

TX Endos RNAseq Plant Responses

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Libraries and Data

Install and load R libraries

```
library(tidyverse)
library(lmPerm)
library(car)
library(writexl)
library(rcompanion)
```

Load and prepare data

```
Plant <- read.csv("RNAseqPlantRespData.csv", header=TRUE, sep=",", stringsAsFactors = TRUE)
str(Plant)
```

```
## 'data.frame': 84 obs. of 12 variables:
## $ SampleID : Factor w/ 84 levels "AltD1","AltD2",...: 1 2 3 4 5 6 7 8 9 10 ...
## $ Fungus : Factor w/ 7 levels "Alt","Cer","Coc",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ FunCode : int 1 1 1 1 1 1 1 1 1 1 ...
## $ PhysCode : int 1 1 1 1 1 1 1 1 1 1 ...
## $ Water : Factor w/ 2 levels "Drought","WellWatered": 1 1 1 1 1 1 2 2 2 ...
## $ Repl : int 1 2 3 4 5 6 1 2 3 4 ...
## $ rgr : num 0.247 0.021 0 0.021 0.195 0 0.279 0.511 0.553 0.174 ...
## $ wilt : int 20 20 19 21 20 12 21 21 21 21 ...
## $ death : int 21 21 21 21 21 15 21 21 21 21 ...
## $ waterloss: num 2.44 2.45 2.25 2.33 2.45 ...
## $ totbiom : num 0.411 0.356 0.451 NA NA NA 0.51 0.462 0.347 NA ...
## $ leafcol : num NA NA NA 0.581 0.737 ...
```

```
# subset data by Water Treatment
```

```
PlantD <- subset(Plant, Water=="Drought")
```

```
PlantW <- subset(Plant, Water=="WellWatered")
```

```
# subset data by Fungus Treatment
```

```
PlantCon <- subset(Plant, Fungus=="Con")
```

```
PlantAlt <- subset(Plant, Fungus=="Alt")
```

```
PlantCer <- subset(Plant, Fungus=="Cer")
```

```
PlantCoc <- subset(Plant, Fungus=="Coc")
```

```
PlantNig <- subset(Plant, Fungus=="Nig")
```

```
PlantPen <- subset(Plant, Fungus=="Pen")
```

```
PlantSor <- subset(Plant, Fungus=="Sor")
```

Check assumptions

```
# normality
```

```
stats::shapiro.test(Plant$rgr)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: Plant$rgr
```

```
## W = 0.94036, p-value = 0.0007238
```

```
stats::shapiro.test(Plant$wilt)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: Plant$wilt
```

```
## W = 0.83443, p-value = 2.846e-08
```

```
stats::shapiro.test(Plant$waterloss)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: Plant$waterloss
```

```
## W = 0.88782, p-value = 2.405e-06
```

```
stats::shapiro.test(Plant$death)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: Plant$death
```

```
## W = 0.69828, p-value = 7.563e-12
```

```
stats::shapiro.test(Plant$totbiom)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: Plant$totbiom
```

```
## W = 0.93284, p-value = 0.01618
```

```
stats::shapiro.test(Plant$leafcol)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: Plant$leafcol
```

```
## W = 0.77892, p-value = 1.621e-06
```

```
# homogeneity of variance
```

```
car::leveneTest(rgr ~Fungus*Water, data=Plant)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value    Pr(>F)
## group 13  4.2582 3.333e-05 ***
##      70
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
car::leveneTest(wilt ~Fungus*Water, data=Plant)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value    Pr(>F)
## group 13  3.0262 0.001413 **
##      70
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
car::leveneTest(waterloss ~Fungus*Water, data=Plant)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value    Pr(>F)
## group 13  4.1822 4.176e-05 ***
##      70
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
car::leveneTest(death ~Fungus*Water, data=Plant)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 13  1.9747 0.0359 *
##      70
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
car::leveneTest(totbiom ~Fungus*Water, data=Plant)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 13  0.6233 0.8143
##      28
```

```
car::leveneTest(leafcol ~Fungus*Water, data=Plant)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 13  0.8597 0.5999
##      28
```

```
# at least one assumption violated for each var; use perMANOVA
```

Permutational ANOVAs and posthocs

RGR - height relative growth rate

```
# Permanova
# use TypeIII SS seqs=FALSE
# use all permutations of Y perm="Exact"
rgr_aovp <- lmPerm::aovp (rgr ~ Fungus * Water, data=Plant, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(rgr_aovp)
```

```
## Component 1 :
##           Df R Sum Sq R Mean Sq Iter  Pr(Prob)
## Fungus      6  5.0092  0.83487 5000 < 2.2e-16 ***
## Water       1  1.5301  1.53009 5000 < 2.2e-16 ***
## Fungus:Water 6  1.1593  0.19321 5000 < 2.2e-16 ***
## Residuals   70  1.0640  0.01520
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(rgr_aovp), path="rgr_aovp.xlsx")
```

```
# Posthoc on fungal main effect
rgr_phf <- rcompanion::pairwisePermutationTest(rgr ~ Fungus, data=Plant, method="fdr")
write_xlsx(rgr_phf, path="rgr_ph_f.xlsx")
rcompanion::pairwisePermutationMatrix(rgr ~ Fungus, data=Plant, method="fdr")
```

```
## $Unadjusted
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt  NA 0.0006431 0.0124100 0.0109000 1.666e-04 1.168e-02 0.1760000
## Cer  NA      NA 0.0000069 0.8314000 1.153e-02 5.506e-03 0.0045530
## Coc  NA      NA      NA 0.0004843 1.711e-05 6.636e-06 0.0003797
## Con  NA      NA      NA      NA 9.449e-02 1.265e-01 0.0515300
## Nig  NA      NA      NA      NA      NA 5.525e-04 0.0004593
## Pen  NA      NA      NA      NA      NA      NA 0.2002000
## Sor  NA      NA      NA      NA      NA      NA      NA
##
## $Method
## [1] "fdr"
##
## $Adjusted
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt 1.0000000 1.501e-03 1.737e-02 0.01737 0.0008746 1.737e-02 0.194500
## Cer 0.0015010 1.000e+00 7.245e-05 0.83140 0.0173700 1.051e-02 0.009561
## Coc 0.0173700 7.245e-05 1.000e+00 0.00145 0.0001198 7.245e-05 0.001450
## Con 0.0173700 8.314e-01 1.450e-03 1.00000 0.1167000 1.476e-01 0.067630
```

```
## Nig 0.0008746 1.737e-02 1.198e-04 0.11670 1.0000000 1.450e-03 0.001450
## Pen 0.0173700 1.051e-02 7.245e-05 0.14760 0.0014500 1.000e+00 0.210200
## Sor 0.1945000 9.561e-03 1.450e-03 0.06763 0.0014500 2.102e-01 1.000000
```

```
# Posthocs on the interaction term
```

```
# By fungus in each water treatment
```

```
rgr_phfw_d <- rcompanion::pairwisePermutationTest(rgr ~ Fungus, data=PlantD, method="fdr")
rgr_phfw_d
```

```
##      Comparison      Stat  p.value p.adjust
## 1  Alt - Cer = 0 -2.997 0.002728 0.01531
## 2  Alt - Coc = 0 0.4071 0.6839 0.68390
## 3  Alt - Con = 0 -2.402 0.01633 0.02634
## 4  Alt - Nig = 0 -2.71 0.00673 0.01767
## 5  Alt - Pen = 0 -2.976 0.002916 0.01531
## 6  Alt - Sor = 0 -1.707 0.0878 0.11520
## 7  Cer - Coc = 0 3.107 0.00189 0.01531
## 8  Cer - Con = 0 2.713 0.006661 0.01767
## 9  Cer - Nig = 0 -1.365 0.1722 0.20090
## 10 Cer - Pen = 0 0.4859 0.627 0.65840
## 11 Cer - Sor = 0 2.528 0.01147 0.02409
## 12 Coc - Con = 0 -2.771 0.005593 0.01767
## 13 Coc - Nig = 0 -2.77 0.005608 0.01767
## 14 Coc - Pen = 0 -3.1 0.001934 0.01531
## 15 Coc - Sor = 0 -2.038 0.04157 0.05820
## 16 Con - Nig = 0 -2.375 0.01756 0.02634
## 17 Con - Pen = 0 -2.641 0.008265 0.01928
## 18 Con - Sor = 0 0.6037 0.5461 0.60360
## 19 Nig - Pen = 0 1.527 0.1268 0.15660
## 20 Nig - Sor = 0 2.393 0.0167 0.02634
## 21 Pen - Sor = 0 2.439 0.01475 0.02634
```

```
write_xlsx(rgr_phfw_d, path="rgr_phfw_d.xlsx")
```

```
rgr_phfw_w <- rcompanion::pairwisePermutationTest(rgr ~ Fungus, data=PlantW, method="fdr")
rgr_phfw_w
```

```
##      Comparison      Stat  p.value p.adjust
## 1  Alt - Cer = 0 -2.704 0.006845 0.008984
## 2  Alt - Coc = 0 2.871 0.004092 0.005729
## 3  Alt - Con = 0 -3.092 0.00199 0.003482
## 4  Alt - Nig = 0 -3.144 0.001667 0.003482
## 5  Alt - Pen = 0 -0.09978 0.9205 0.920500
## 6  Alt - Sor = 0 -1.14 0.2543 0.267000
## 7  Cer - Coc = 0 3.293 0.0009927 0.003482
## 8  Cer - Con = 0 -3.044 0.002336 0.003510
## 9  Cer - Nig = 0 -3.171 0.001519 0.003482
## 10 Cer - Pen = 0 3.043 0.00234 0.003510
## 11 Cer - Sor = 0 2.592 0.009555 0.011800
## 12 Coc - Con = 0 -3.293 0.0009929 0.003482
## 13 Coc - Nig = 0 -3.301 0.0009619 0.003482
## 14 Coc - Pen = 0 -3.158 0.001587 0.003482
## 15 Coc - Sor = 0 -3.13 0.00175 0.003482
```

```

## 16 Con - Nig = 0    -1.467    0.1425 0.166200
## 17 Con - Pen = 0     3.21    0.00133 0.003482
## 18 Con - Sor = 0     3.107    0.001889 0.003482
## 19 Nig - Pen = 0     3.243    0.001182 0.003482
## 20 Nig - Sor = 0     3.167    0.001538 0.003482
## 21 Pen - Sor = 0    -1.385    0.1661 0.183600

write_xlsx(rgr_phfw_w, path="rgr_phfw_w.xlsx")

# By water in each fungus treatment
rgr_phfw_Alt <- lmPerm::aovp(rgr ~ Water, data=PlantAlt, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

summary(rgr_phfw_Alt)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water           1 0.33367  0.33367 5000  0.0106 *
## Residuals      10 0.17528  0.01753
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

write_xlsx(summary(rgr_phfw_Alt), path="rgr_phfw_Alt.xlsx")

rgr_phfw_Cer <- lmPerm::aovp(rgr ~ Water, data=PlantCer, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

summary(rgr_phfw_Cer)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water           1 0.138460  0.13846 5000  0.0064 **
## Residuals      10 0.063603  0.00636
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

write_xlsx(summary(rgr_phfw_Cer), path="rgr_phfw_Cer.xlsx")

rgr_phfw_Coc <- lmPerm::aovp(rgr ~ Water, data=PlantCoc, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

summary(rgr_phfw_Coc)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water           1 0.0002341 0.00023408  51  0.9412
## Residuals      10 0.0311168 0.00311168

```

```

write_xlsx(summary(rgr_phfw_Coc), path="rgr_phfw_Coc.xlsx")

rgr_phfw_Con <- lmPerm::aovp(rgr ~ Water, data=PlantCon, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

summary(rgr_phfw_Con)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1  1.56313   1.56313  5000    6e-04 ***
## Residuals  10  0.05756   0.00576
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

write_xlsx(summary(rgr_phfw_Con), path="rgr_phfw_Con.xlsx")

rgr_phfw_Nig <- lmPerm::aovp(rgr ~ Water, data=PlantNig, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

summary(rgr_phfw_Nig)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1  0.40959   0.40959  3367   0.02911 *
## Residuals  10  0.49124   0.04912
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

write_xlsx(summary(rgr_phfw_Nig), path="rgr_phfw_Nig.xlsx")

rgr_phfw_Pen <- lmPerm::aovp(rgr ~ Water, data=PlantPen, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

summary(rgr_phfw_Pen)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1  0.005125  0.0051253  146    0.411
## Residuals  10  0.077418  0.0077418

write_xlsx(summary(rgr_phfw_Pen), path="rgr_phfw_Pen.xlsx")

rgr_phfw_Sor <- lmPerm::aovp(rgr ~ Water, data=PlantSor, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

```

```
summary(rgr_phfw_Sor)
```

```
## Component 1 :  
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)  
## Water      1 0.23914 0.239136 5000 0.0062 **  
## Residuals 10 0.16777 0.016777  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(rgr_phfw_Sor), path="rgr_phfw_Sor.xlsx")
```

Total biomass - root + shoot

```
# subset for only replicates with biomass data  
Plant_biom <- dplyr::filter(Plant, !is.na(totbiom))  
  
# Permanova  
# use TypeIII SS seqs=FALSE  
# use all permutations of Y perm="Exact"  
totbiom_aovp <- lmPerm::aovp (totbiom ~ Fungus * Water, data=Plant_biom, perm="Exact", seqs=FALSE, center=FALSE)  
  
## [1] "Settings: unique SS "
```

```
summary(totbiom_aovp)
```

```
## Component 1 :  
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)  
## Fungus      6 0.034072 0.0056787 5000 0.1628  
## Water       1 0.003983 0.0039829   84 0.5476  
## Fungus:Water 6 0.020992 0.0034987  993 0.4099  
## Residuals   28 0.096740 0.0034550
```

```
write_xlsx(summary(totbiom_aovp), path="totbiom_aovp.xlsx")
```

```
# Posthoc on fungal main effect - NS  
# Posthocs on the interaction term - NS
```

Wilt - days to first wilt

```
# Permanova  
# use TypeIII SS seqs=FALSE  
# use all permutations of Y perm="Exact"  
wilt_aovp <- lmPerm::aovp (wilt ~ Fungus * Water, data=Plant, perm="Exact", seqs=FALSE, center=FALSE)  
  
## [1] "Settings: unique SS "
```

```
summary(wilt_aovp)
```



```
## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Fungus      6 1045.48   174.25 5000  <2e-16 ***
## Water       1 1265.19  1265.19 5000  <2e-16 ***
## Fungus:Water 6   235.14    39.19 5000  0.0104 *
## Residuals   70   958.00    13.69
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(wilt_aovp), path="wilt_aovp.xlsx")
```

```
# Posthoc on fungal main effect
```

```
wilt_phf <- rcompanion::pairwisePermutationTest(wilt ~ Fungus, data=Plant, method="fdr")
write_xlsx(wilt_phf, path="wilt_ph_f.xlsx")
rcompanion::pairwisePermutationMatrix(wilt ~ Fungus, data=Plant, method="fdr")
```

```
## $Unadjusted
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt  NA 0.02455 0.0002576 0.04445 0.1629 0.298900 0.0004056
## Cer  NA      NA 0.1401000 0.70090 0.2864 0.096890 0.1406000
## Coc  NA      NA      NA 0.05644 0.0103 0.001379 0.9424000
## Con  NA      NA      NA      NA 0.4749 0.179600 0.0594900
## Nig  NA      NA      NA      NA      NA 0.539200 0.0120200
## Pen  NA      NA      NA      NA      NA      NA 0.0019280
## Sor  NA      NA      NA      NA      NA      NA      NA
##
## $Method
## [1] "fdr"
##
## $Adjusted
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt 1.000000 0.07365 0.004259 0.1167 0.24440 0.369200 0.004259
## Cer 0.073650 1.00000 0.227100 0.7359 0.36920 0.185000 0.227100
## Coc 0.004259 0.22710 1.000000 0.1249 0.04207 0.009653 0.942400
## Con 0.116700 0.73590 0.124900 1.0000 0.55400 0.251400 0.124900
## Nig 0.244400 0.36920 0.042070 0.5540 1.00000 0.596000 0.042070
## Pen 0.369200 0.18500 0.009653 0.2514 0.59600 1.000000 0.010120
## Sor 0.004259 0.22710 0.942400 0.1249 0.04207 0.010120 1.000000
```

```
# Posthocs on the interaction term - NS
```

WaterLoss - average weekly whole-plant water loss

```
# Permanova
```

```
# use TypeIII SS seqs=FALSE
```

```
# use all permutations of Y perm="Exact"
```

```
waterloss_aovp <- lmPerm::aovp (waterloss ~ Fungus * Water, data=Plant, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(waterloss_aovp)
```

```
## Component 1 :
##           Df R Sum Sq R Mean Sq Iter  Pr(Prob)
## Fungus      6 11.5061   1.9177 5000 < 2.2e-16 ***
## Water       1  9.4094   9.4094 5000 < 2.2e-16 ***
## Fungus:Water 6  9.8063   1.6344 5000 < 2.2e-16 ***
## Residuals   70  2.6125   0.0373
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(waterloss_aovp), path="waterlossavg_aovp.xlsx")
```

```
# Posthoc on fungal main effect
```

```
waterloss_phf <- rcompanion::pairwisePermutationTest(waterloss ~ Fungus, data=Plant, method="fdr")
write_xlsx(waterloss_phf, path="waterlossavg_ph_f.xlsx")
rcompanion::pairwisePermutationMatrix(waterloss ~ Fungus, data=Plant, method="fdr")
```

```
## $Unadjusted
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt  NA 0.006773 0.06390 0.007443 0.142300 0.08140 0.0024000
## Cer  NA      NA 0.02494 0.969300 0.007191 0.03073 0.1313000
## Coc  NA      NA      NA 0.033130 0.432000 0.88100 0.0024340
## Con  NA      NA      NA      NA 0.009646 0.03849 0.1479000
## Nig  NA      NA      NA      NA      NA 0.55870 0.0009942
## Pen  NA      NA      NA      NA      NA      NA 0.0037790
## Sor  NA      NA      NA      NA      NA      NA      NA
##
## $Method
## [1] "fdr"
##
## $Adjusted
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt 1.00000 0.02233 0.10320 0.02233 0.18270 0.12210 0.01704
## Cer 0.02233 1.00000 0.05819 0.96930 0.02233 0.06325 0.18270
## Coc 0.10320 0.05819 1.00000 0.06325 0.50400 0.92500 0.01704
## Con 0.02233 0.96930 0.06325 1.00000 0.02532 0.06736 0.18270
## Nig 0.18270 0.02233 0.50400 0.02532 1.00000 0.61750 0.01704
## Pen 0.12210 0.06325 0.92500 0.06736 0.61750 1.00000 0.01984
## Sor 0.01704 0.18270 0.01704 0.18270 0.01704 0.01984 1.00000
```

```
# Posthocs on the interaction term
```

```
# By fungus in each water treatment
```

```
waterloss_phfw_d <- rcompanion::pairwisePermutationTest(waterloss ~ Fungus, data=PlantD, method="fdr")
waterloss_phfw_d
```

```
##      Comparison  Stat  p.value p.adjust
## 1  Alt - Cer = 0 -3.298 0.0009746 0.002214
## 2  Alt - Coc = 0 -3.242 0.001188 0.002214
## 3  Alt - Con = 0 -3.31 0.0009333 0.002214
## 4  Alt - Nig = 0 -3.269 0.001079 0.002214
## 5  Alt - Pen = 0 -3.283 0.001028 0.002214
```

```
## 6  Alt - Sor = 0 -3.304 0.0009524 0.002214
## 7  Cer - Coc = 0  2.898  0.003753 0.004636
## 8  Cer - Con = 0 0.1187    0.9055 0.905500
## 9  Cer - Nig = 0  3.191  0.001419 0.002214
## 10 Cer - Pen = 0  3.179  0.001476 0.002214
## 11 Cer - Sor = 0 -3.092  0.001986 0.002780
## 12 Coc - Con = 0 -2.991  0.002785 0.003655
## 13 Coc - Nig = 0  1.995   0.04603 0.053700
## 14 Coc - Pen = 0  1.461    0.144 0.159200
## 15 Coc - Sor = 0 -3.204  0.001357 0.002214
## 16 Con - Nig = 0  3.255  0.001135 0.002214
## 17 Con - Pen = 0   3.26  0.001115 0.002214
## 18 Con - Sor = 0 -3.184  0.001454 0.002214
## 19 Nig - Pen = 0 -1.319    0.1872 0.196600
## 20 Nig - Sor = 0 -3.271  0.00107 0.002214
## 21 Pen - Sor = 0 -3.271  0.001071 0.002214
```

```
write_xlsx(waterloss_phfw_d, path="waterlossavg_phfw_d.xlsx")
```

```
waterloss_phfw_w <- rcompanion::pairwisePermutationTest(waterloss ~ Fungus, data=PlantW, method="fdr")
waterloss_phfw_w
```

```
##      Comparison      Stat p.value p.adjust
## 1  Alt - Cer = 0    -1.29  0.1969  0.5964
## 2  Alt - Coc = 0   0.02989 0.9762  0.9838
## 3  Alt - Con = 0    -1.04  0.2982  0.5964
## 4  Alt - Nig = 0   0.8198  0.4123  0.6184
## 5  Alt - Pen = 0    -1.01  0.3124  0.5964
## 6  Alt - Sor = 0   0.3643  0.7157  0.8460
## 7  Cer - Coc = 0    1.235  0.2169  0.5964
## 8  Cer - Con = 0   0.02035 0.9838  0.9838
## 9  Cer - Nig = 0    1.656 0.09773 0.5964
## 10 Cer - Pen = 0   0.8469  0.3971  0.6184
## 11 Cer - Sor = 0    1.427  0.1535  0.5964
## 12 Coc - Con = 0   -1.014  0.3105  0.5964
## 13 Coc - Nig = 0   0.6436  0.5198  0.6822
## 14 Coc - Pen = 0  -0.8629  0.3882  0.6184
## 15 Coc - Sor = 0   0.2876  0.7737  0.8551
## 16 Con - Nig = 0    1.355  0.1755  0.5964
## 17 Con - Pen = 0   0.6532  0.5136  0.6822
## 18 Con - Sor = 0    1.175  0.2401  0.5964
## 19 Nig - Pen = 0   -1.831 0.06703 0.5964
## 20 Nig - Sor = 0  -0.3517  0.7251  0.8460
## 21 Pen - Sor = 0    1.247  0.2125  0.5964
```

```
write_xlsx(waterloss_phfw_w, path="waterlossavg_phfw_w.xlsx")
```

```
# By water in each fungus treatment
```

```
waterloss_phfw_Alt <- lmPerm::aovp(waterloss ~ Water, data=PlantAlt, perm="Exact", seqs=FALSE, center=F)
```

```
## [1] "Settings:  unique SS "
```

```
summary(waterloss_phfw_Alt)
```

```
## Component 1 :  
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)  
## Water      1 11.5558  11.5558 5000  0.0028 **  
## Residuals 10  0.1509   0.0151  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(waterloss_phfw_Alt), path="waterlossavg_phfw_Alt.xlsx")
```

```
waterloss_phfw_Cer <- lmPerm::aovp(waterloss ~ Water, data=PlantCer, perm="Exact", seqs=FALSE, center=F
```

```
## [1] "Settings: unique SS "
```

```
summary(waterloss_phfw_Cer)
```

```
## Component 1 :  
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)  
## Water      1  0.40568   0.40568 5000  0.0176 *  
## Residuals 10  0.62890   0.06289  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(waterloss_phfw_Cer), path="waterlossavg_phfw_Cer.xlsx")
```

```
waterloss_phfw_Coc <- lmPerm::aovp(waterloss ~ Water, data=PlantCoc, perm="Exact", seqs=FALSE, center=F
```

```
## [1] "Settings: unique SS "
```

```
summary(waterloss_phfw_Coc)
```

```
## Component 1 :  
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)  
## Water      1  1.45812   1.45812 5000  0.0016 **  
## Residuals 10  0.39757   0.03976  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(waterloss_phfw_Coc), path="waterlossavg_phfw_Coc.xlsx")
```

```
waterloss_phfw_Con <- lmPerm::aovp(waterloss ~ Water, data=PlantCon, perm="Exact", seqs=FALSE, center=F
```

```
## [1] "Settings: unique SS "
```

```
summary(waterloss_phfw_Con)
```

```

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1  0.40893   0.40893   776   0.1147
## Residuals  10  0.93457   0.09346

write_xlsx(summary(waterloss_phfw_Con), path="waterlossavg_phfw_Con.xlsx")

waterloss_phfw_Nig <- lmPerm::aovp(waterloss ~ Water, data=PlantNig, perm="Exact", seqs=FALSE, center=F)

## [1] "Settings: unique SS "

summary(waterloss_phfw_Nig)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1  2.18359   2.18359  5000   0.002 **
## Residuals  10  0.13057   0.01306
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

write_xlsx(summary(waterloss_phfw_Nig), path="waterlossavg_phfw_Nig.xlsx")

waterloss_phfw_Pen <- lmPerm::aovp(waterloss ~ Water, data=PlantPen, perm="Exact", seqs=FALSE, center=F)

## [1] "Settings: unique SS "

summary(waterloss_phfw_Pen)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1  2.51351   2.51351  5000   0.0024 **
## Residuals  10  0.11159   0.01116
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

write_xlsx(summary(waterloss_phfw_Pen), path="waterlossavg_phfw_Pen.xlsx")

waterloss_phfw_Sor <- lmPerm::aovp(waterloss ~ Water, data=PlantSor, perm="Exact", seqs=FALSE, center=F)

## [1] "Settings: unique SS "

summary(waterloss_phfw_Sor)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1  0.69000   0.69000  5000   0.005 **
## Residuals  10  0.25845   0.02584
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
write_xlsx(summary(waterloss_phfw_Sor), path="waterlossavg_phfw_Sor.xlsx")
```

Survival - days to first tiller death

```
# Permanova
# use TypeIII SS seqs=FALSE
# use all permutations of Y perm="Exact"
death_aovp <- lmPerm::aovp (death ~ Fungus * Water, data=Plant, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(death_aovp)
```

```
## Component 1 :
##              Df R Sum Sq R Mean Sq Iter   Pr(Prob)
## Fungus         6  491.57    81.93 5000 < 2.2e-16 ***
## Water          1  906.86   906.86 5000 < 2.2e-16 ***
## Fungus:Water    6   365.14    60.86 5000 < 2.2e-16 ***
## Residuals      70 1044.00    14.91
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(death_aovp), path="death_aovp.xlsx")
```

```
# Posthoc on fungal main effect
death_phf <- rcompanion::pairwisePermutationTest(death ~ Fungus, data=Plant, method="fdr")
write_xlsx(death_phf, path="death_ph_f.xlsx")
rcompanion::pairwisePermutationMatrix(death ~ Fungus, data=Plant, method="fdr")
```

```
## $Unadjusted
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt  NA 0.03498 0.00443 0.01609 0.27830 0.50190 0.01931
## Cer  NA      NA 0.49090 0.77330 0.26150 0.05751 0.65580
## Coc  NA      NA      NA 0.68920 0.06619 0.00752 0.85280
## Con  NA      NA      NA      NA 0.15600 0.02688 0.85700
## Nig  NA      NA      NA      NA      NA 0.43870 0.13860
## Pen  NA      NA      NA      NA      NA      NA 0.03020
## Sor  NA      NA      NA      NA      NA      NA      NA
##
## $Method
## [1] "fdr"
##
## $Adjusted
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt 1.00000 0.1049 0.07896 0.1014 0.4496 0.65870 0.1014
## Cer 0.10490 1.0000 0.65870 0.8547 0.4496 0.15100 0.8041
## Coc 0.07896 0.6587 1.00000 0.8041 0.1544 0.07896 0.8570
## Con 0.10140 0.8547 0.80410 1.0000 0.2978 0.10490 0.8570
## Nig 0.44960 0.4496 0.15440 0.2978 1.0000 0.65800 0.2911
## Pen 0.65870 0.1510 0.07896 0.1049 0.6580 1.00000 0.1049
## Sor 0.10140 0.8041 0.85700 0.8570 0.2911 0.10490 1.0000
```

```

# Posthocs on the interaction term
# By fungus in each water treatment
death_phfw_d <- rcompanion::pairwisePermutationTest(death ~ Fungus, data=PlantD, method="fdr")
death_phfw_d

```

```

##      Comparison      Stat  p.value p.adjust
## 1  Alt - Cer = 0    2.445  0.01447  0.06077
## 2  Alt - Coc = 0    2.269  0.02324  0.06972
## 3  Alt - Con = 0    2.935  0.003332  0.04347
## 4  Alt - Nig = 0    0.9619  0.3361  0.54290
## 5  Alt - Pen = 0    0.7237  0.4692  0.68900
## 6  Alt - Sor = 0    2.599  0.009341  0.06077
## 7  Cer - Coc = 0      0      1  1.00000
## 8  Cer - Con = 0    0.5536  0.5798  0.68900
## 9  Cer - Nig = 0   -1.475  0.1402  0.26770
## 10 Cer - Pen = 0   -2.309  0.02092  0.06972
## 11 Cer - Sor = 0    0.5863  0.5577  0.68900
## 12 Coc - Con = 0    0.4861  0.6269  0.69290
## 13 Coc - Nig = 0   -1.386  0.1656  0.28980
## 14 Coc - Pen = 0   -2.124  0.03364  0.08830
## 15 Coc - Sor = 0    0.538  0.5906  0.68900
## 16 Con - Nig = 0   -1.938  0.05263  0.12280
## 17 Con - Pen = 0   -2.867  0.00414  0.04347
## 18 Con - Sor = 0    0.178  0.8587  0.90160
## 19 Nig - Pen = 0   -0.6568  0.5113  0.68900
## 20 Nig - Sor = 0    1.797  0.07233  0.15190
## 21 Pen - Sor = 0     2.5  0.01242  0.06077

```

```

write_xlsx(death_phfw_d, path="death_phfw_d.xlsx")

```

```

death_phfw_w <- rcompanion::pairwisePermutationTest(death ~ Fungus, data=PlantW, method="fdr")

```

```

## Warning in .local(.Object, ...): The conditional covariance matrix has zero
## diagonal elements

```

```

## Warning in .local(.Object, ...): The conditional covariance matrix has zero
## diagonal elements

```

```

## Warning in .local(.Object, ...): The conditional covariance matrix has zero
## diagonal elements

```

```

## Warning in .local(.Object, ...): The conditional covariance matrix has zero
## diagonal elements

```

```

## Warning in .local(.Object, ...): The conditional covariance matrix has zero
## diagonal elements

```

```

## Warning in .local(.Object, ...): The conditional covariance matrix has zero
## diagonal elements

```

```

death_phfw_w

```

```
##      Comparison      Stat p.value p.adjust
## 1  Alt - Cer = 0      NaN      NaN      NaN
## 2  Alt - Coc = 0    2.548 0.01082  0.04058
## 3  Alt - Con = 0      NaN      NaN      NaN
## 4  Alt - Nig = 0       1    0.3173  0.34000
## 5  Alt - Pen = 0      NaN      NaN      NaN
## 6  Alt - Sor = 0       1    0.3173  0.34000
## 7  Cer - Coc = 0    2.548 0.01082  0.04058
## 8  Cer - Con = 0      NaN      NaN      NaN
## 9  Cer - Nig = 0       1    0.3173  0.34000
## 10 Cer - Pen = 0      NaN      NaN      NaN
## 11 Cer - Sor = 0       1    0.3173  0.34000
## 12 Coc - Con = 0   -2.548 0.01082  0.04058
## 13 Coc - Nig = 0   -2.225 0.02609  0.06522
## 14 Coc - Pen = 0   -2.548 0.01082  0.04058
## 15 Coc - Sor = 0   -2.225 0.02609  0.06522
## 16 Con - Nig = 0       1    0.3173  0.34000
## 17 Con - Pen = 0      NaN      NaN      NaN
## 18 Con - Sor = 0       1    0.3173  0.34000
## 19 Nig - Pen = 0      -1    0.3173  0.34000
## 20 Nig - Sor = 0       0       1    1.00000
## 21 Pen - Sor = 0       1    0.3173  0.34000
```

```
write_xlsx(death_phfw_w, path="death_phfw_w.xlsx")
```

```
# By water in each fungus treatment
```

```
death_phfw_Alt <- lmPerm::aovp(death ~ Water, data=PlantAlt, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(death_phfw_Alt)
```

```
## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1      3      3      51      1
## Residuals 10     30      3
```

```
write_xlsx(summary(death_phfw_Alt), path="death_phfw_Alt.xlsx")
```

```
death_phfw_Cer <- lmPerm::aovp(death ~ Water, data=PlantCer, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(death_phfw_Cer)
```

```
## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1    300    300.0 5000  0.0184 *
## Residuals 10    174     17.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```

write_xlsx(summary(death_phfw_Cer), path="death_phfw_Cer.xlsx")

death_phfw_Coc <- lmPerm::aovp(death ~ Water, data=PlantCoc, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

summary(death_phfw_Coc)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1  126.75   126.75 1384  0.06792 .
## Residuals 10   271.50    27.15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

write_xlsx(summary(death_phfw_Coc), path="death_phfw_Coc.xlsx")

death_phfw_Con <- lmPerm::aovp(death ~ Water, data=PlantCon, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

summary(death_phfw_Con)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1  396.75   396.75 5000  0.0012 **
## Residuals 10    61.50    6.15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

write_xlsx(summary(death_phfw_Con), path="death_phfw_Con.xlsx")

death_phfw_Nig <- lmPerm::aovp(death ~ Water, data=PlantNig, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

summary(death_phfw_Nig)

## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Water      1   36.75    36.75  58  0.6379
## Residuals 10   271.50    27.15

write_xlsx(summary(death_phfw_Nig), path="death_phfw_Nig.xlsx")

death_phfw_Pen <- lmPerm::aovp(death ~ Water, data=PlantPen, perm="Exact", seqs=FALSE, center=FALSE)

## [1] "Settings: unique SS "

```

```
summary(death_phfw_Pen)
```

```
## Component 1 :  
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)  
## Water      1      12      12  440  0.1864  
## Residuals  10      30       3
```

```
write_xlsx(summary(death_phfw_Pen), path="death_phfw_Pen.xlsx")
```

```
death_phfw_Sor <- lmPerm::aovp(death ~ Water, data=PlantSor, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(death_phfw_Sor)
```

```
## Component 1 :  
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)  
## Water      1  396.75  396.75 5000  0.0158 *  
## Residuals  10  205.50   20.55  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(death_phfw_Sor), path="death_phfw_Sor.xlsx")
```

Leaf colonization

```
# subset for only replicates with leaf colonization data
```

```
Plant_LC <- dplyr::filter(Plant, !is.na(leafcol))
```

```
PlantD_LC <- subset(Plant_LC, Water=="Drought")
```

```
PlantW_LC <- subset(Plant_LC, Water=="WellWatered")
```

```
PlantCon_LC <- subset(Plant_LC, Fungus=="Con")
```

```
PlantAlt_LC <- subset(Plant_LC, Fungus=="Alt")
```

```
PlantCer_LC <- subset(Plant_LC, Fungus=="Cer")
```

```
PlantCoc_LC <- subset(Plant_LC, Fungus=="Coc")
```

```
PlantNig_LC <- subset(Plant_LC, Fungus=="Nig")
```

```
PlantPen_LC <- subset(Plant_LC, Fungus=="Pen")
```

```
PlantSor_LC <- subset(Plant_LC, Fungus=="Sor")
```

```
# Permanova
```

```
# use TypeIII SS seqs=FALSE
```

```
# use all permutations of Y perm="Exact"
```

```
leafcol_aovp <- lmPerm::aovp (leafcol ~ Fungus * Water, data=Plant_LC, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(leafcol_aovp)
```

```
## Component 1 :
##           Df R Sum Sq R Mean Sq Iter Pr(Prob)
## Fungus      6  2.78967   0.46494 5000  <2e-16 ***
## Water       1  0.03721   0.03721 5000   6e-03 **
## Fungus:Water 6  0.17555   0.02926 5000   2e-04 ***
## Residuals   28  0.13361   0.00477
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
write_xlsx(summary(leafcol_aovp), path="leafcol_aovp.xlsx")
```

```
# Posthoc on fungal main effect
```

```
leafcol_phf <- rcompanion::pairwisePermutationTest(leafcol ~ Fungus, data=Plant_LC, method="fdr")
write_xlsx(leafcol_phf, path="leafcol_ph_f.xlsx")
rcompanion::pairwisePermutationMatrix(leafcol ~ Fungus, data=Plant_LC, method="fdr")
```

```
## $Unadjusted
```

```
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt  NA 0.4458 0.49080 0.0011930 0.051840 0.62610 0.573400
## Cer  NA      NA 0.01022 0.0009378 0.039710 0.30010 0.065360
## Coc  NA      NA      NA 0.0009283 0.007947 0.90640 0.928900
## Con  NA      NA      NA      NA 0.001224 0.00158 0.001002
## Nig  NA      NA      NA      NA      NA 0.05983 0.013710
## Pen  NA      NA      NA      NA      NA      NA 0.884100
## Sor  NA      NA      NA      NA      NA      NA      NA
```

```
## $Method
```

```
## [1] "fdr"
```

```
##
```

```
## $Adjusted
```

```
##      Alt      Cer      Coc      Con      Nig      Pen      Sor
## Alt 1.000000 0.624100 0.644200 0.005141 0.098970 0.73040 0.708300
## Cer 0.624100 1.000000 0.026830 0.005141 0.083390 0.45010 0.105600
## Coc 0.644200 0.026830 1.000000 0.005141 0.023840 0.92890 0.928900
## Con 0.005141 0.005141 0.005141 1.000000 0.005141 0.00553 0.005141
## Nig 0.098970 0.083390 0.023840 0.005141 1.000000 0.10470 0.031990
## Pen 0.730400 0.450100 0.928900 0.005530 0.104700 1.00000 0.928900
## Sor 0.708300 0.105600 0.928900 0.005141 0.031990 0.92890 1.000000
```

```
# Posthocs on the interaction term
```

```
# By fungus in each water treatment
```

```
leafcol_phfw_d <- rcompanion::pairwisePermutationTest(leafcol ~ Fungus, data=PlantD_LC, method="fdr")
leafcol_phfw_d
```

```
##      Comparison      Stat p.value p.adjust
## 1 Alt - Cer = 0 -0.498 0.6185 0.66010
## 2 Alt - Coc = 0 -1.232 0.218 0.26300
## 3 Alt - Con = 0 2.209 0.02716 0.07345
## 4 Alt - Nig = 0 0.3945 0.6932 0.69320
## 5 Alt - Pen = 0 -2.067 0.03874 0.07396
## 6 Alt - Sor = 0 -1.376 0.1688 0.23630
## 7 Cer - Coc = 0 -1.303 0.1927 0.25290
## 8 Cer - Con = 0 2.23 0.02573 0.07345
```

```
## 9 Cer - Nig = 0 1.212 0.2254 0.26300
## 10 Cer - Pen = 0 -2.185 0.02892 0.07345
## 11 Cer - Sor = 0 -1.479 0.1392 0.20880
## 12 Coc - Con = 0 2.231 0.02569 0.07345
## 13 Coc - Nig = 0 1.78 0.0751 0.12130
## 14 Coc - Pen = 0 -2.151 0.03148 0.07345
## 15 Coc - Sor = 0 -0.4835 0.6287 0.66010
## 16 Con - Nig = 0 -2.228 0.0259 0.07345
## 17 Con - Pen = 0 -2.236 0.02537 0.07345
## 18 Con - Sor = 0 -2.229 0.02579 0.07345
## 19 Nig - Pen = 0 -2.192 0.02841 0.07345
## 20 Nig - Sor = 0 -1.833 0.06684 0.11700
## 21 Pen - Sor = 0 2.1 0.0357 0.07396
```

```
write_xlsx(leafcol_phfw_d, path="leafcol_phfw_d.xlsx")
```

```
leafcol_phfw_w <- rcompanion::pairwisePermutationTest(leafcol ~ Fungus, data=PlantW_LC, method="fdr")
leafcol_phfw_w
```

```
##      Comparison  Stat p.value p.adjust
## 1 Alt - Cer = 0  1.162 0.2454 0.30670
## 2 Alt - Coc = 0  0.1051 0.9163 0.91630
## 3 Alt - Con = 0  2.184 0.02896 0.08962
## 4 Alt - Nig = 0  1.84 0.06575 0.12550
## 5 Alt - Pen = 0  1.416 0.1568 0.23520
## 6 Alt - Sor = 0  0.3278 0.7431 0.78030
## 7 Cer - Coc = 0 -2.118 0.03414 0.08962
## 8 Cer - Con = 0  2.233 0.02552 0.08962
## 9 Cer - Nig = 0  1.975 0.04832 0.11270
## 10 Cer - Pen = 0  1.053 0.2921 0.34080
## 11 Cer - Sor = 0 -1.154 0.2483 0.30670
## 12 Coc - Con = 0  2.235 0.02544 0.08962
## 13 Coc - Nig = 0  2.121 0.03392 0.08962
## 14 Coc - Pen = 0  1.788 0.07371 0.12900
## 15 Coc - Sor = 0  0.413 0.6796 0.75110
## 16 Con - Nig = 0 -2.201 0.02773 0.08962
## 17 Con - Pen = 0 -2.193 0.02834 0.08962
## 18 Con - Sor = 0 -2.207 0.02729 0.08962
## 19 Nig - Pen = 0 -1.302 0.1929 0.27010
## 20 Nig - Sor = 0 -1.916 0.05541 0.11640
## 21 Pen - Sor = 0 -1.421 0.1553 0.23520
```

```
write_xlsx(leafcol_phfw_w, path="leafcol_phfw_w.xlsx")
```

```
# By water in each fungus treatment
```

```
leafcol_phfw_Alt <- lmPerm::aovp(leafcol ~ Water, data=PlantAlt_LC, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(leafcol_phfw_Alt)
```

```
## Component 1 :
```

```
##           Df R Sum Sq R Mean Sq Pr(Exact)
## Water      1 0.015041  0.015041      1
## Residuals  4 0.059641  0.014910
```

```
write_xlsx(summary(leafcol_phfw_Alt), path="leafcol_phfw_Alt.xlsx")
```

```
leafcol_phfw_Cer <- lmPerm::aovp(leafcol ~ Water, data=PlantCer_LC, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(leafcol_phfw_Cer)
```

```
## Component 1 :
##           Df  R Sum Sq R Mean Sq Pr(Exact)
## Water      1 0.0014039 0.0014039      1
## Residuals  4 0.0047035 0.0011759
```

```
write_xlsx(summary(leafcol_phfw_Cer), path="leafcol_phfw_Cer.xlsx")
```

```
leafcol_phfw_Coc <- lmPerm::aovp(leafcol ~ Water, data=PlantCoc_LC, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(leafcol_phfw_Coc)
```

```
## Component 1 :
##           Df  R Sum Sq R Mean Sq Pr(Exact)
## Water      1 0.0003392 0.0003392      1
## Residuals  4 0.0043183 0.00107958
```

```
write_xlsx(summary(leafcol_phfw_Coc), path="leafcol_phfw_Coc.xlsx")
```

```
leafcol_phfw_Con <- lmPerm::aovp(leafcol ~ Water, data=PlantCon_LC, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(leafcol_phfw_Con)
```

```
## Component 1 :
##           Df    R Sum Sq R Mean Sq Pr(Exact)
## Water      1 0.00002010 2.0104e-05      1
## Residuals  4 0.00083138 2.0784e-04
```

```
write_xlsx(summary(leafcol_phfw_Con), path="leafcol_phfw_Con.xlsx")
```

```
leafcol_phfw_Nig <- lmPerm::aovp(leafcol ~ Water, data=PlantNig_LC, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(leafcol_phfw_Nig)
```

```
## Component 1 :  
##           Df R Sum Sq R Mean Sq Pr(Exact)  
## Water      1 0.035745  0.035745      1  
## Residuals  4 0.016085  0.004021
```

```
write_xlsx(summary(leafcol_phfw_Nig), path="leafcol_phfw_Nig.xlsx")
```

```
leafcol_phfw_Pen <- lmPerm::aovp(leafcol ~ Water, data=PlantPen_LC, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

```
summary(leafcol_phfw_Pen)
```

```
## Component 1 :  
##           Df R Sum Sq R Mean Sq Pr(Exact)  
## Water      1 0.159297  0.159297      1  
## Residuals  4 0.021646  0.005411
```

```
write_xlsx(summary(leafcol_phfw_Pen), path="leafcol_phfw_Pen.xlsx")
```

```
leafcol_phfw_Sor <- lmPerm::aovp(leafcol ~ Water, data=PlantSor_LC, perm="Exact", seqs=FALSE, center=FALSE)
```

```
## [1] "Settings: unique SS "
```

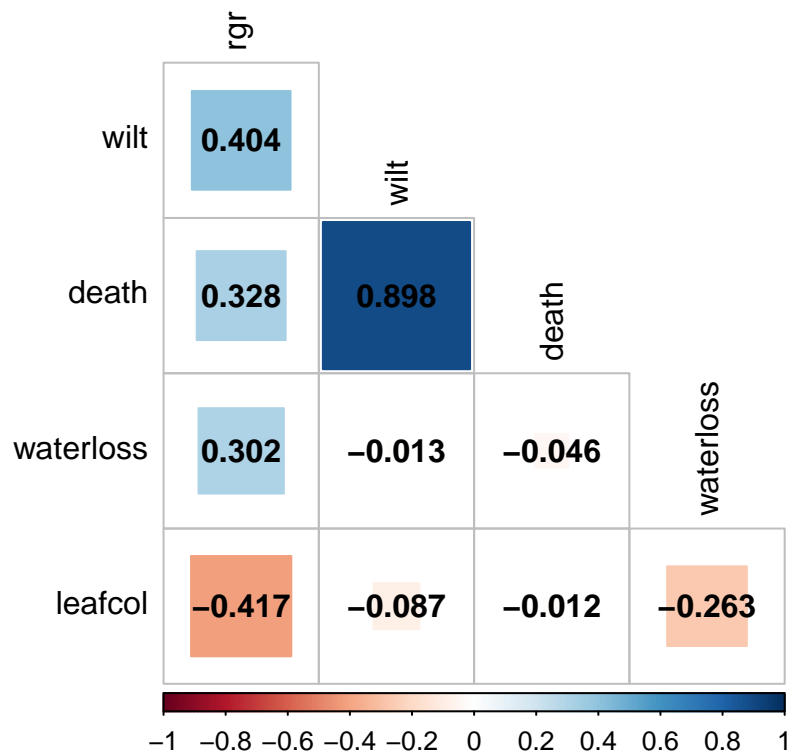
```
summary(leafcol_phfw_Sor)
```

```
## Component 1 :  
##           Df  R Sum Sq R Mean Sq Pr(Exact)  
## Water      1 0.0009149 0.0009149      1  
## Residuals  4 0.0263895 0.0065974
```

```
write_xlsx(summary(leafcol_phfw_Sor), path="leafcol_phfw_Sor.xlsx")
```

Correlations

```
PlantCorr <- select(Plant, c(rgr, wilt, death, waterloss, leafcol))  
PlantCorr <- as.matrix(PlantCorr)  
c <- cor(PlantCorr, use="pairwise.complete.obs")  
corrplot::corrplot(c, method="square",  
                    number.digits = 3,  
                    type="lower",  
                    addCoef.col="black",  
                    diag=FALSE,  
                    tl.col="black"  
                    )
```



Session Info

```
sessionInfo()
```

```
## R version 4.2.2 (2022-10-31 ucrt)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19044)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.utf8
## [2] LC_CTYPE=English_United States.utf8
## [3] LC_MONETARY=English_United States.utf8
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.utf8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] rcompanion_2.4.21 writexl_1.4.2      car_3.1-1          carData_3.0-5
## [5] lmPerm_2.1.0      forcats_0.5.2     stringr_1.5.0      dplyr_1.0.10
## [9] purrr_1.0.1       readr_2.1.3       tidyr_1.2.1        tibble_3.1.8
```

```

## [13] ggplot2_3.4.0      tidyverse_1.3.2
##
## loaded via a namespace (and not attached):
## [1] matrixStats_0.63.0  fs_1.6.0             lubridate_1.9.0
## [4] httr_1.4.4          tools_4.2.2          backports_1.4.1
## [7] utf8_1.2.2          R6_2.5.1             nortest_1.0-4
## [10] DBI_1.1.3           colorspace_2.1-0     withr_2.5.0
## [13] tidyselect_1.2.0    Exact_3.2            compiler_4.2.2
## [16] cli_3.6.0           rvest_1.0.3          expm_0.999-7
## [19] xml2_1.3.3          sandwich_3.0-2       scales_1.2.1
## [22] lmtest_0.9-40       mvtnorm_1.1-3        proxy_0.4-27
## [25] multcompView_0.1-8  digest_0.6.31        rmarkdown_2.20
## [28] pkgconfig_2.0.3     htmltools_0.5.4      highr_0.10
## [31] dbplyr_2.3.0        fastmap_1.1.0        rlang_1.0.6
## [34] readxl_1.4.1        rstudioapi_0.14      generics_0.1.3
## [37] zoo_1.8-11          jsonlite_1.8.4       googlesheets4_1.0.1
## [40] magrittr_2.0.3      modeltools_0.2-23    Matrix_1.5-3
## [43] Rcpp_1.0.10         DescTools_0.99.47    munsell_0.5.0
## [46] fansi_1.0.4         abind_1.4-5          lifecycle_1.0.3
## [49] multcomp_1.4-20     stringi_1.7.12       yaml_2.3.6
## [52] MASS_7.3-58.1       rootSolve_1.8.2.3    plyr_1.8.8
## [55] grid_4.2.2          parallel_4.2.2       crayon_1.5.2
## [58] lmom_2.9            lattice_0.20-45      haven_2.5.1
## [61] splines_4.2.2       hms_1.1.2            knitr_1.42
## [64] pillar_1.8.1        boot_1.3-28.1        gld_2.6.6
## [67] codetools_0.2-18    stats4_4.2.2         reprex_2.0.2
## [70] glue_1.6.2          evaluate_0.20        data.table_1.14.6
## [73] modelr_0.1.10       vctrs_0.5.2          tzdb_0.3.0
## [76] cellranger_1.1.0    gtable_0.3.1         assertthat_0.2.1
## [79] xfun_0.36           coin_1.4-2           libcoin_1.0-9
## [82] broom_1.0.3         e1071_1.7-13         class_7.3-20
## [85] survival_3.4-0      googledrive_2.0.0    gargle_1.3.0
## [88] corrplot_0.92       timechange_0.2.0     TH.data_1.1-1
## [91] ellipsis_0.3.2

```