S = 691.77, p-value = 0.5597  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.1522409

# 2MAT soil, 3MAT leaf --> No sig correlation  
  
cor.test(x = M2\_M3$PSME, y = M2\_M3$PLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M2\_M3$PLA), exact = NULL)

## Warning in cor.test.default(x = M2\_M3$PSME, y = M2\_M3$PLA, alternative =  
## "two.sided", : Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: M2\_M3$PSME and M2\_M3$PLA  
## S = 490.58, p-value = 0.2962  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.2785557

cor.test(x = M2\_M3$PMM, y = M2\_M3$PLA, alternative = "two.sided", method = "spearman", exact = NULL)

## Warning in cor.test.default(x = M2\_M3$PMM, y = M2\_M3$PLA, alternative =  
## "two.sided", : Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: M2\_M3$PMM and M2\_M3$PLA  
## S = 349.76, p-value = 0.05651  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.4856513

# 3MAT soil, 4MAT leaf --> No sig relationship  
  
cor.test(x = M3\_M4$PSME, y = M3\_M4$PLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M3\_M4$PLA), exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M3\_M4$PSME and M3\_M4$PLA  
## S = 116, p-value = 0.1456  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.4727273

cor.test(x = M3\_M4$PMM, y = M3\_M4$PLA, alternative = "two.sided", method = "spearman", exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M3\_M4$PMM and M3\_M4$PLA  
## S = 124, p-value = 0.1825  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.4363636

# 4MAT soil, 5MAT leaf --> No sig relationship  
  
cor.test(x = M4\_M5$PSME, y = M4\_M5$PLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M4\_M5$PLA), exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M4\_M5$PSME and M4\_M5$PLA  
## S = 116, p-value = 0.1456  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.4727273

cor.test(x = M4\_M5$PMM, y = M4\_M5$PLA, alternative = "two.sided", method = "spearman", exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M4\_M5$PMM and M4\_M5$PLA  
## S = 124, p-value = 0.1825  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.4363636

# K  
# 1MAT soil, 2MAT leaf --> No sig correlation  
  
cor.test(x = M1\_M2$KSME, y = M1\_M2$KLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M1\_M2$KLA), exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M1\_M2$KSME and M1\_M2$KLA  
## S = 750, p-value = 0.7584  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.08088235

cor.test(x = M1\_M2$KMM, y = M1\_M2$KLA, alternative = "two.sided", method = "spearman", exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M1\_M2$KMM and M1\_M2$KLA  
## S = 1020, p-value = 0.3318  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## -0.25

# 2MAT soil, 3MAT leaf --> No sig correlation  
  
cor.test(x = M2\_M3$KSME, y = M2\_M3$KLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M2\_M3$KLA), exact = NULL)

## Warning in cor.test.default(x = M2\_M3$KSME, y = M2\_M3$KLA, alternative =  
## "two.sided", : Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: M2\_M3$KSME and M2\_M3$KLA  
## S = 610.95, p-value = 0.7083  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.1015453

cor.test(x = M2\_M3$KMM, y = M2\_M3$KLA, alternative = "two.sided", method = "spearman", exact = NULL)

## Warning in cor.test.default(x = M2\_M3$KMM, y = M2\_M3$KLA, alternative =  
## "two.sided", : Cannot compute exact p-value with ties

##   
## Spearman's rank correlation rho  
##   
## data: M2\_M3$KMM and M2\_M3$KLA  
## S = 682, p-value = 0.9914  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## -0.002943341

# 3MAT soil, 4MAT leaf --> No sig relationship  
  
cor.test(x = M3\_M4$KSME, y = M3\_M4$KLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M3\_M4$KLA), exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M3\_M4$KSME and M3\_M4$KLA  
## S = 146, p-value = 0.313  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.3363636

cor.test(x = M3\_M4$KMM, y = M3\_M4$KLA, alternative = "two.sided", method = "spearman", exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M3\_M4$KMM and M3\_M4$KLA  
## S = 176, p-value = 0.5576  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.2

# 4MAT soil, 5MAT leaf --> No sig relationship  
  
cor.test(x = M4\_M5$KSME, y = M4\_M5$KLA, alternative = "two.sided", method = "spearman", na.action = na.omit(M4\_M5$KLA), exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M4\_M5$KSME and M4\_M5$KLA  
## S = 146, p-value = 0.313  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.3363636

cor.test(x = M4\_M5$KMM, y = M4\_M5$KLA, alternative = "two.sided", method = "spearman", exact = NULL)

##   
## Spearman's rank correlation rho  
##   
## data: M4\_M5$KMM and M4\_M5$KLA  
## S = 176, p-value = 0.5576  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho   
## 0.2