Appendix 3B - Tests, diagnostic plots and assumption testing

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June 18, 2020

All tests are organized by the results-section of the main document

```
library(lmerTest)
library(psycho)
library(psych)
library(lme4)
library(tidyverse)
library(rcompanion)
library(ggplot2)
library(ggpubr)
library(data.table)
library(car)
library(multcomp)
library(emmeans)
library(vegan)
library(betapart)
library(boxcoxmix)
library(bestNormalize)
library(MuMIn)

knitr::opts_knit$set(root.dir = "C:/Users/lhamberg/Dropbox/TreePaper/r_files/r_mark")
```

3.3.1 - Soil depth and characteristics

Soil depth test

The distribution did not fulfill normality assumptions as per Shapiro test (see below), switched to Wilcoxon signed-rank test which do not assume normality.

```
sdepth <-read.csv("soil_depth.csv")

sdepth[,'Measurement_no']<-factor(sdepth[,'Measurement_no'])

sumdepth <- summary(sdepth)

tdepth <- t.test(Depth ~ Depth_type, data = sdepth, paired = TRUE)

leveneTest(sdepth$Depth ~ sdepth$Depth_type)
```

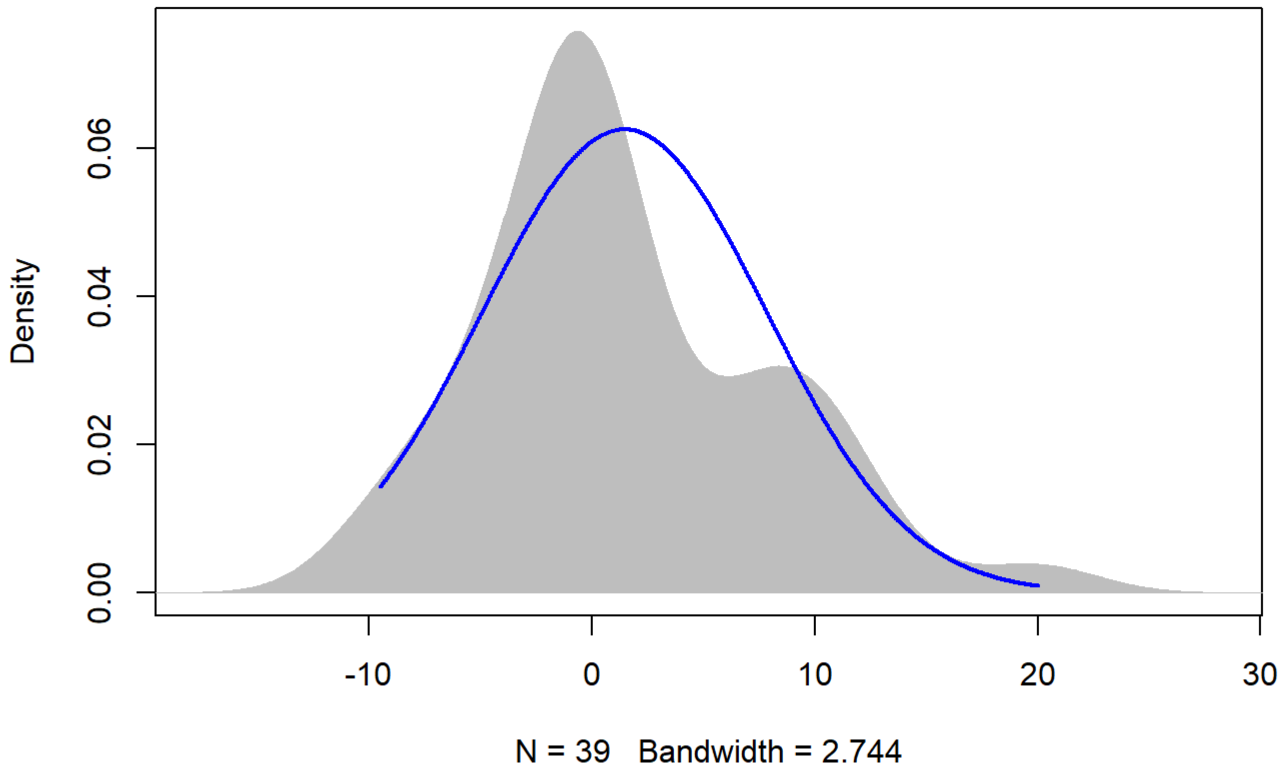
```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
```

```
## group  1   1.361  0.247
##       76
```

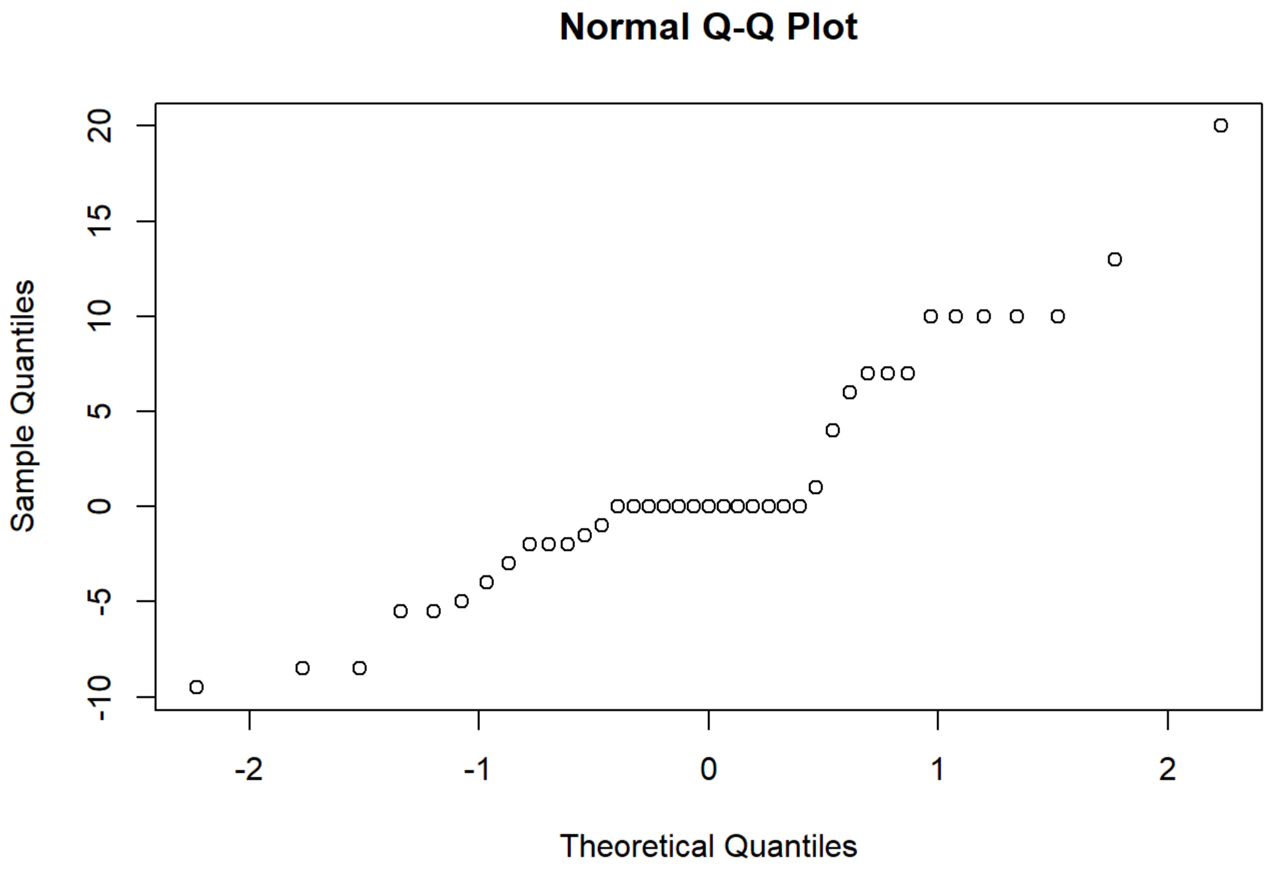
```
shapiro.test(sdepth$DugMinusAvg_rem)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  sdepth$DugMinusAvg_rem
## W = 0.92245, p-value = 0.01037
```

```
plotNormalDensity(sdepth$DugMinusAvg_rem)
```



```
qqnorm(sdepth$DugMinusAvg_rem)
```



```
wilcox.test(Depth ~ Depth_type, data = sdepth, paired = TRUE)
```

```
## Warning in wilcox.test.default(x = c(10, 16, 17, 26, 29, 10, 22, 26, 13, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(x = c(10, 16, 17, 26, 29, 10, 22, 26, 13, :
## cannot compute exact p-value with zeroes
```

```
##
##  Wilcoxon signed rank test with continuity correction
##
## data:  Depth by Depth_type
## V = 122, p-value = 0.1777
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(sdepth$Digging.depth, sdepth$A_horz_avg, paired = TRUE)
```

```
## Warning in wilcox.test.default(sdepth$Digging.depth, sdepth$A_horz_avg, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(sdepth$Digging.depth, sdepth$A_horz_avg, :
## cannot compute exact p-value with zeroes
```

```
##
##  Wilcoxon signed rank test with continuity correction
##
## data:  sdepth$Digging.depth and sdepth$A_horz_avg
## V = 229, p-value = 0.1777
## alternative hypothesis: true location shift is not equal to 0
```

Soil moisture test - ANOVA on lmer and diagnostic plots

2015 Reforestation

```
smoist <-read.csv("soil_moisture.csv")

smoistYA2015 <- filter(smoist, Field == "YA2015")

summary(smoistYA2015$moist)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    1.40    7.40    9.80   10.11   12.97   23.00
```

```
fit <- lmer(moist ~ Plot_treat + Sub_plot_treat + (1 | Plot), data=smoistYA2015, na.action = n
a.fail)

anova(fit, type = "III", ddf="Kenward-Roger")
```

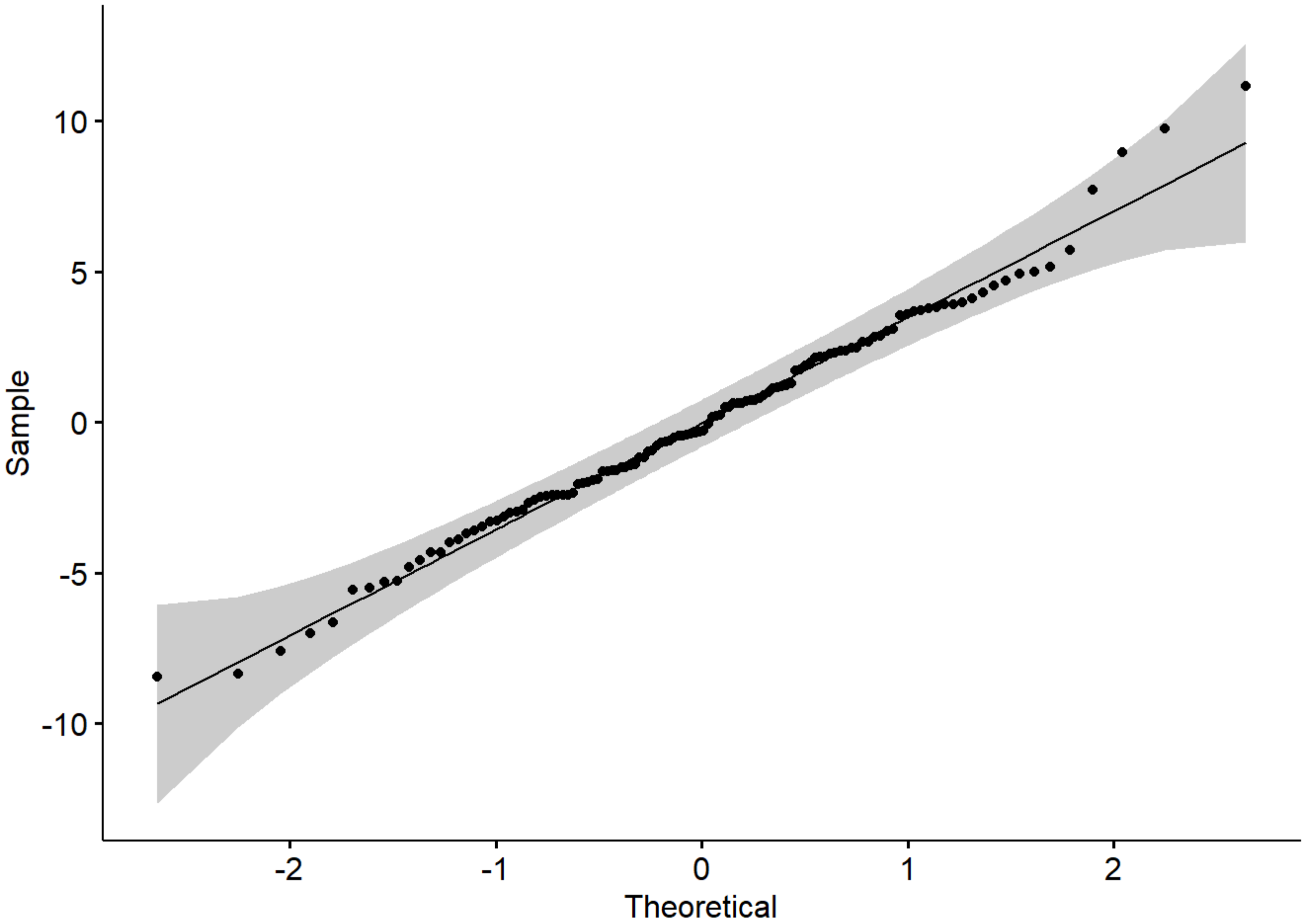
```
## Type III Analysis of Variance Table with Kenward-Roger's method
##                Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## Plot_treat     24.506  12.253     2  13.31  0.8819 0.4369
## Sub_plot_treat 59.385  19.795     3 106.00  1.4375 0.2360
```

```
r.squaredGLMM(fit)
```

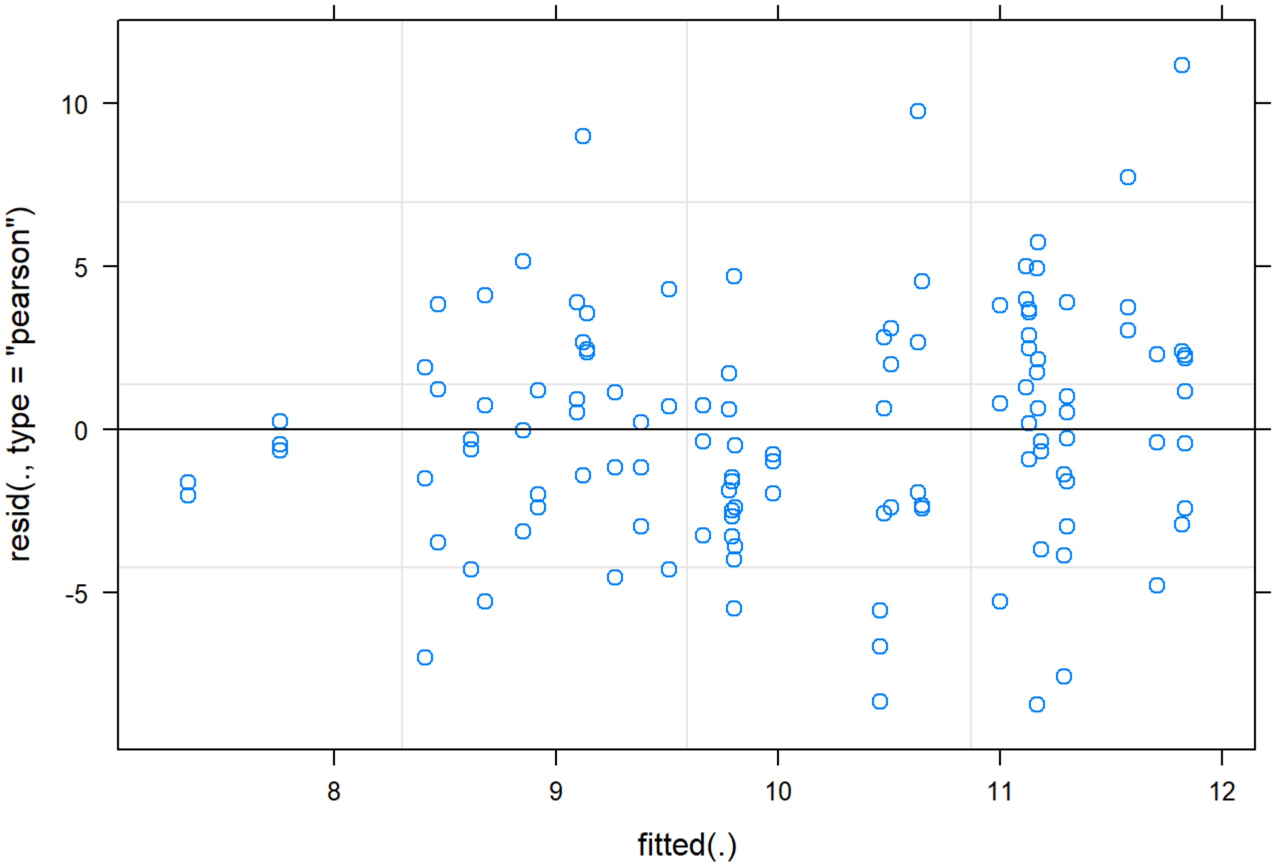
```
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help
## page.
```

```
##             R2m       R2c
## [1,] 0.04425071 0.1689093
```

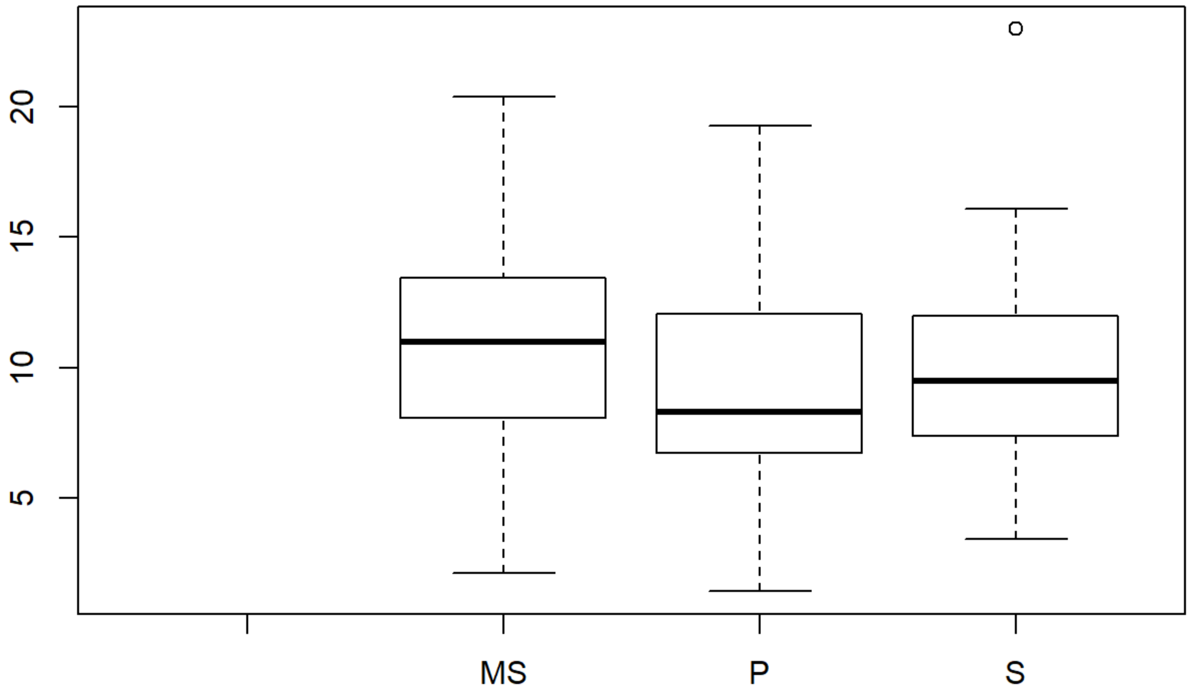
```
ggqqplot(residuals(fit))
```



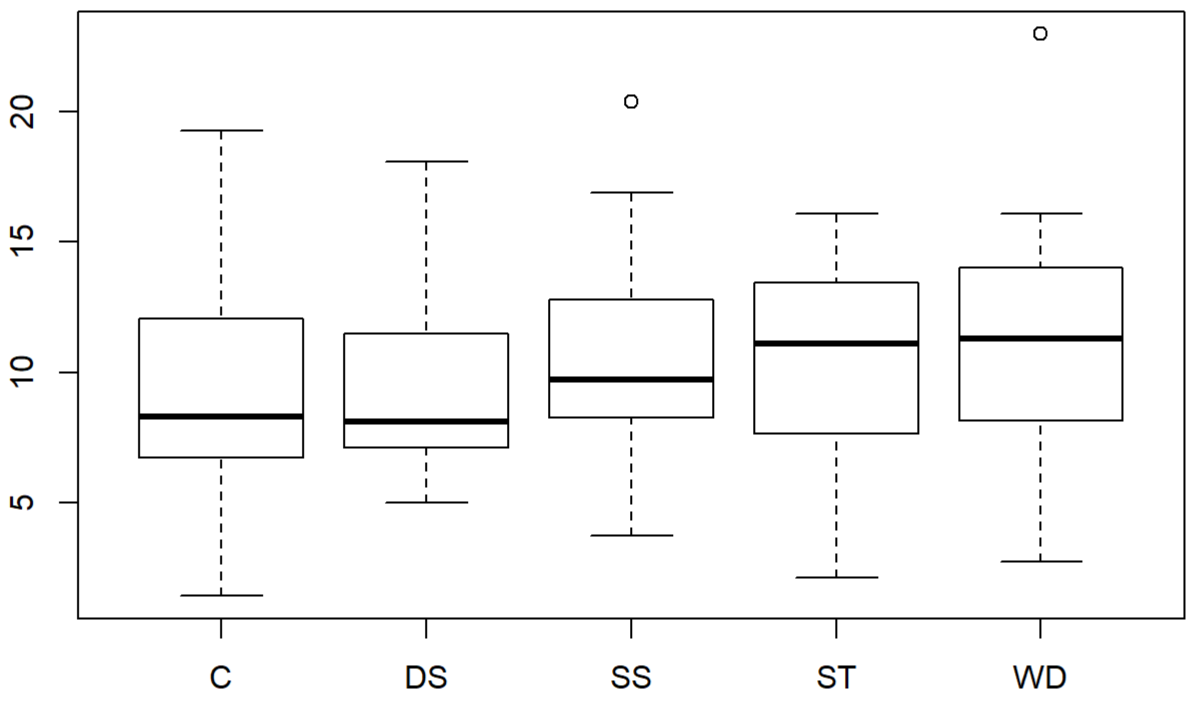
```
plot(fit)
```



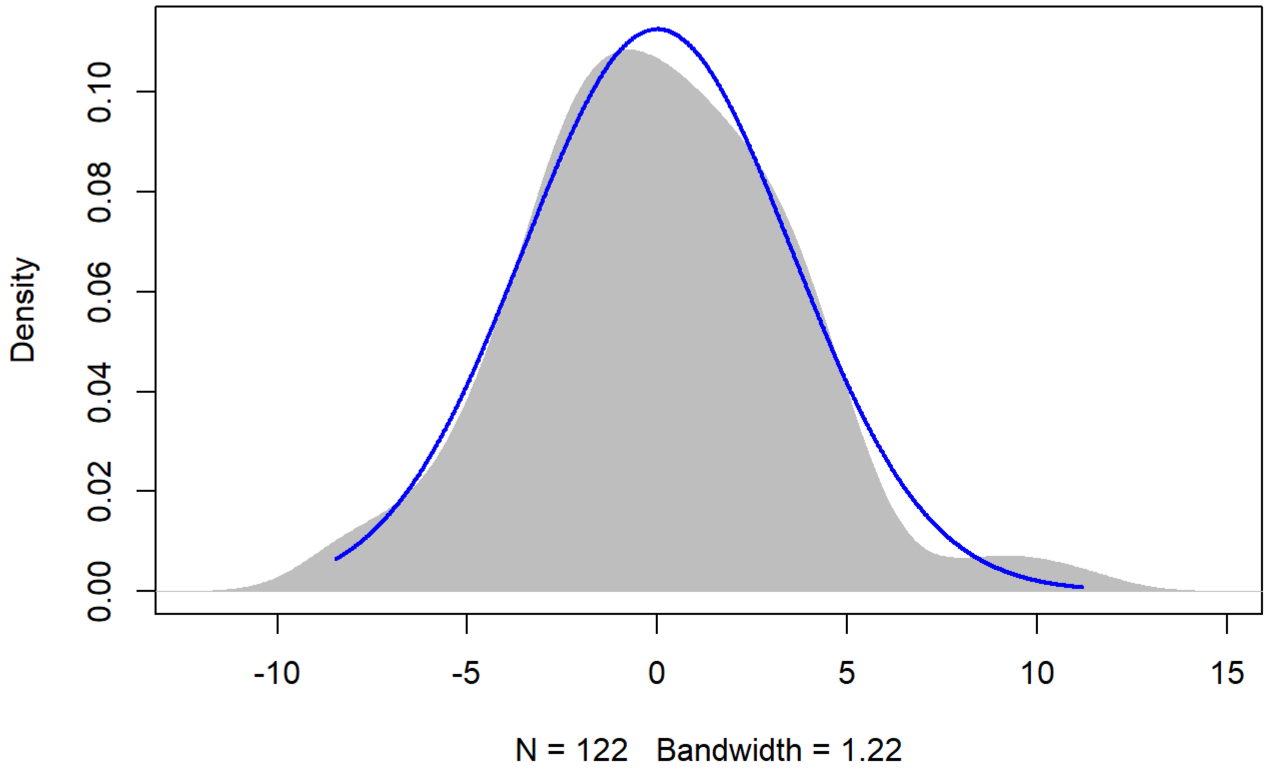
```
boxplot(smoistYA2015$moist ~ smoistYA2015$Plot_treat)
```



```
boxplot(smoistYA2015$moist ~ smoistYA2015$Sub_plot_treat)
```



```
plotNormalDensity(resid(fit))
```



2016 Reforestation site

```
smoist <-read.csv("soil_moisture.csv")

smoistYA2016 <- filter(smoist, Field == "YA2016")

summary(smoistYA2016$moist)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##    3.60    7.15   11.40   11.12   14.00   21.50 
```

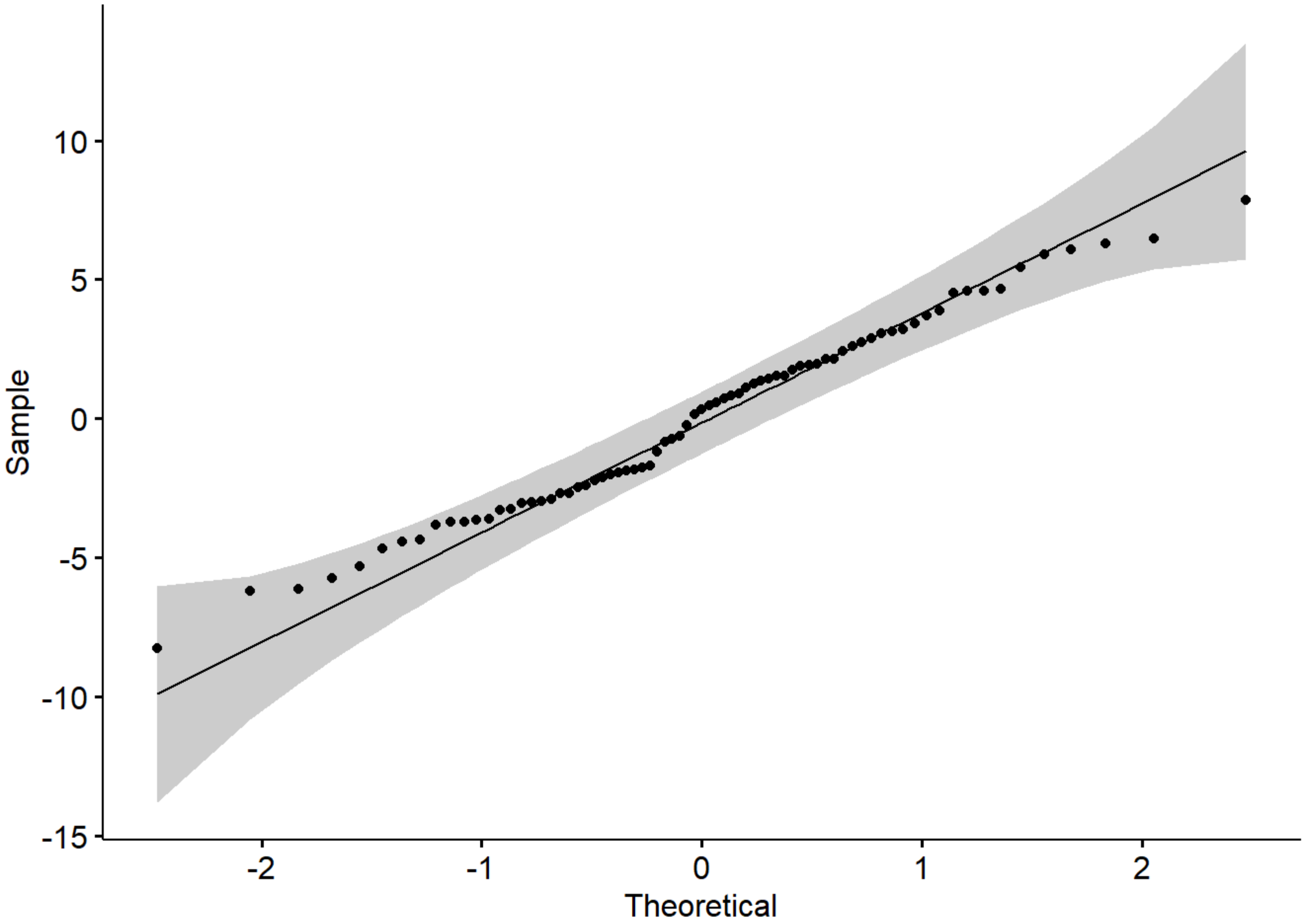
```
fit <- lmer(moist ~ Plot_treat + Sub_plot_treat + (1 | Plot), data=smoistYA2016, na.action = n
a.fail)

anova(fit, type = "III", ddf="Kenward-Roger")
```

```
## Type III Analysis of Variance Table with Kenward-Roger's method
##                Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## Plot_treat      0.037  0.0369     1 15.639  0.0026 0.9598
## Sub_plot_treat 32.614 10.8713     3 62.539  0.7735 0.5132
```

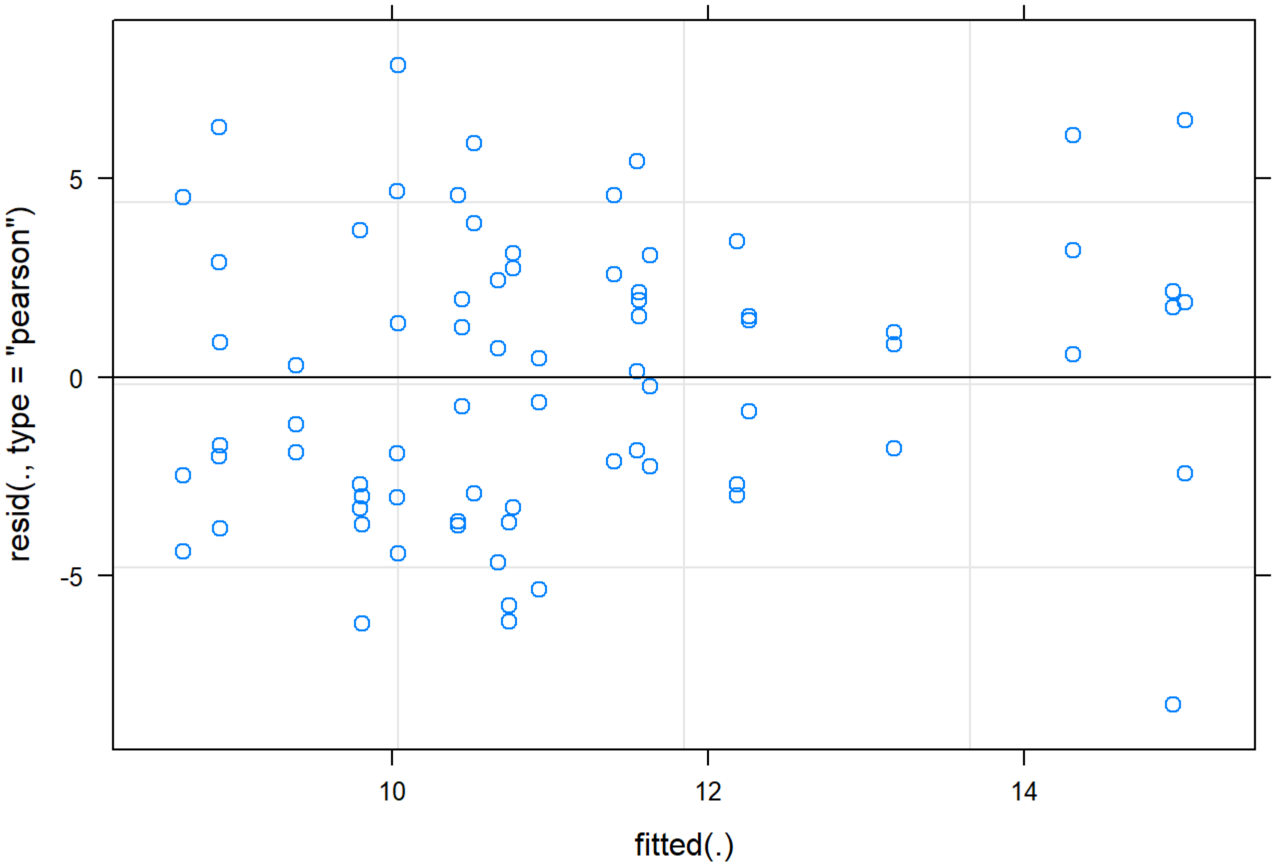
```
r.squaredGLMM(fit)
```

```
##               R2m        R2c
## [1,] 0.03841962 0.2348211
```

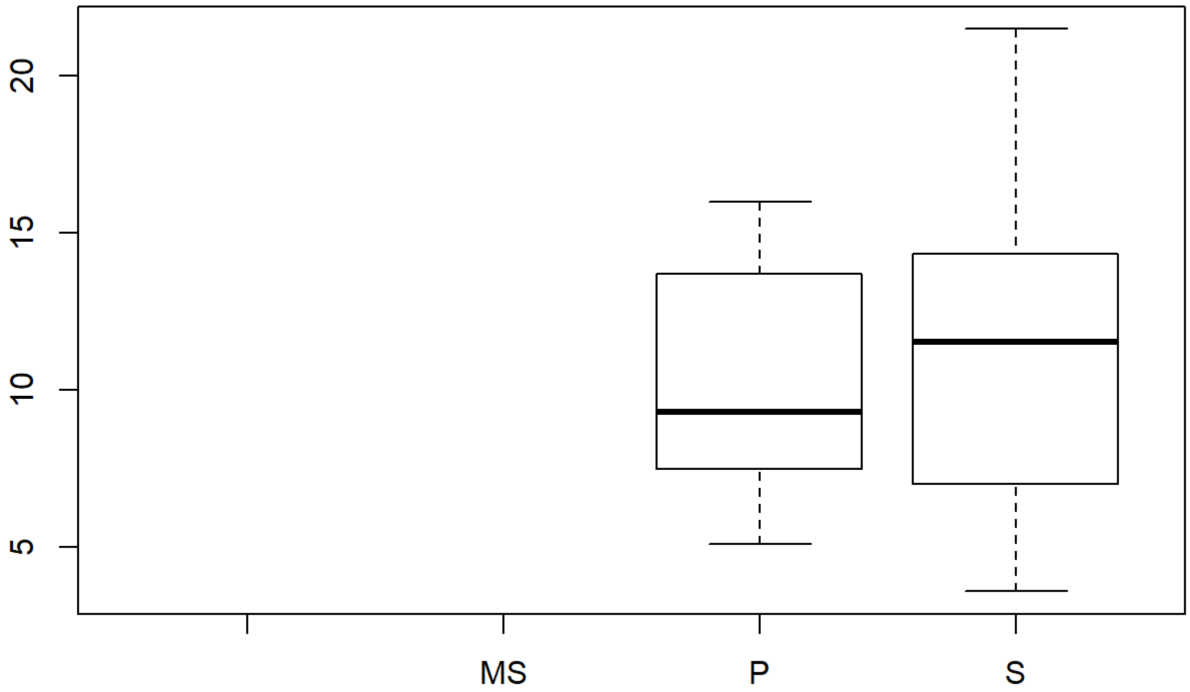
```
ggqqplot(residuals(fit))
```



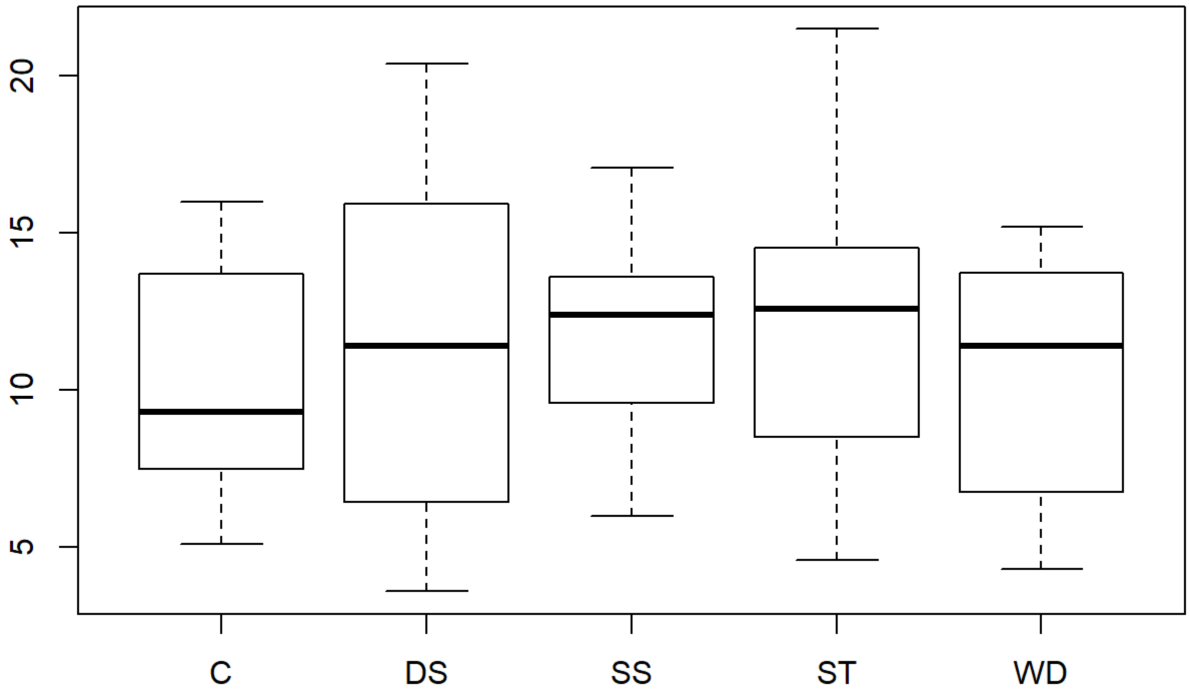
```
plot(fit)
```



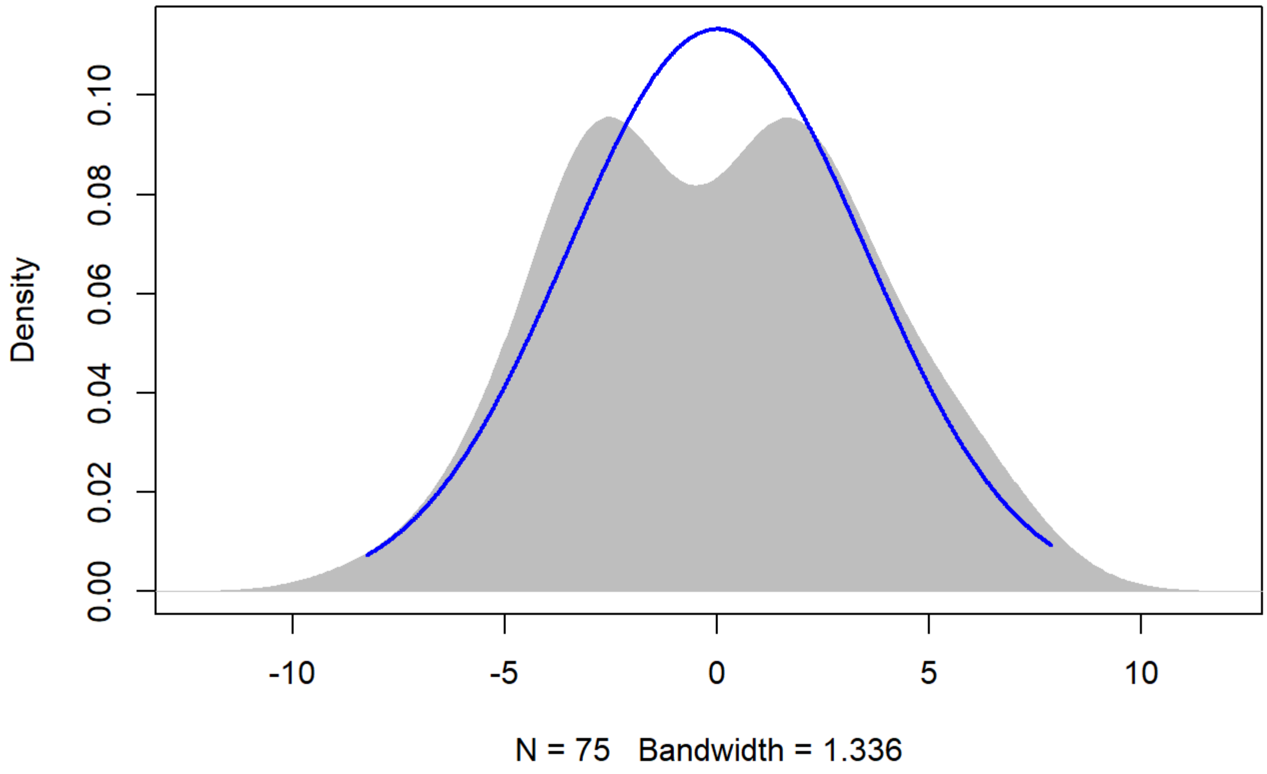
```
boxplot(smoistYA2016$moist ~ smoistYA2016$Plot_treat)
```



```
boxplot(smoistYA2016$moist ~ smoistYA2016$Sub_plot_treat)
```



```
plotNormalDensity(resid(fit))
```



Gravel pit site

```
smoist <-read.csv("soil_moisture.csv")
smoistavg <-read.csv("soil_moisture_avg.csv")


smoistPE <- filter(smoist, Field == "PE")
smoistPEavg <- filter(smoistavg, Field == "PE")

summary(smoistPE$moist)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##   0.000   0.950   4.000   4.549   7.200  16.200
```

```
fit <- lmer(moist ~ Sub_plot_treat + (1 | Plot), data=smoistPE, na.action = na.fail)

anova(fit, type = "III", ddf="Kenward-Roger")
```

```
## Type III Analysis of Variance Table with Kenward-Roger's method
##                 Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)   
## Sub_plot_treat 171.41  42.853     4    66  3.8404 0.007249 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

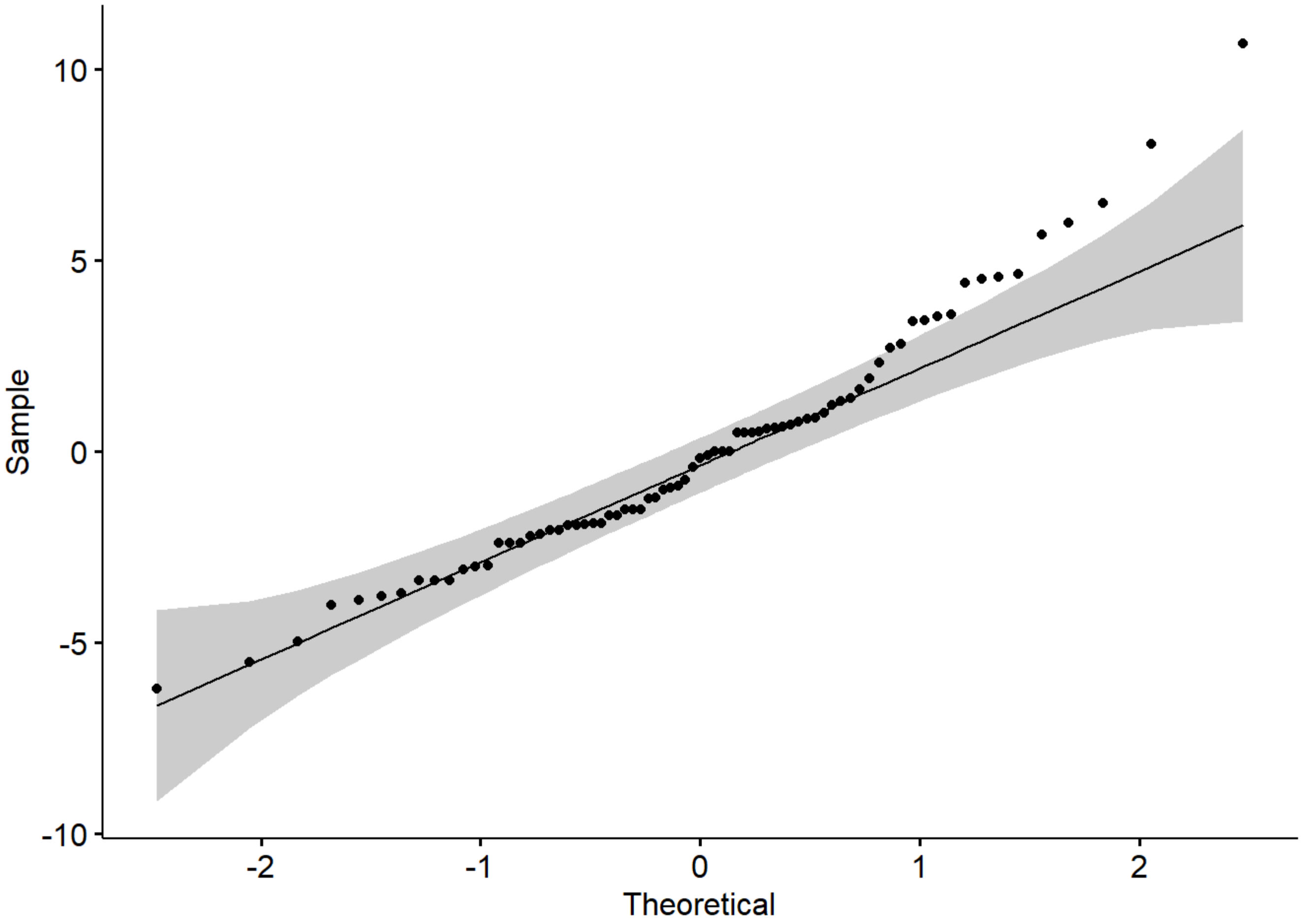
```
r.squaredGLMM(fit)
```

```
##              R2m       R2c
## [1,] 0.1391446 0.3297098
```

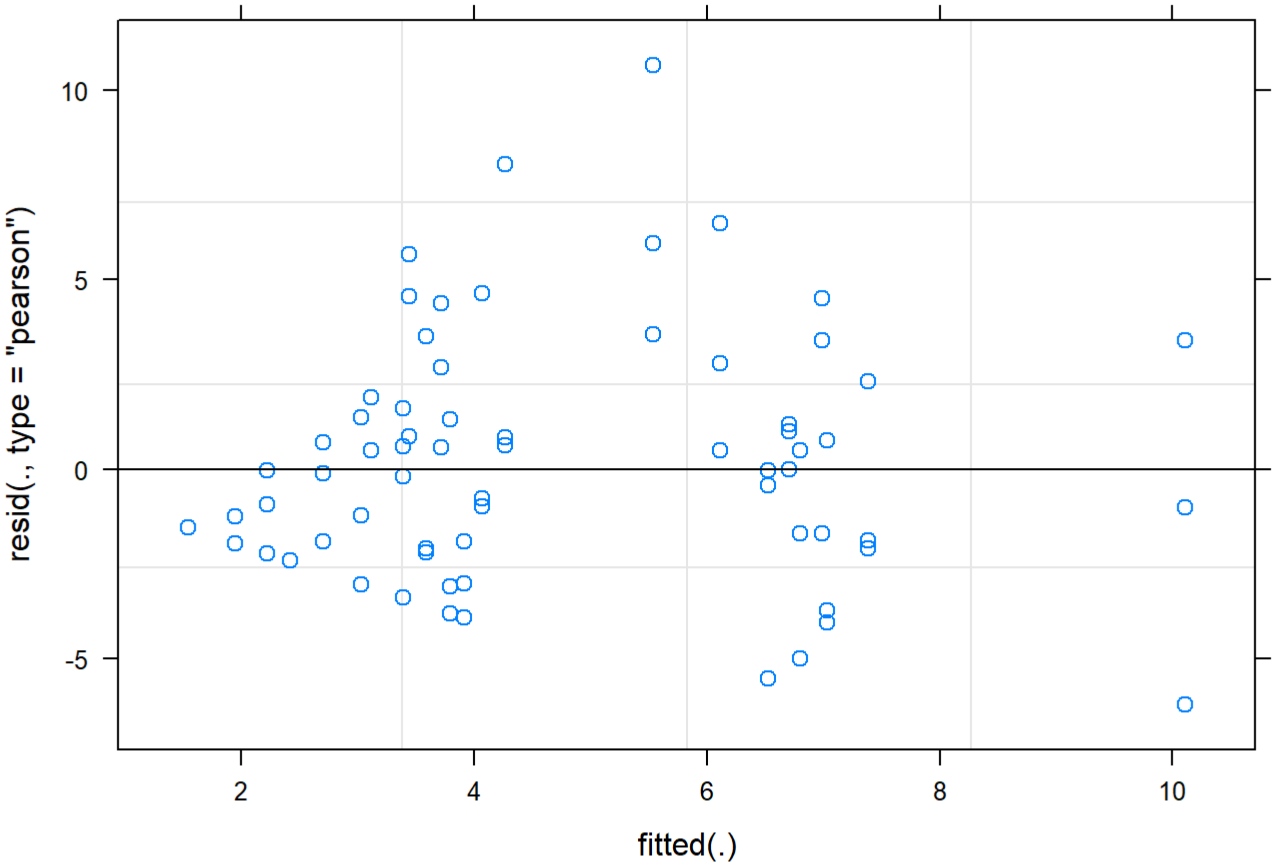
```
sprem <- emmeans(fit, list(pairwise ~ Sub_plot_treat), adjust = "Tukey")
sprem
```

```
## $`emmeans of Sub_plot_treat`
##  Sub_plot_treat emmean   SE df lower.CL upper.CL
##  C                2.73 1.17 12    0.175     5.29
##  DS               4.23 1.17 12    1.668     6.79
##  SS               7.31 1.17 12    4.748     9.87
##  ST               3.90 1.17 12    1.341     6.46
##  WD               4.58 1.17 12    2.021     7.14
## 
## Degrees-of-freedom method: kenward-roger 
## Confidence level used: 0.95 
## 
## $`pairwise differences of Sub_plot_treat`
##  contrast estimate   SE df t.ratio p.value
##  C - DS     -1.493 1.22 66 -1.224  0.7373 
##  C - SS     -4.573 1.22 66 -3.749  0.0033 
##  C - ST     -1.167 1.22 66 -0.956  0.8734 
##  C - WD     -1.847 1.22 66 -1.514  0.5573 
##  DS - SS    -3.080 1.22 66 -2.525  0.0974 
##  DS - ST     0.327 1.22 66  0.268  0.9988 
##  DS - WD    -0.353 1.22 66 -0.290  0.9984 
##  SS - ST     3.407 1.22 66  2.793  0.0515 
##  SS - WD     2.727 1.22 66  2.235  0.1797 
##  ST - WD    -0.680 1.22 66 -0.557  0.9806 
## 
## P value adjustment: tukey method for comparing a family of 5 estimates
```

```
ggqqplot(residuals(fit))
```



```
plot(fit)
```



```
fit <- glmer(moist ~ Sub_plot_treat + (1 | Plot), data=smoistPE, family = gaussian(link = "log
"), mustart=pmax(smoistPE$moist,0.5))

fit <- lmer(log(moist+0.5) ~ Sub_plot_treat + (1 | Plot), data=smoistPE, na.action = na.fail)

anova(fit, type = "III", ddf="Kenward-Roger")
```

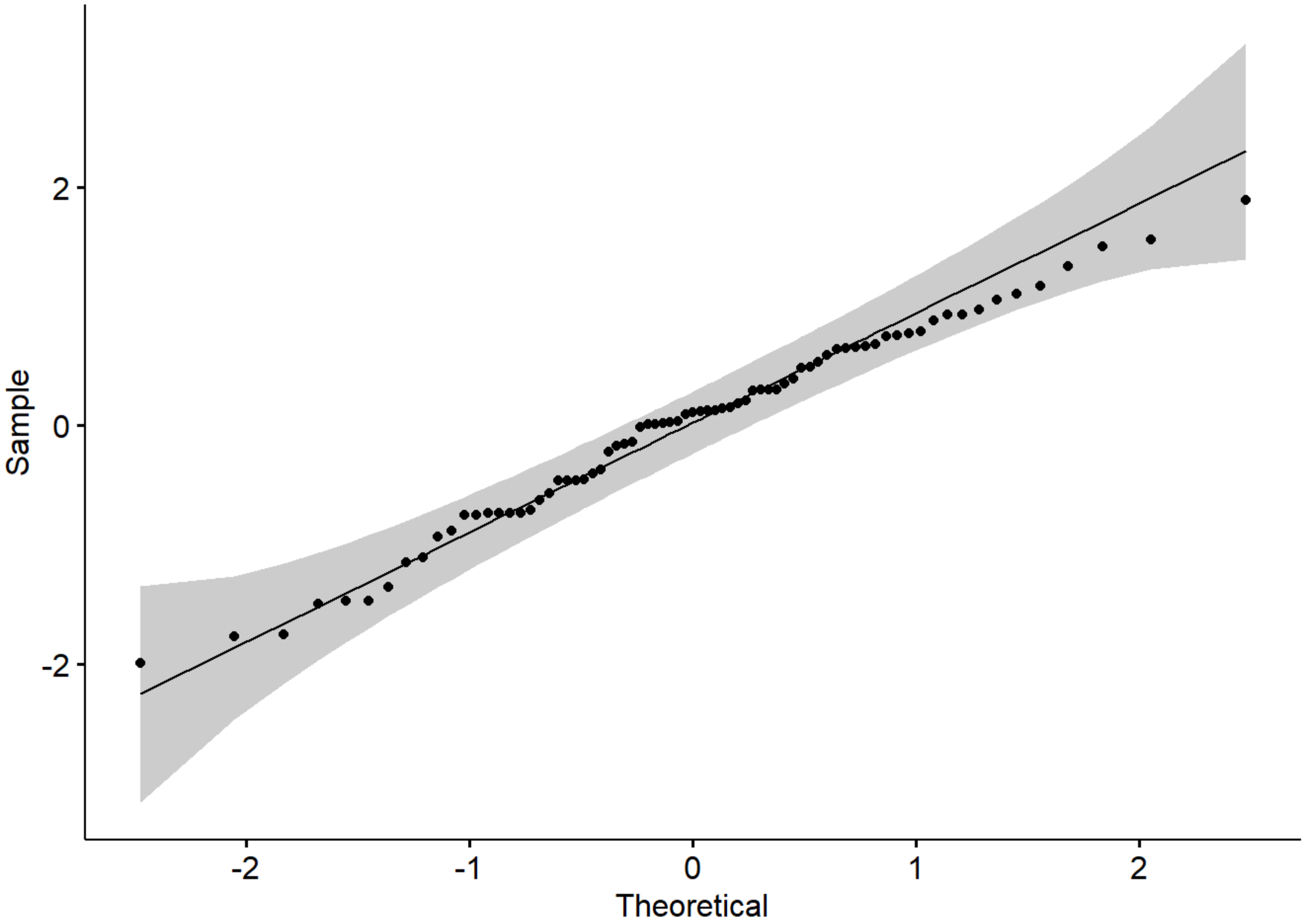
```
## Type III Analysis of Variance Table with Kenward-Roger's method
##                Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)    
## Sub_plot_treat 22.375  5.5937     4    66  7.1669 7.438e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sprem <- emmeans(fit, list(pairwise ~ Sub_plot_treat), adjust = "Tukey")
sprem
```

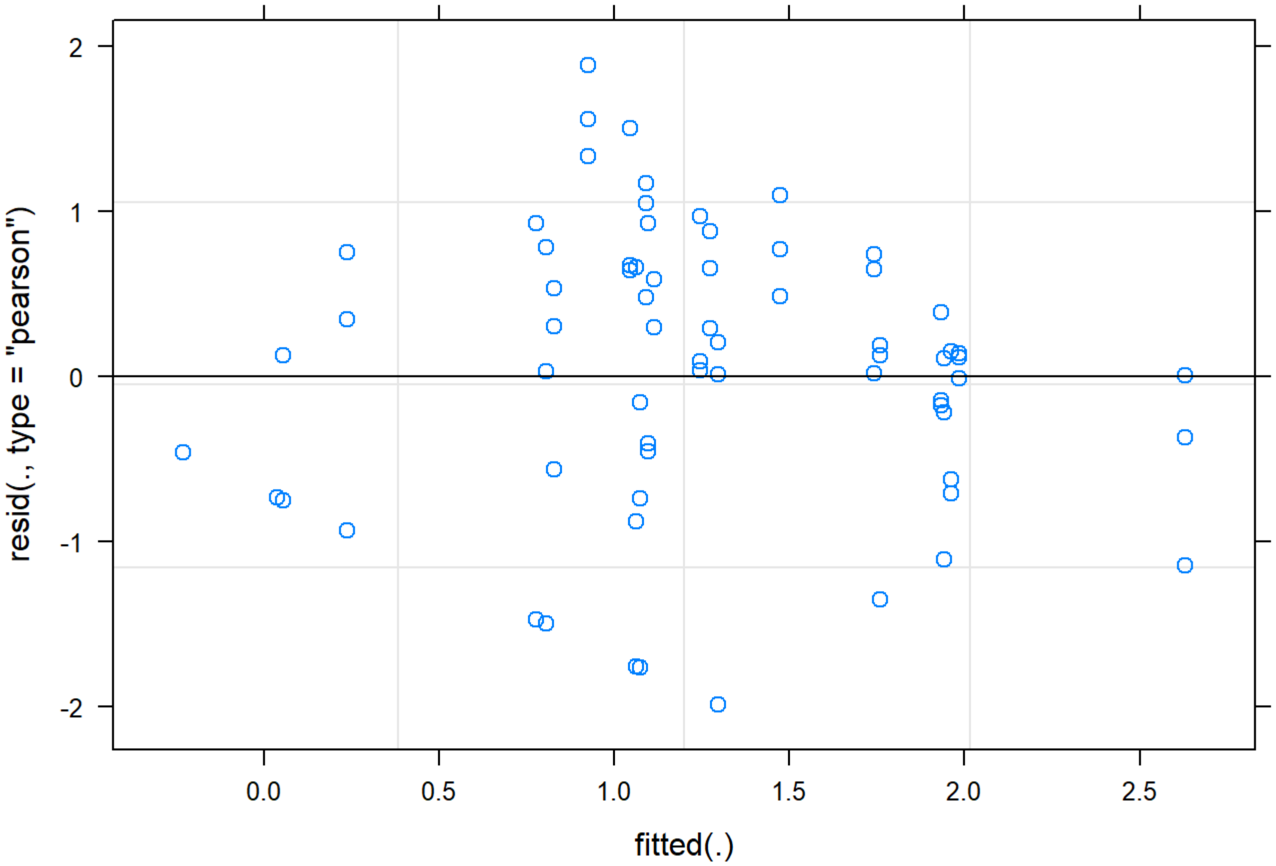
```
## $`emmeans of Sub_plot_treat`
##  Sub_plot_treat emmean    SE   df lower.CL upper.CL
##  C               0.206 0.314 11.6   -0.481    0.893
##  DS              1.241 0.314 11.6    0.554    1.928
##  SS              1.909 0.314 11.6    1.222    2.596
##  ST              1.265 0.314 11.6    0.578    1.951
##  WD              1.213 0.314 11.6    0.526    1.900
## 
```

```
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of Sub_plot_treat`
##  contrast estimate    SE df t.ratio p.value
##  C - DS    -1.0352 0.323 66 -3.209  0.0170
##  C - SS    -1.7032 0.323 66 -5.280  <.0001
##  C - ST    -1.0589 0.323 66 -3.282  0.0138
##  C - WD    -1.0073 0.323 66 -3.122  0.0216
##  DS - SS   -0.6680 0.323 66 -2.071  0.2450
##  DS - ST   -0.0237 0.323 66 -0.073  1.0000
##  DS - WD    0.0279 0.323 66  0.087  1.0000
##  SS - ST    0.6444 0.323 66  1.997  0.2787
##  SS - WD    0.6960 0.323 66  2.157  0.2089
##  ST - WD    0.0516 0.323 66  0.160  0.9998
##
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 5 estimates
```

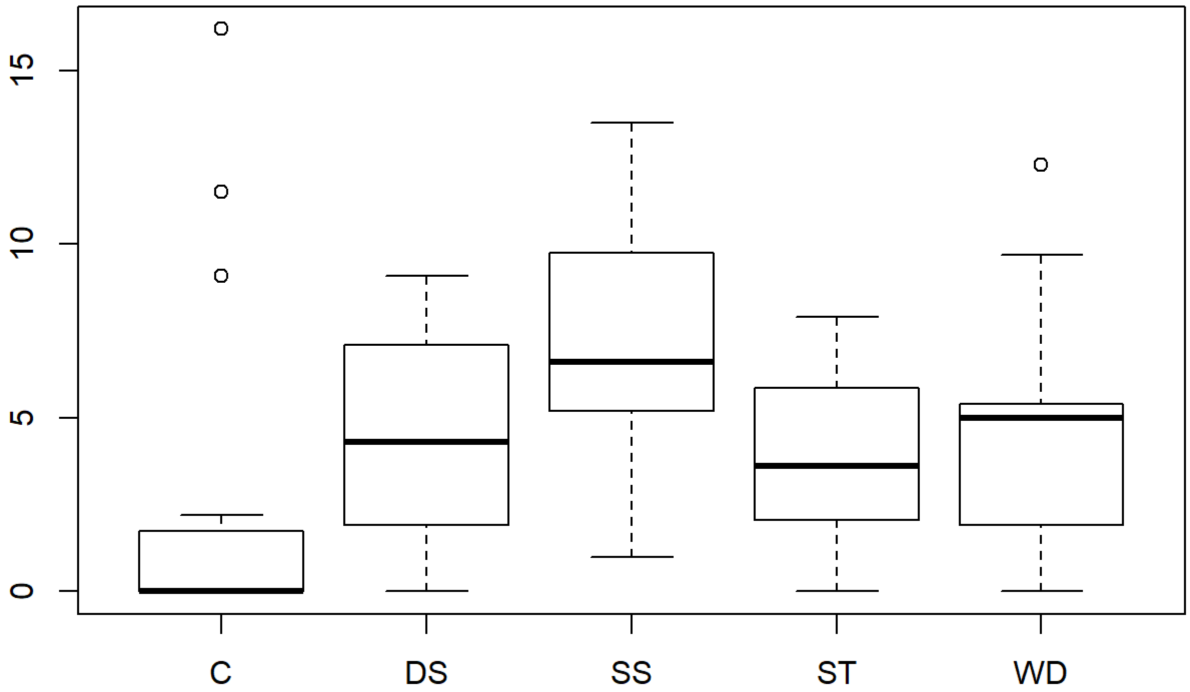
```
ggqqplot(residuals(fit))
```



```
plot(fit)
```

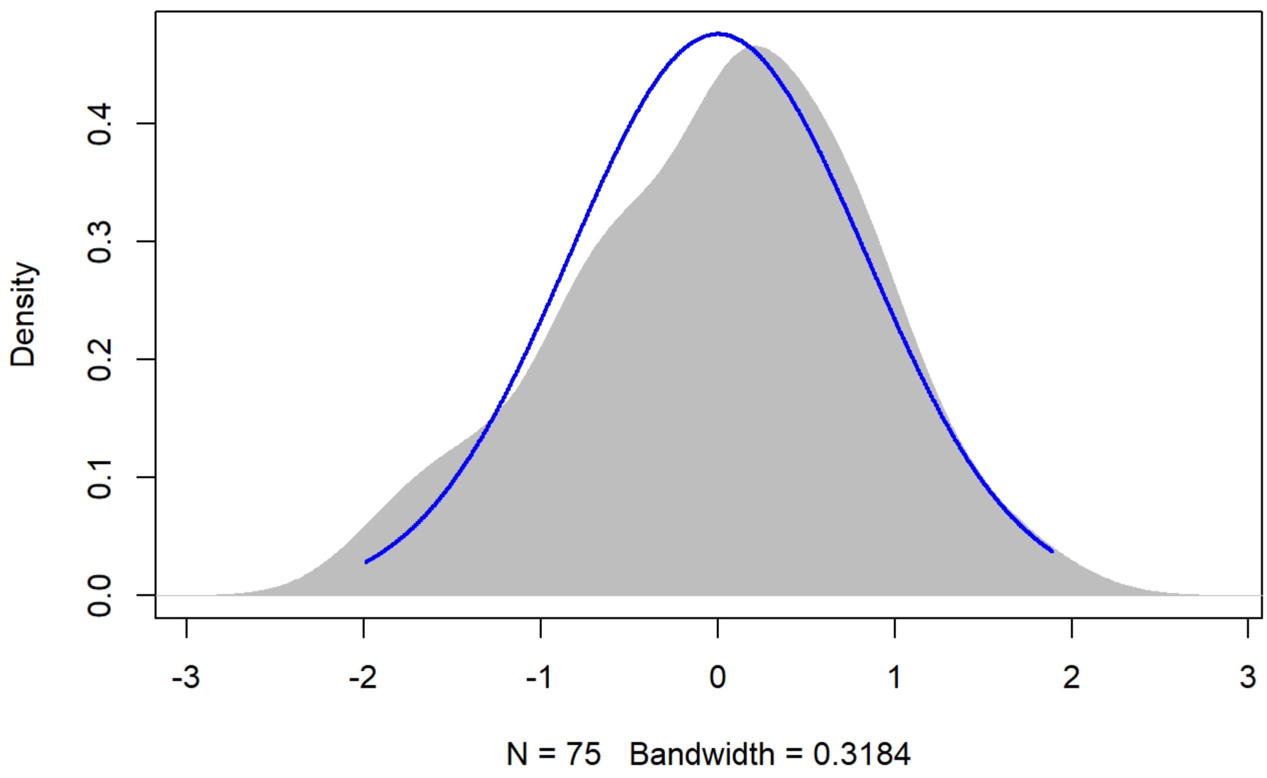


```
boxplot(smoistPE$moist ~ smoistPE$Sub_plot_treat)
```



```
plotNormalDensity(resid(fit))
```

There are



zero-inflation issues with the PE moisture data transformed by log+0.5 to achieve equal variance

3.3.2 Tree survival, damage, and growth results

3.3.2.1. Tree survival and damage

Comparison of survival of trees by plot-type in both reforestation sites - untransformed (including testing assumptions)

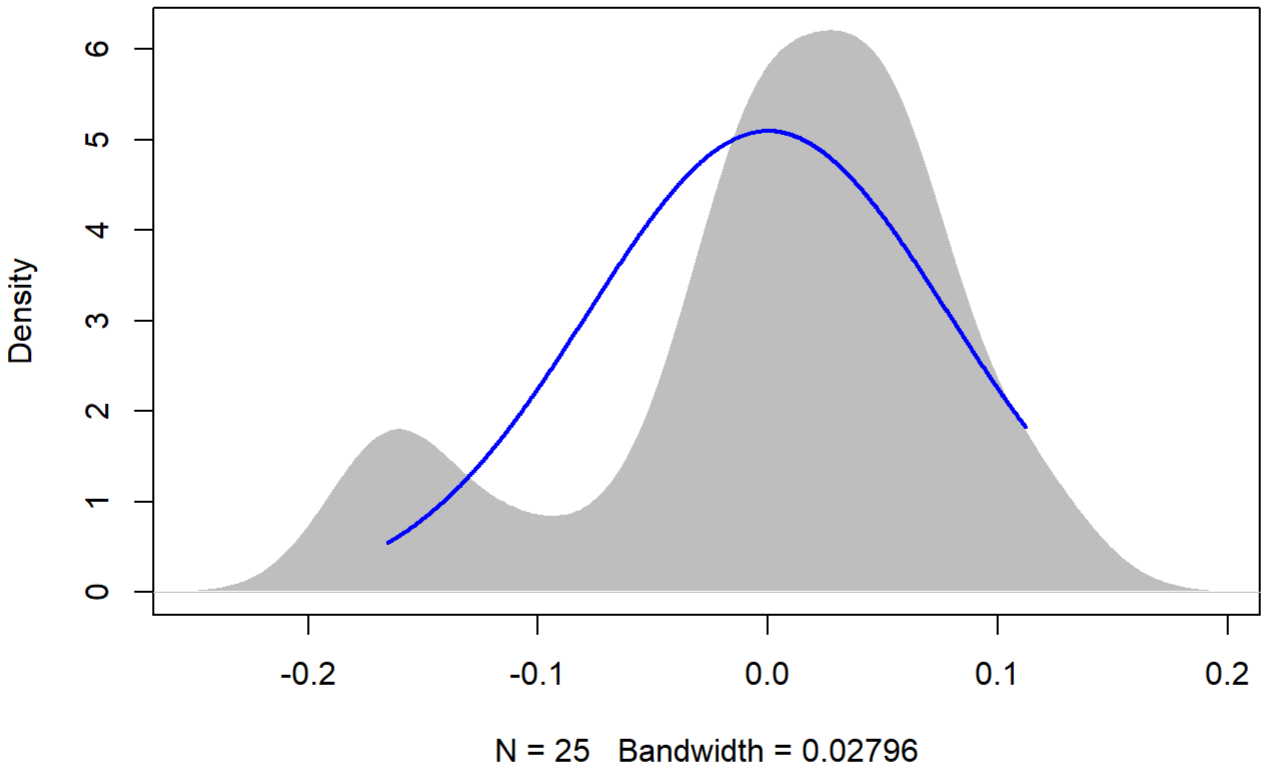
```
TreeSurv <- read.csv("tree_survival.csv")

model = lm(ratio_survival ~ Plot_type, data = TreeSurv)

Anova(model, type="III")
```

```
## Anova Table (Type III tests)
##
## Response: ratio_survival
##             Sum Sq Df  F value Pr(>F)
## (Intercept) 4.4389  1 664.4465 <2e-16 ***
## Plot_type   0.0267  2   2.0006 0.1591
## Residuals   0.1470 22
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

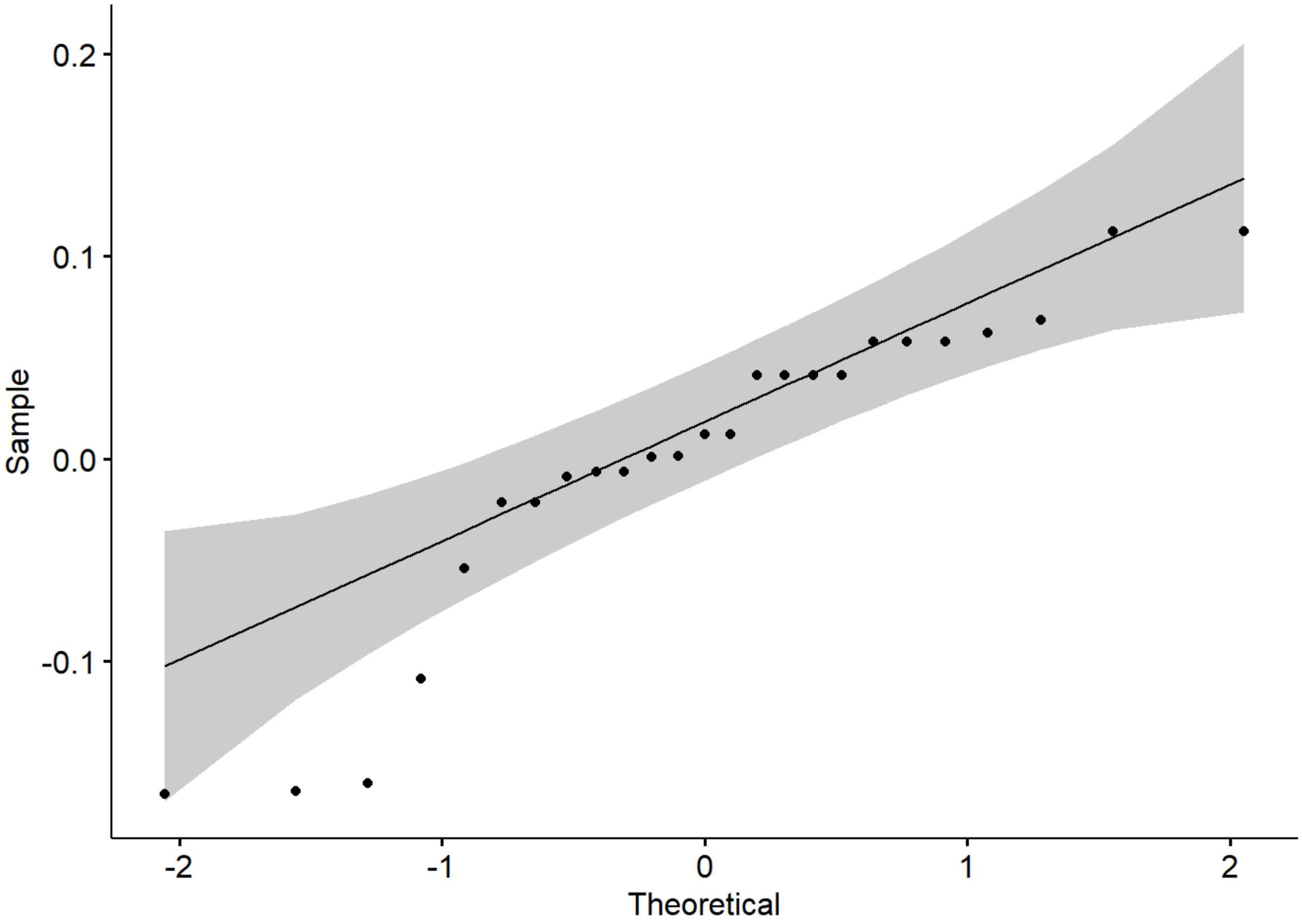
```
outlierTest(model)
```

```
## No Studentized residuals with Bonferonni p < 0.05
## Largest |rstudent|:
##    rstudent unadjusted p-value Bonferonni p
## 5 -2.504471           0.020578      0.51446
```

```
plotNormalDensity(residuals(model))
```



```
ggqqplot(residuals(model))
```



```
TreeSurvomit <- na.omit(TreeSurv)
leveneTest(residuals(model) ~ TreeSurvomit$Plot_type)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  2  1.0871 0.3546
##       22
```

```
DT <- data.table(TreeSurv)
DT[, .(W = shapiro.test(resid(model))$statistic, P.value = shapiro.test(resid(model))$p.value)
,
   by = .(Plot_type)]
```

```
##    Plot_type        W     P.value
## 1:        MS 0.885057 0.008801553
## 2:         P 0.885057 0.008801553
## 3:         T 0.885057 0.008801553
```

Data and residuals are not normal - but homoskedacity is met - therefore performing Kruskal-Wallis instead - http://www.biostathandbook.com/kruskalwallis.html and https://rcompanion.org/rcompanion/d_06.html and http://www.sthda.com/english/wiki/kruskal-wallis-test-in-r

Kruskal-Wallis on survival ratio

```
kruskal.test(ratio_survival ~ Plot_type, data = TreeSurv)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  ratio_survival by Plot_type
## Kruskal-Wallis chi-squared = 3.523, df = 2, p-value = 0.1718
```

Tree Damage - untransformed (including assumptions)

```
tree_dmg <- read.csv("tree_dmg.csv")

model = lm(Total ~ Plot_type, data = tree_dmg)
Anova(model, type= "III")
```

```
## Anova Table (Type III tests)
##
## Response: Total
##              Sum Sq Df  F value    Pr(>F)
## (Intercept) 3.9443  1 395.2905 1.508e-15 ***
## Plot_type   0.0268  2   1.3423    0.2818
## Residuals   0.2195 22
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

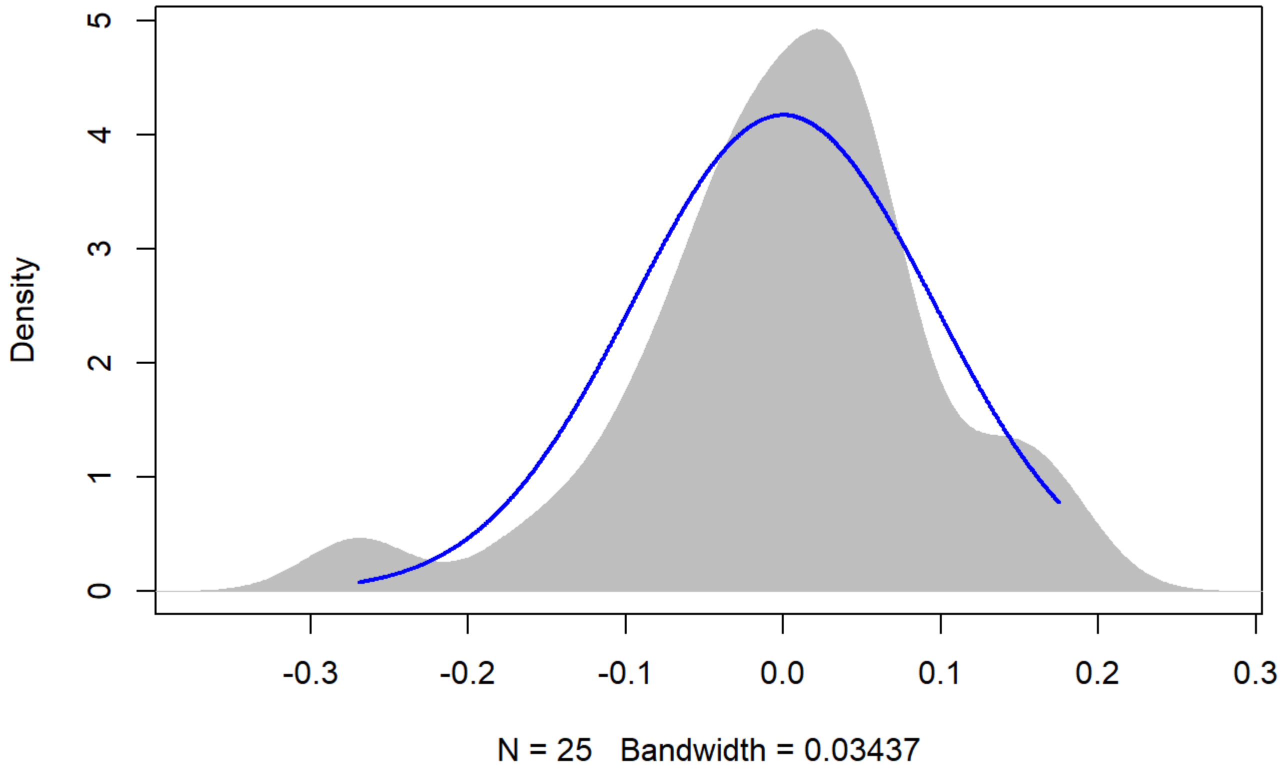
```
DT <- data.table(tree_dmg)
DT[, .(W = shapiro.test(resid(model))$statistic, P.value = shapiro.test(resid(model))$p.value)
,
   by = .(Plot_type)]
```

```
##    Plot_type         W   P.value
## 1:        MS 0.9554371 0.3311029
## 2:         P 0.9554371 0.3311029
## 3:         T 0.9554371 0.3311029
```

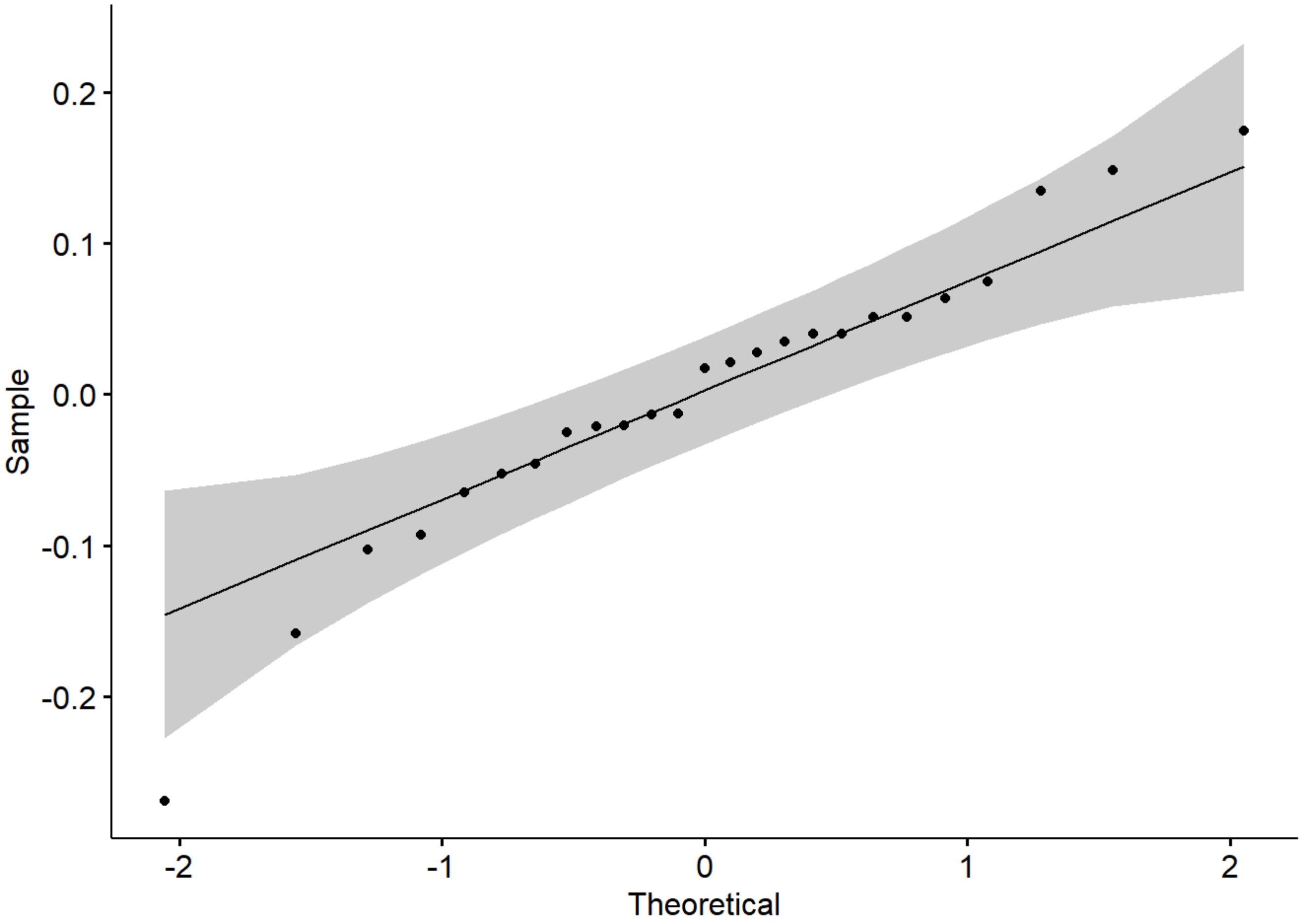
```
outlierTest(model)
```

```
## No Studentized residuals with Bonferonni p < 0.05
## Largest |rstudent|:
##    rstudent unadjusted p-value Bonferonni p
## 8 -3.488638          0.0021902     0.054756
```

```
plotNormalDensity(residuals(model))
```



```
ggqqplot(residuals(model))
```



```
TreeDmgomit <- na.omit(tree_dmg)
leveneTest(residuals(model) ~ TreeDmgomit$Plot_type)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  2  1.0438 0.3689
##       22
```

3.3.2.2. Change in tree height and diameter by plot-type

LMER test for height change - Field and plots as random intercept factor

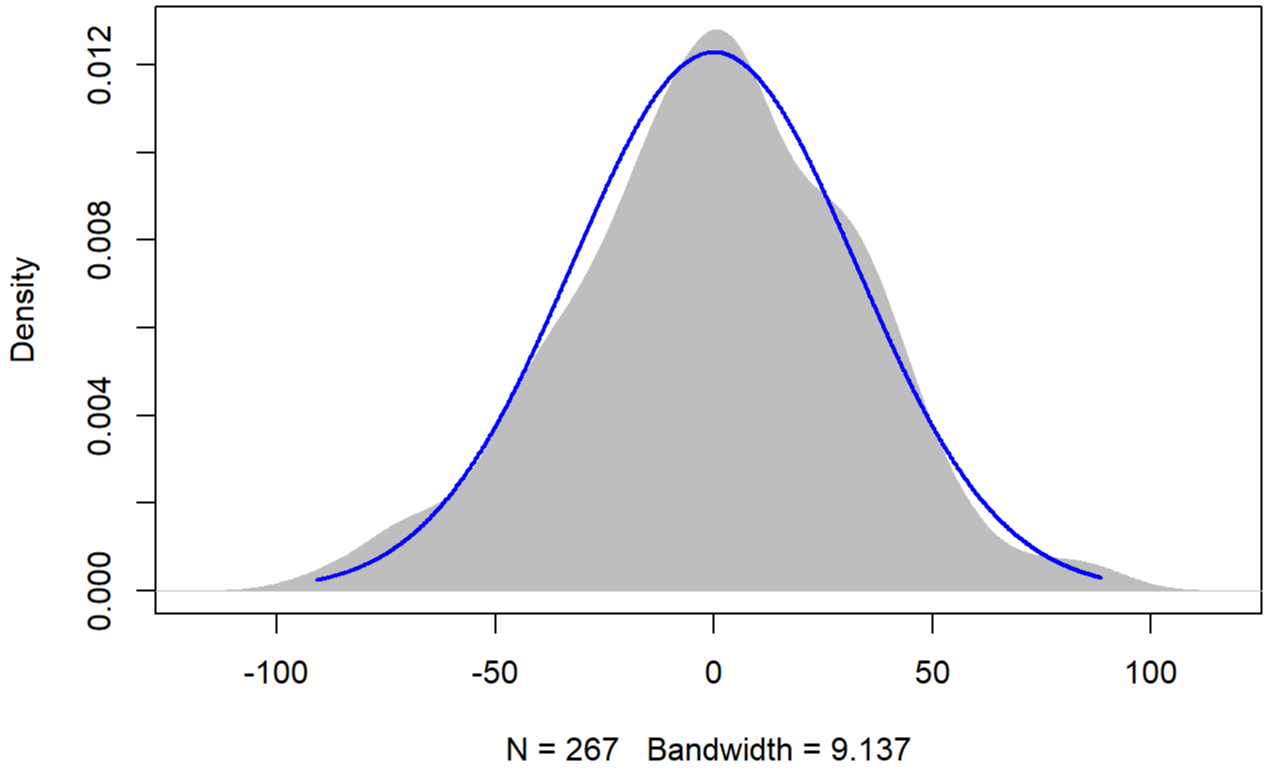
```
tree_data6 <- read.csv("tree_data6.csv")

all <- lmer(height_change.20 ~ Plot_type + (1|p_size_gen) + (1|Field/Plot), data=tree_data6)

anova(all, ddf="Kenward-Roger")
```

```
## Type III Analysis of Variance Table with Kenward-Roger's method
##           Sum Sq Mean Sq NumDF  DenDF F value Pr(>F)
## Plot_type 4544.6  2272.3     2 23.029   1.965  0.163
```

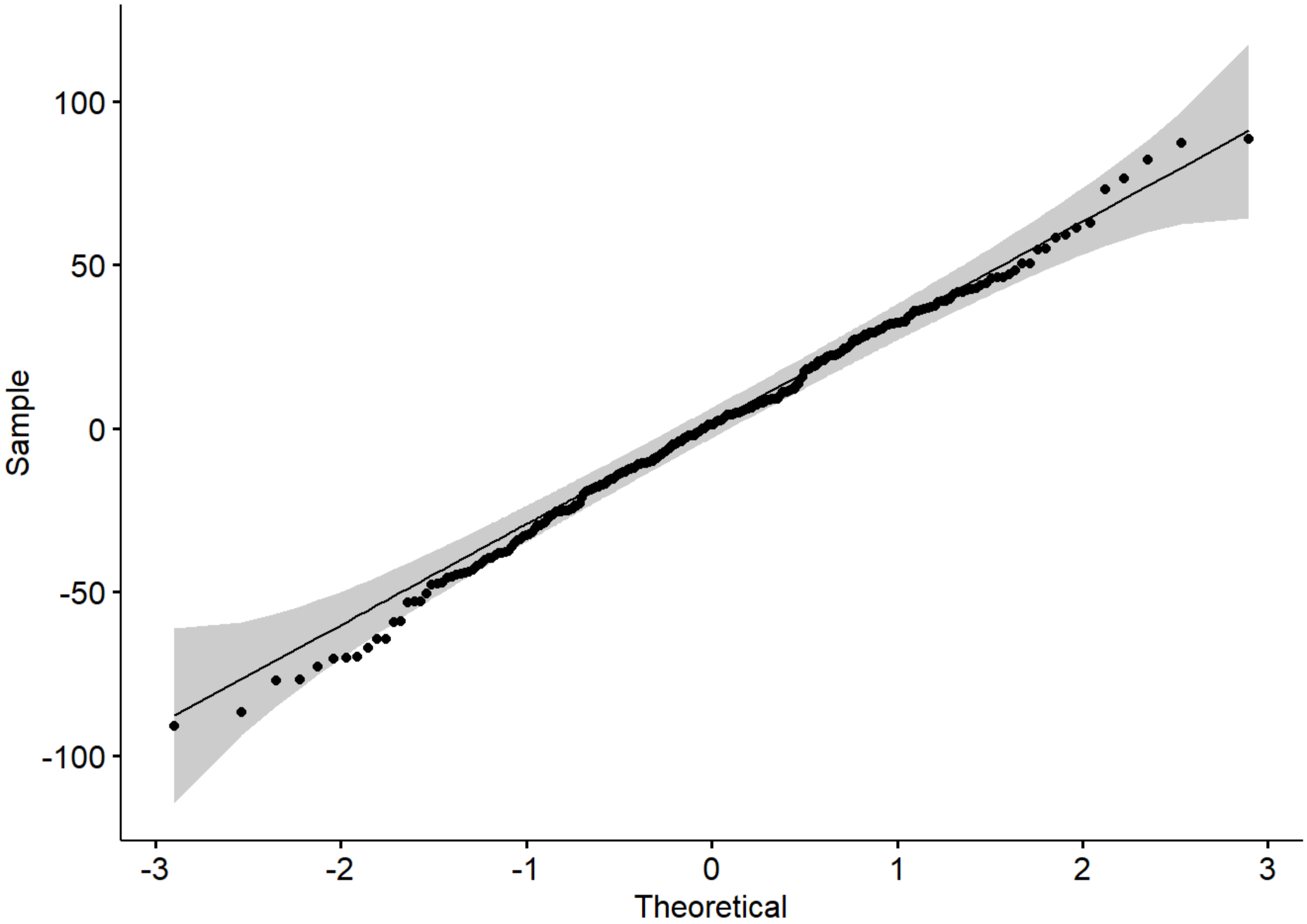
```
emmeans(all, list(pairwise ~ Plot_type), adjust = "tukey")
```

```
## $`emmeans of Plot_type`
##  Plot_type emmean   SE   df lower.CL upper.CL
##  MS         107.5 13.1 5.81     75.1      140
##  P           90.7 10.5 3.17     58.3      123
##  T          104.0 10.6 3.26     71.8      136
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of Plot_type`
##  contrast estimate    SE   df t.ratio p.value
##  MS - P      16.79 11.19 25.3  1.500  0.3080
##  MS - T       3.56 11.21 25.9  0.318  0.9460
##  P - T      -13.22  7.65 20.1 -1.729  0.2190
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

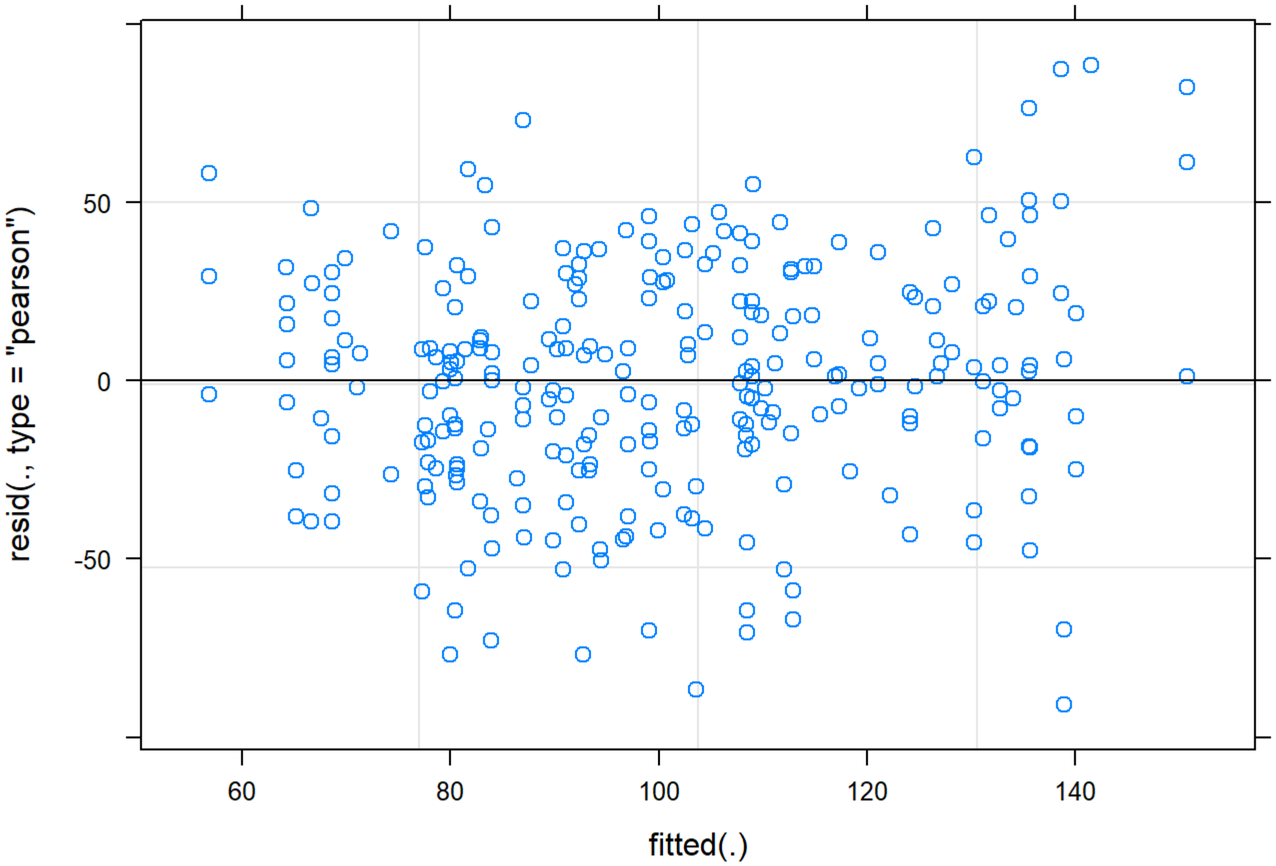
```
plotNormalDensity(residuals(all))
```



```
ggqqplot(residuals(all))
```

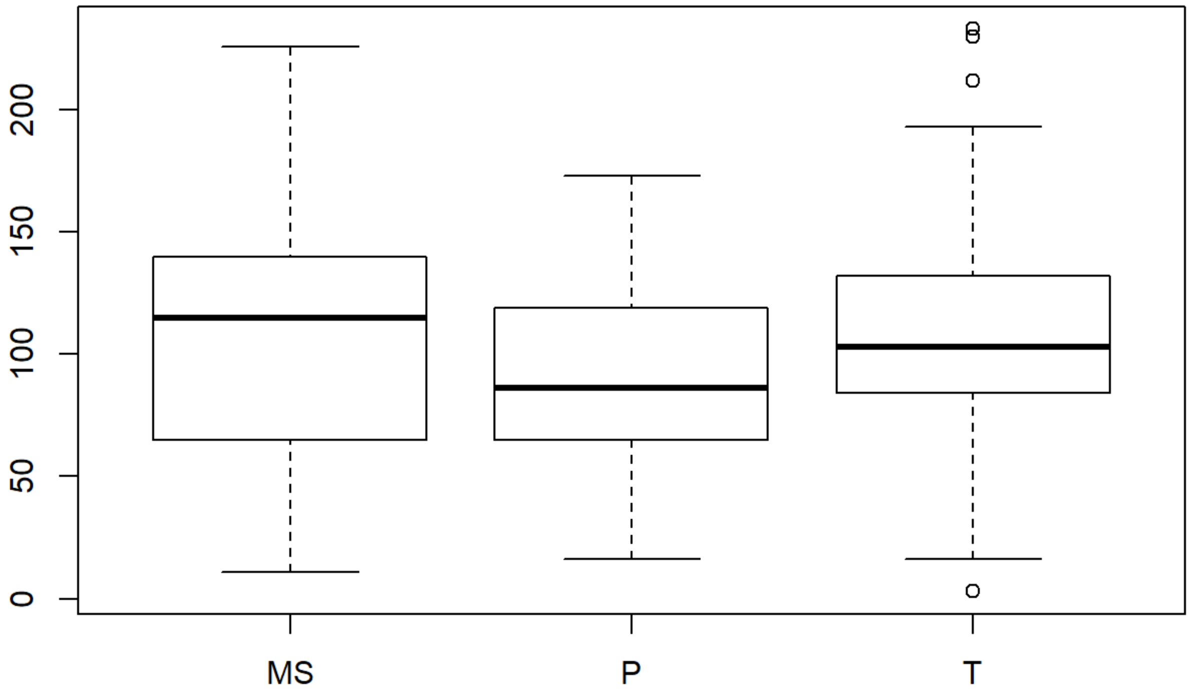


```
plot(all)
```



```
boxplot(tree_data6$height_change.20 ~ tree_data6$Plot_type)
```

LMER



test for width change - Field and plots as random intercept factor

```
tree_data6 <- read.csv("tree_data6.csv")

all <- lmer(width_change ~ Plot_type + (1|p_size_gen) + (1|Field/Plot), data=tree_data6)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 0.00228465
## (tol = 0.002, component 1)
```

```
anova(all, ddf="Kenward-Roger")
```

```
## Type III Analysis of Variance Table with Kenward-Roger's method
##           Sum Sq Mean Sq NumDF DenDF F value  Pr(>F)
## Plot_type 296.51  148.25     2 23.09  3.7085 0.04012 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

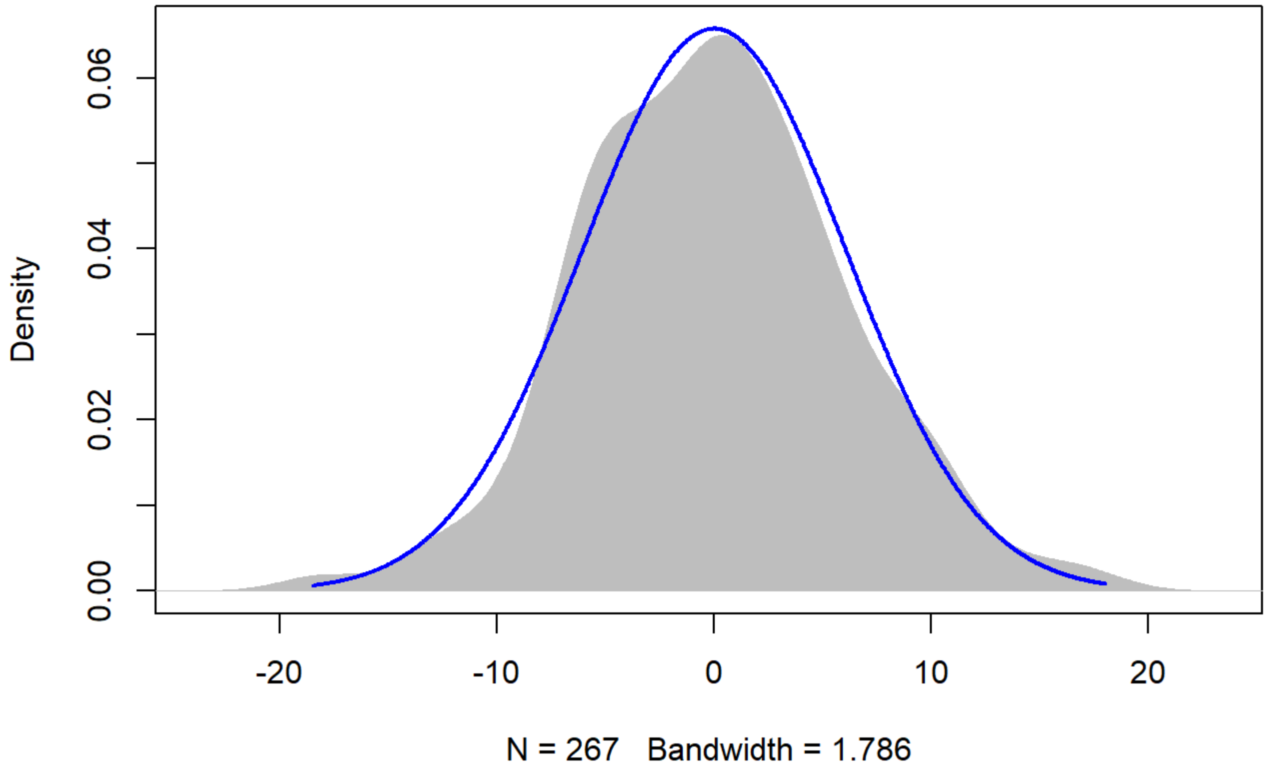
```
r.squaredGLMM(all)
```

```
##             R2m       R2c
## [1,] 0.03476587 0.4506367
```

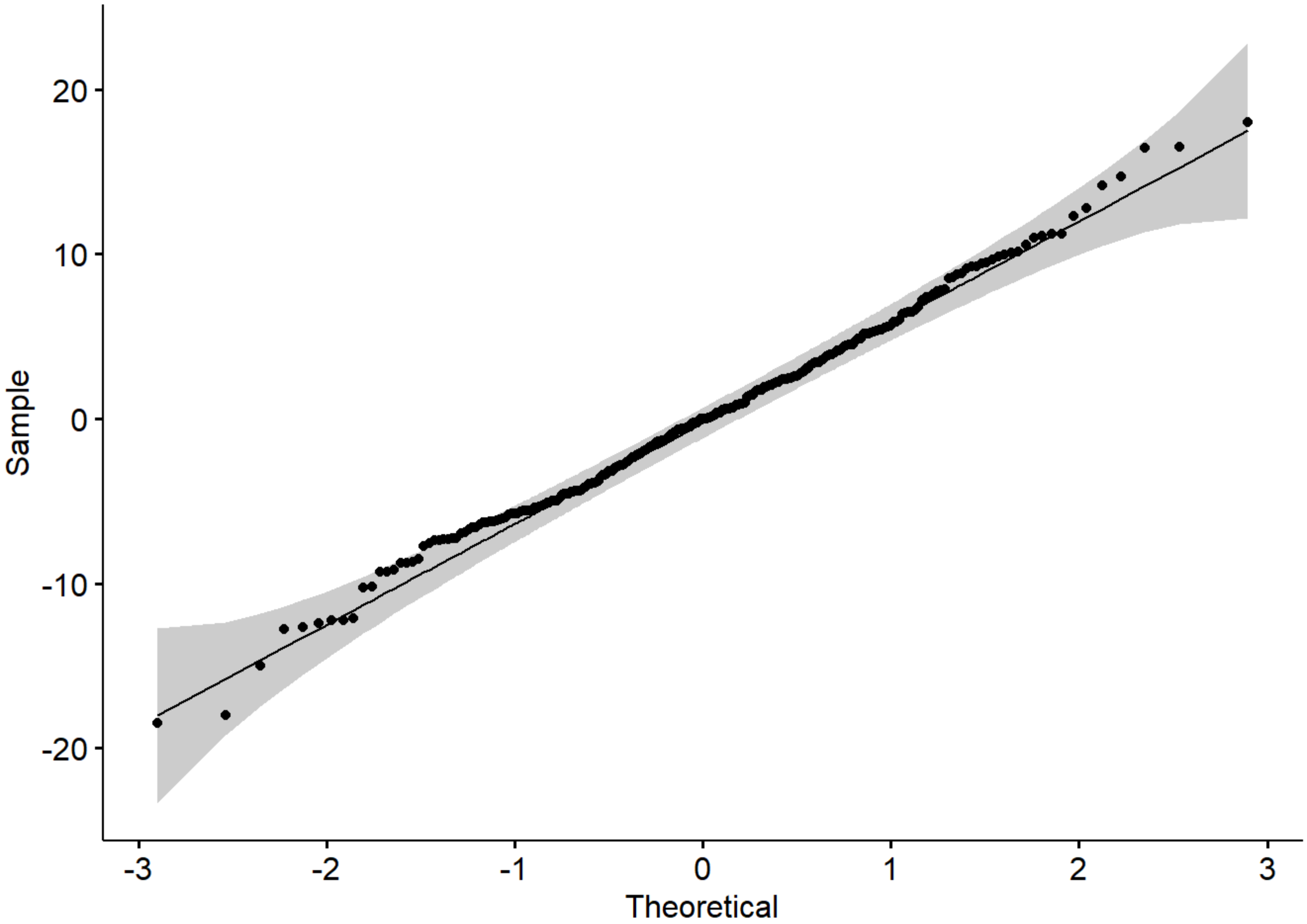
```
emmeans(all, list(pairwise ~ Plot_type), adjust = "tukey")
```

```
## $`emmeans of Plot_type`
##  Plot_type emmean   SE   df lower.CL upper.CL
##  MS          16.8 2.94 2.76     6.99     26.6
##  P           13.6 2.66 1.94     1.81     25.4
##  T           16.8 2.67 1.97     5.10     28.4
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of Plot_type`
##  contrast estimate   SE   df t.ratio p.value
##  MS - P     3.2219 1.79 25.6  1.803  0.1887
##  MS - T     0.0552 1.80 26.5  0.031  0.9995
##  P - T     -3.1667 1.25 20.0 -2.536  0.0495
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

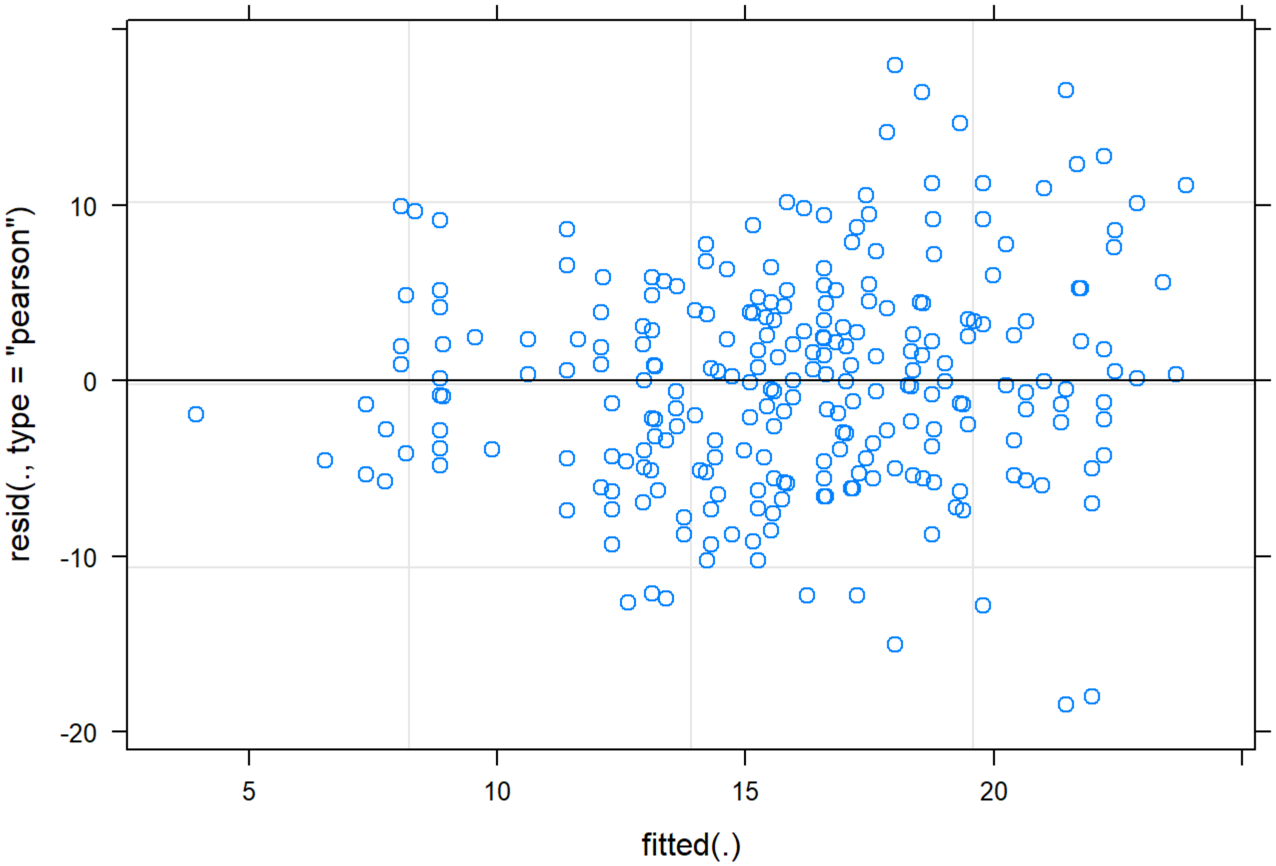
```
plotNormalDensity(residuals(all))
```



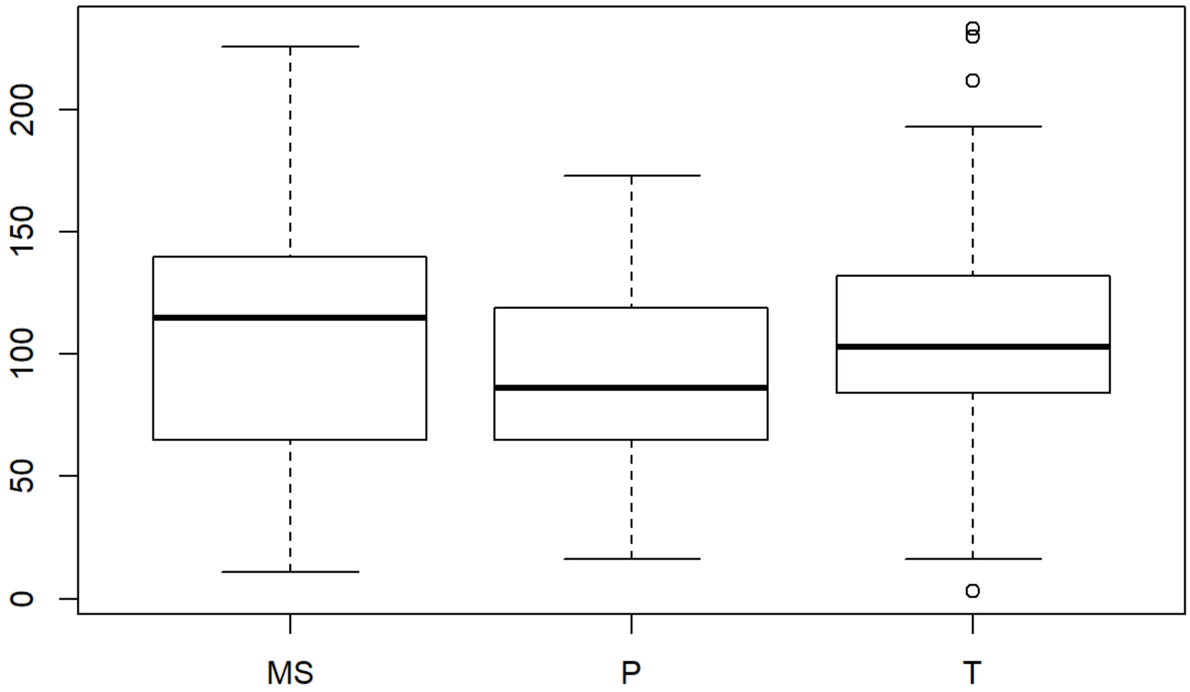
```
ggqqplot(residuals(all))
```



```
plot(all)
```



```
boxplot(tree_data6$height_change.20 ~ tree_data6$Plot_type)
```



3.3.3. Plant richness and diversity results

3.3.3.1. Spring vegetation sampling results

3.3.3.1.1. Comparing native forest species richness and diversity between plot and sub-plot treatments

Poisson GLMER for spring species richness (control for field) - and post hoc test

```
sprich <- read.csv("spring_veg_richness.csv")

all_spr <- glmer(sp_rich ~ Field_plottype + (1|Plot) + (1|Sub_treat), data = sprich, family =
poisson())
```

```
## boundary (singular) fit: see ?isSingular
```

```
allmeans <- emmeans(all_spr, list(pairwise ~ Field_plottype), adjust = "Tukey")

gspr <- glmer(NF_sp_rich ~ Field_plottype * Sub_treat + (1|Plot), data = sprich, family = pois
son())
```

```
## fixed-effect model matrix is rank deficient so dropping 18 columns / coefficients
## boundary (singular) fit: see ?isSingular
```

```r
Anova(gspr, type="III")
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: NF_sp_rich
##                              Chisq Df Pr(>Chisq)
## (Intercept)               255.2542  1  < 2.2e-16 ***
## Field_plottype             57.2476  7  5.337e-10 ***
## Sub_treat                   0.3004  3     0.9600
## Field_plottype:Sub_treat    2.1687 11     0.9978
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
r.squaredGLMM(gspr)
```

```
## Warning: The null model is correct only if all variables used by the
## original model remain unchanged.
```

```
##                  R2m       R2c
## delta     0.9036135 0.9036135
## lognormal 0.9100441 0.9100441
## trigamma  0.8962265 0.8962265
```

```r
gsprpost <- glmer(NF_sp_rich ~ Field_plottype + (1|Sub_treat) + (1|Plot), data = sprich, family = poisson())
```

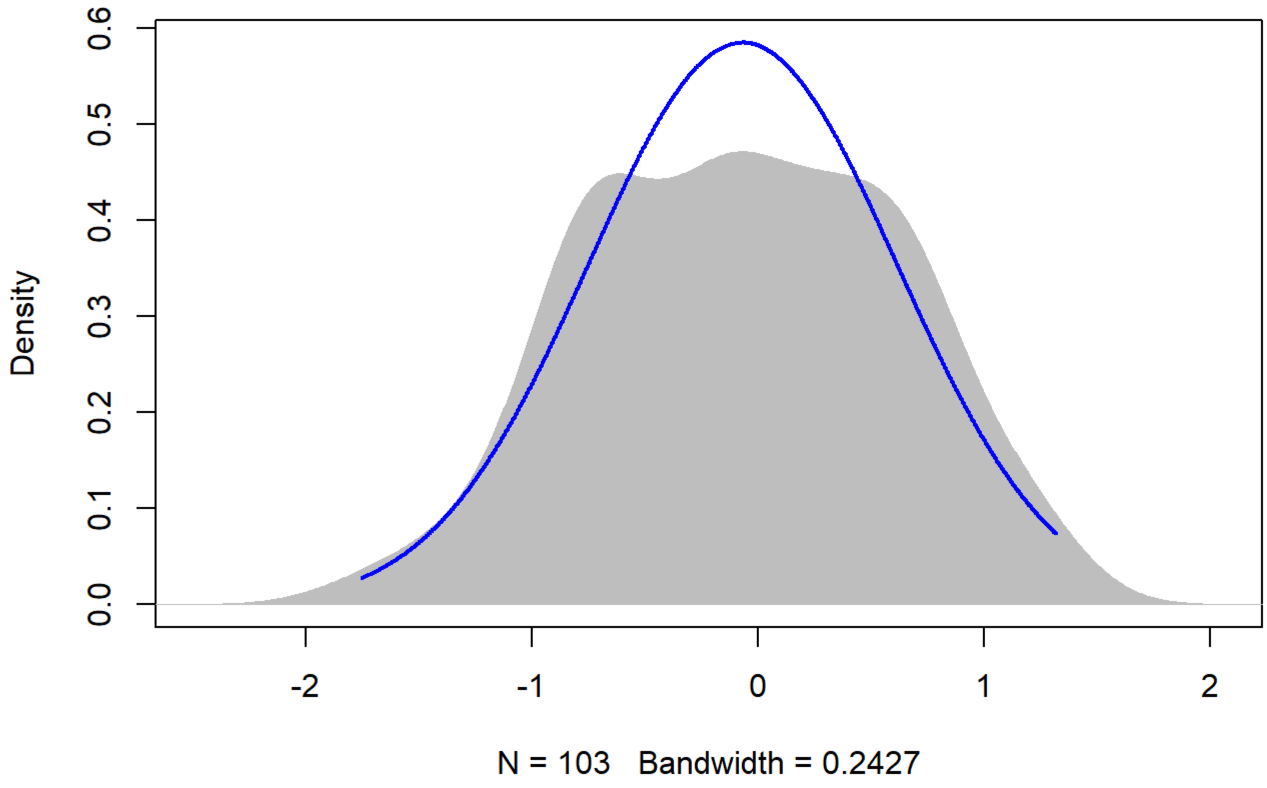
```
## boundary (singular) fit: see ?isSingular
```

```r
sprem <- emmeans(gsprpost, list(pairwise ~ Field_plottype), adjust = "Tukey")
spemm2 <- as.emmGrid(sprem$`emmeans of Field_plottype`)
CLD(spemm2, alpha = 0.05)
```

```
##  Field_plottype emmean     SE  df asymp.LCL asymp.UCL .group
##  YA2015_MSC     -0.981 0.4082 Inf    -1.781    -0.181  1
##  YA2016_PC      -0.916 0.7071 Inf    -2.302     0.470  1
##  YA2015_PC       0.182 0.4082 Inf    -0.618     0.982  1
##  YA2015_ST       1.649 0.0981 Inf     1.456     1.841   2
##  YA2016_ST       1.967 0.0836 Inf     1.803     2.131   23
##  PE_ST           2.079 0.0791 Inf     1.924     2.234    3
##  NF_ST           2.152 0.0880 Inf     1.979     2.324    3
##  NF_PC           2.282 0.1429 Inf     2.002     2.562    3
##
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 8 estimates
## significance level used: alpha = 0.05
```

```
plotNormalDensity(residuals(gspr))
```

```
## Warning in sqrt(object$devResid()): NaNs produced
```

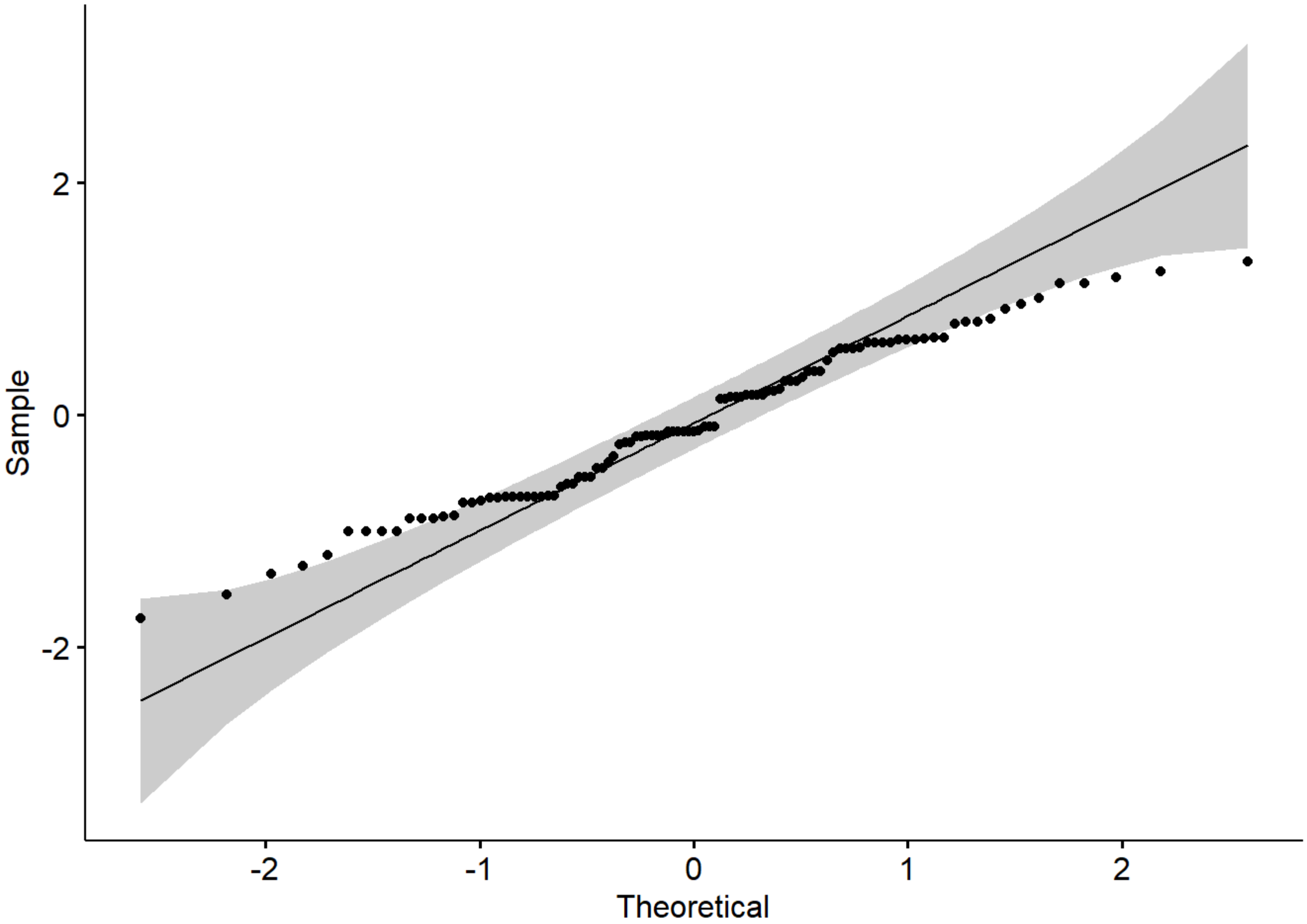


```
ggqqplot(residuals(gspr))
```

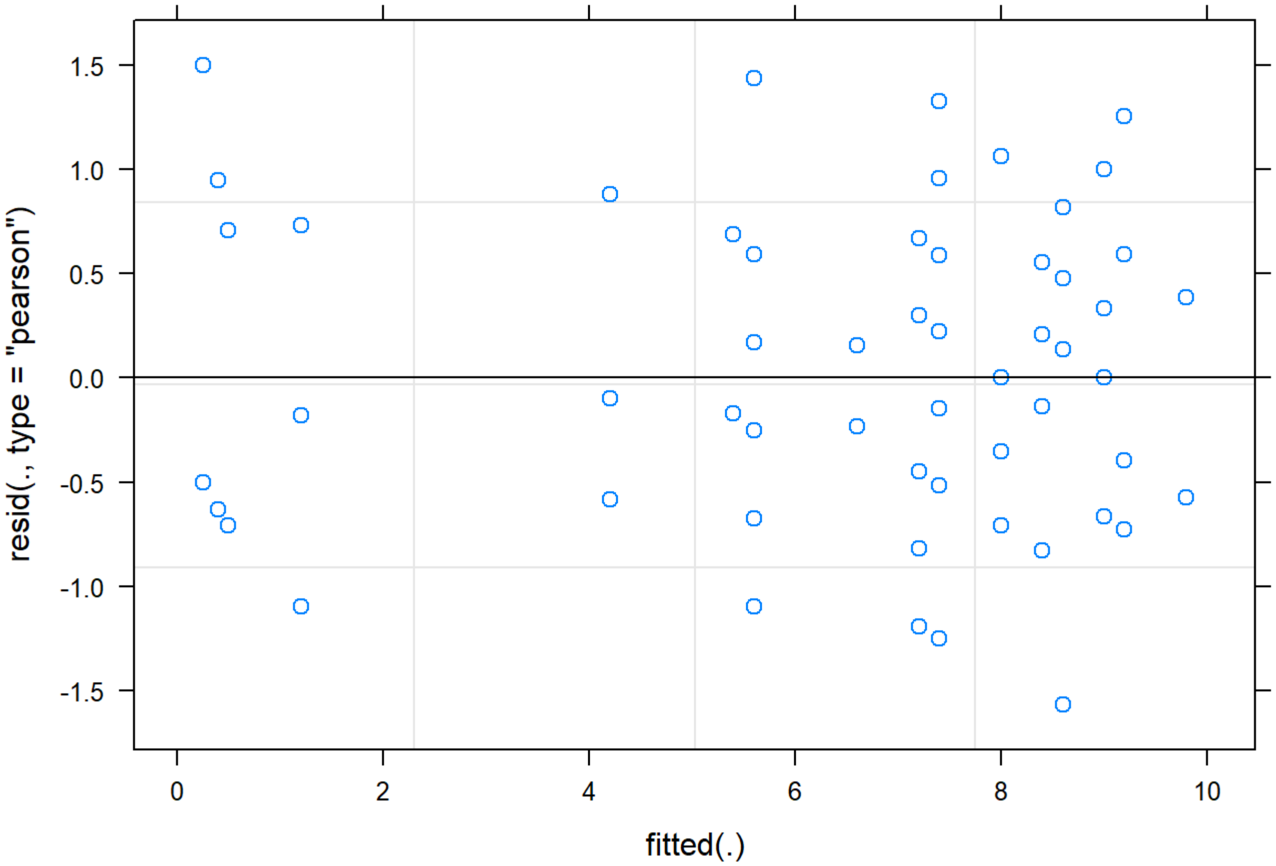
```
## Warning in sqrt(object$devResid()): NaNs produced
```

```
## Warning: Removed 3 rows containing non-finite values (stat_qq).
```

```
## Warning: Removed 3 rows containing non-finite values (stat_qq_line).

## Warning: Removed 3 rows containing non-finite values (stat_qq_line).
```

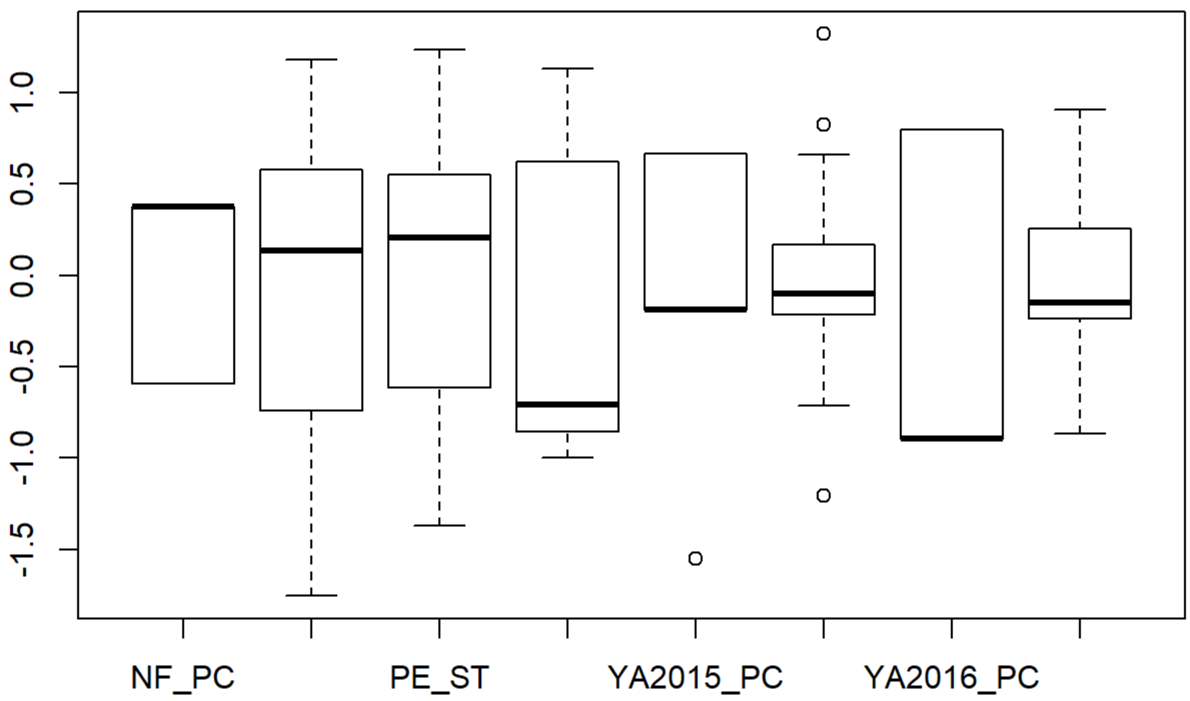


```
plot(gspr)
```



```
boxplot(residuals(gspr) ~ sprich$Field_plottype)
```

```
## Warning in sqrt(object$devResid()): NaNs produced
```



Non NF species richness difference for 2015 and 2016

```
sprich <- read.csv("spring_veg_richness.csv")

nonsp2016 <-filter(sprich, Field == "YA2016")

all_spr <- glmer(non_NF_sp ~ Field_plottype + (1|Plot) + (1|Sub_treat), data = nonsp2016, fami
ly = poisson())
```

```
## boundary (singular) fit: see ?isSingular
```

```
Anova(all_spr,type="III")
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: non_NF_sp
##                   Chisq Df Pr(>Chisq)
## (Intercept)    217.2508  1  < 2.2e-16 ***
## Field_plottype   7.2265  1   0.007184 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
r.squaredGLMM(all_spr)
```

```
## Warning: The null model is correct only if all variables used by the
## original model remain unchanged.
```

```
## boundary (singular) fit: see ?isSingular
```

```
##                  R2m       R2c
## delta     0.1906755 0.1906755
## lognormal 0.2024855 0.2024855
## trigamma  0.1785611 0.1785611
```

```
allmeans <- emmeans(all_spr, list(pairwise ~ Field_plottype), adjust = "Tukey")
```

```
sprich <- read.csv("spring_veg_richness.csv")

nonsp2015 <-filter(sprich, Field == "YA2015")

all_spr <- glmer(non_NF_sp ~ Field_plottype + (1|Plot) + (1|Sub_treat), data = nonsp2015, fami
ly = poisson())
```

```
## boundary (singular) fit: see ?isSingular
```

```
Anova(all_spr,type="III")
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: non_NF_sp
##                    Chisq Df Pr(>Chisq)
## (Intercept)    190.0915  1     <2e-16 ***
## Field_plottype   1.9353  2       0.38
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
allmeans <- emmeans(all_spr, list(pairwise ~ Field_plottype), adjust = "Tukey")
allmeans
```

```
## $`emmeans of Field_plottype`
##  Field_plottype emmean     SE  df asymp.LCL asymp.UCL
##  YA2015_MSC       1.57 0.1140 Inf      1.35      1.79
##  YA2015_PC        1.82 0.1796 Inf      1.47      2.18
##  YA2015_ST        1.74 0.0937 Inf      1.56      1.92
##
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of Field_plottype`
##  contrast               estimate    SE  df z.ratio p.value
##  YA2015_MSC - YA2015_PC  -0.2533 0.213 Inf -1.191  0.4585
```

```
##  YA2015_MSC - YA2015_ST  -0.1692 0.148 Inf -1.147  0.4849
##  YA2015_PC - YA2015_ST    0.0841 0.203 Inf  0.415  0.9094
##
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 3 estimates
```

3.3.3.1.2. Comparing plant community beta diversity between plot-types and sub-plot treatments

PERMANOVA and assumption testing of similar multivariate dispersion + NMDS plot for spring plant community by plot-type

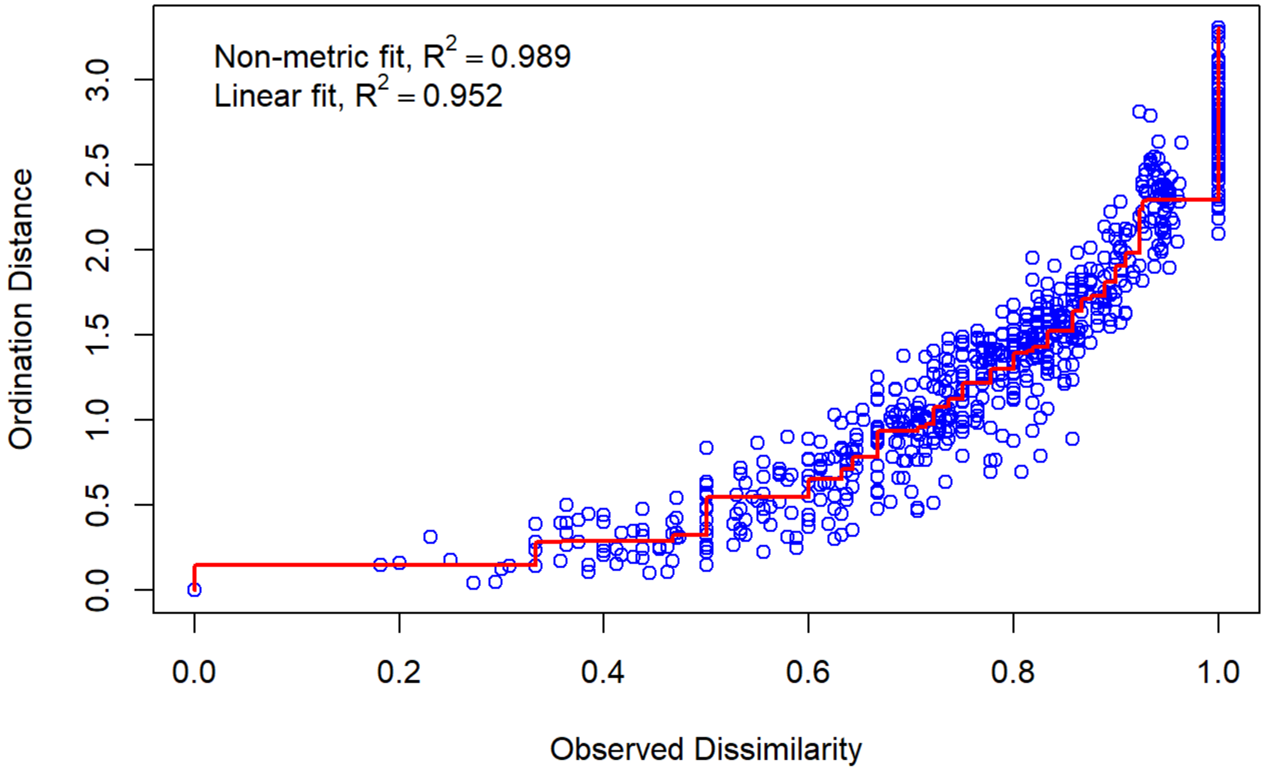
```
spec <- read.csv("veg_spring_plotwise_mini.csv", header = TRUE, row.names = 1)
meta <- read.csv("veg_spring_plotwise.csv")

comm.bc.dist <- vegdist(spec, method = "jaccard")

ad <- adonis(comm.bc.dist ~ Field_plottype, meta, method = "jaccard",  permutations = 100000)
ad
```

```
##
## Call:
## adonis(formula = comm.bc.dist ~ Field_plottype, data = meta,      permutations = 1e+05, met
hod = "jaccard")
##
## Permutation: free
## Number of permutations: 1e+05
##
## Terms added sequentially (first to last)
##
##                Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Field_plottype  7    7.5471 1.07815  8.2025 0.64939  1e-05 ***
## Residuals      31    4.0747 0.13144         0.35061
## Total          38   11.6218                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
bd<-betadisper(comm.bc.dist, group = meta$Field_plottype)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df  Sum Sq  Mean Sq F value  Pr(>F)
## Groups     7 0.20889 0.029842  2.2411 0.05757 .
## Residuals 31 0.41279 0.013316
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
comm.bc.mds <- metaMDS(spec, dist = "jaccard", binary = TRUE, try = 1000, trace = FALSE)
stressplot(comm.bc.mds)
```



```
tiff("spring_NMDS_plot.tiff", width = 8, height = 8, units = 'in', res = 150)
par(mar=c(2, 2, 5, 2), xpd=TRUE)

mds.fig <- ordiplot(comm.bc.mds, type = "none", xlim = c(-2.5,2), ylim = c(-2,2))
points(mds.fig, "sites", pch = 19, col = "darkolivegreen", select = meta$Field_plottype == "NF_ST")
points(mds.fig, "sites", pch = 18, cex =1.1, col = "deepskyblue3", select = meta$Field_plottype == "NF_PC")
points(mds.fig, "sites", pch = 17, col = "goldenrod", select = meta$Field_plottype == "YA2016_PC")
points(mds.fig, "sites", pch = 16, col = "deeppink2", select = meta$Field_plottype == "YA2016_ST")
points(mds.fig, "sites", pch = 15, col = "darkorange1", select = meta$Field_plottype == "YA2015_ST")
points(mds.fig, "sites", pch = 15, col = "darkorchid2", select = meta$Field_plottype == "YA2015_MSC")
points(mds.fig, "sites", pch = 16, col = "firebrick2", select = meta$Field_plottype == "YA2015_PC")
points(mds.fig, "sites", pch = 17, cex = 1.1, col = "black", select = meta$Field_plottype == "PE_ST")

ordihull(comm.bc.mds, meta$Field_plottype, draw = "polygon", col = c("deepskyblue3","darkolivegreen", "black", "darkorchid2","firebrick2", "darkorange1","goldenrod","deeppink2"), label = FALSE, alpha = 50)
```

```
legend("top", inset=c(0.,-0.12), bg = "white", ncol = 2, legend = c("P. Forest - Lift-and-drop
",  "P. Forest - Passive" ,"RF 2016 - Passive", "RF 2016 - Topsoil Recipient", "RF 2015 - Tops
oil Recipient", "RF 2015 - Passive", "RF 2015 - Mow-and-Spray", "Gravel Pit - Topsoil Recipien
t"), pch = c(19,18,16,17,15,15,16,17),
       col = c("darkolivegreen",  "deepskyblue3", "deeppink2", "goldenrod" , "darkorange1", "d
arkorchid2", "firebrick2", "black"))

dev.off()
```

```
## png
##   2
```

Pair-wise testing of spring communities, with Benjamini-Hochberg adjustment of p-values at the end - four groups, and betadisper assumption test for each

```
ppsp <- read.csv("pair_perm_spring_plot.csv")

filmeta <- filter(meta, Field_type == "YA_C" | Field_type =="NF")
partspec <- filmeta[-c(1:11)]
comm.bc.dist <- vegdist(partspec, method = "jaccard", binary = TRUE)
ad <- adonis(comm.bc.dist ~ Field_type, filmeta, binary = TRUE, method = "jaccard", permutatio
ns = 100000)
ppsp[1,2] <- ad$aov.tab$F.Model[1]
ppsp[1,3] <- ad$aov.tab$R2[1]
ppsp[1,4] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Field_type)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df   Sum Sq  Mean Sq F value Pr(>F)
## Groups     1 0.000146 0.000146  0.0112 0.9167
## Residuals 22 0.286516 0.013023
```

```
filmeta <- filter(meta, Field_type == "YA_C" | Field_type =="YA_ST")
partspec <- filmeta[-c(1:11)]
comm.bc.dist <- vegdist(partspec, method = "jaccard", binary = TRUE)
ad <- adonis(comm.bc.dist ~ Field_type, filmeta, method = "jaccard", binary = TRUE, permutatio
ns = 100000)
ppsp[2,2] <- ad$aov.tab$F.Model[1]
ppsp[2,3] <- ad$aov.tab$R2[1]
ppsp[2,4] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Field_type)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
```

```
##            Df   Sum Sq  Mean Sq F value Pr(>F)
## Groups     1 0.021267 0.021267  1.9651 0.1749
## Residuals 22 0.238099 0.010823
```

```
filmeta <- filter(meta, Field_type == "YA_C" | Field_type =="PE")
partspec <- filmeta[-c(1:11)]
comm.bc.dist <- vegdist(partspec, method = "jaccard", binary = TRUE)
ad <- adonis(comm.bc.dist ~ Field_type, filmeta, method = "jaccard", binary = TRUE, permutatio
ns = 100000)
ppsp[3,2] <- ad$aov.tab$F.Model[1]
ppsp[3,3] <- ad$aov.tab$R2[1]
ppsp[3,4] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Field_type)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##            Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.000398 0.0003981  0.0273 0.8707
## Residuals 17 0.247962 0.0145860
```

```
filmeta <- filter(meta, Field_type == "NF" | Field_type =="YA_ST")
partspec <- filmeta[-c(1:11)]
comm.bc.dist <- vegdist(partspec, method = "jaccard", binary = TRUE)
ad <- adonis(comm.bc.dist ~ Field_type, filmeta, method = "jaccard", binary = TRUE, permutatio
ns = 100000)
ppsp[4,2] <- ad$aov.tab$F.Model[1]
ppsp[4,3] <- ad$aov.tab$R2[1]
ppsp[4,4] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Field_type)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##            Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.021238 0.0212376  2.3153 0.1455
## Residuals 18 0.165108 0.0091727
```

```
filmeta <- filter(meta, Field_type == "NF" | Field_type =="PE")
partspec <- filmeta[-c(1:11)]
comm.bc.dist <- vegdist(partspec, method = "jaccard", binary = TRUE)
ad <- adonis(comm.bc.dist ~ Field_type, filmeta, method = "jaccard", binary = TRUE, permutatio
ns = 100000)
ppsp[5,2] <- ad$aov.tab$F.Model[1]
ppsp[5,3] <- ad$aov.tab$R2[1]
ppsp[5,4] <- ad$aov.tab$`Pr(>F)`[1]
```

```
bd<-betadisper(comm.bc.dist, group = filmeta$Field_type)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.000978 0.0009783   0.073 0.7913
## Residuals 13 0.174228 0.0134021
```

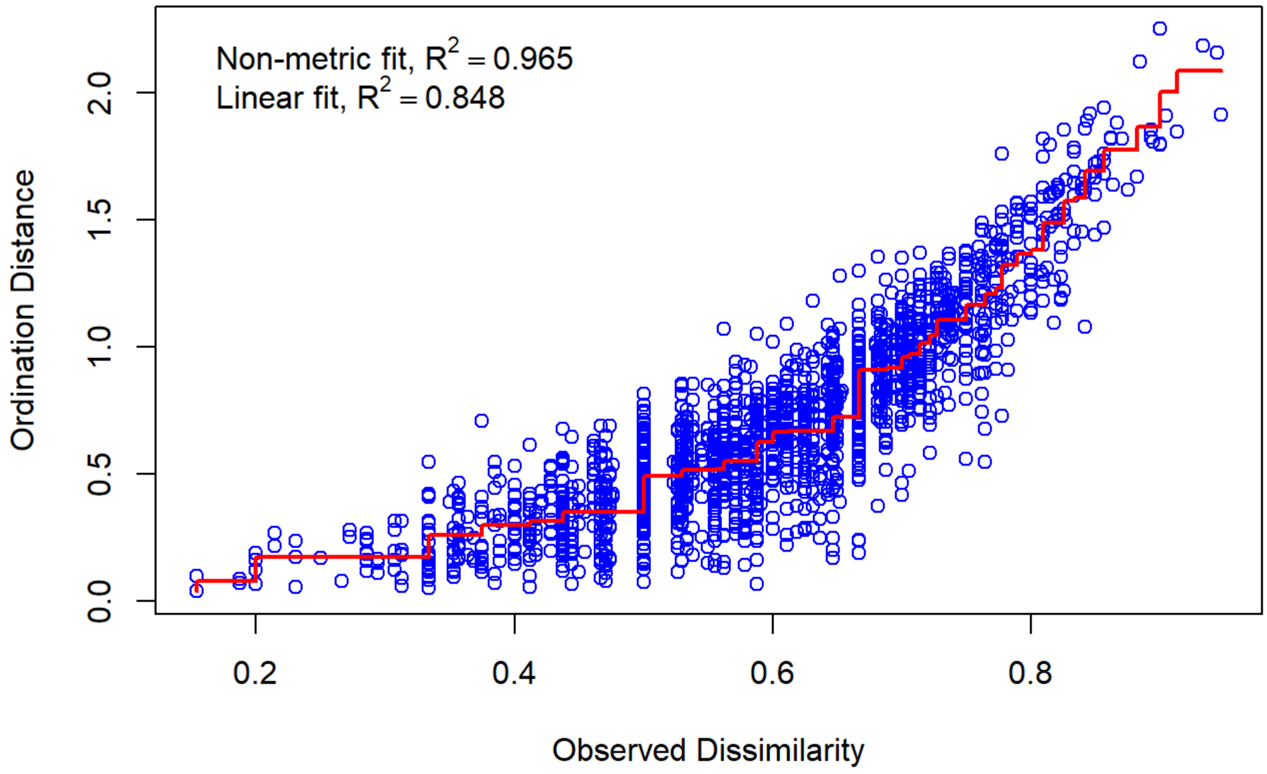
```
filmeta <- filter(meta, Field_type == "YA_ST" | Field_type =="PE")
partspec <- filmeta[-c(1:11)]
comm.bc.dist <- vegdist(partspec, method = "jaccard", binary = TRUE)
ad <- adonis(comm.bc.dist ~ Field_type, filmeta, method = "jaccard", binary = TRUE, permutatio
ns = 100000)
ppsp[6,2] <- ad$aov.tab$F.Model[1]
ppsp[6,3] <- ad$aov.tab$R2[1]
ppsp[6,4] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Field_type)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.008075 0.0080754  0.8384 0.3765
## Residuals 13 0.125217 0.0096321
```

```
ppsp[5] <-p.adjust(ppsp$p, method = "BH")

write.csv(ppsp,"spring_pair.csv")
```

NMDS for soil-transfer sub-plots in Reforestation and Gravel Pit sites for spring

```
spec <- read.csv("spring_veg_plotname.csv", header = TRUE, row.names = 1)
meta <- read.csv("spring_veg_sub.csv")

specYAPEst <- spec[c(21:40,62:81, 87:106),]
metaYAPEst <- meta[c(21:40,62:81, 87:106),]

comm.bc.dist <- vegdist(spec, method = "jaccard")

comm.bc.mds <- metaMDS(specYAPEst, dist = "jaccard", try = 1000, trace = FALSE)

stressplot(comm.bc.mds)
```



```
tiff("spring_sub_NMDS.tiff")
par(mar=c(2, 2, 4, 2), xpd=TRUE)
mds.fig <- ordiplot(comm.bc.mds, type = "none")
points(mds.fig, "sites", pch = 19, col = "darkolivegreen", select = metaYAPEst$Treat_new == "ST")
points(mds.fig, "sites", pch = 18, cex =1.1, col = "deepskyblue3", select = metaYAPEst$Treat_new == "WD")
points(mds.fig, "sites", pch = 17, col = "goldenrod", select = metaYAPEst$Treat_new == "DS")
points(mds.fig, "sites", pch = 16, col = "deeppink2", select = metaYAPEst$Treat_new == "SS")
points(mds.fig, "sites", pch = 0, col = "grey", select = metaYAPEst$Treat_new == "PE_ST")
points(mds.fig, "sites", pch = 1, cex =1.1, col = "blue", select = metaYAPEst$Treat_new == "PE_WD")
points(mds.fig, "sites", pch = 2, col = "black", select = metaYAPEst$Treat_new == "PE_DS")
points(mds.fig, "sites", pch = 5, col = "orange", select = metaYAPEst$Treat_new == "PE_SS")
ordihull(comm.bc.mds, metaYAPEst$Fieldcomb_plottype, draw = "lines", col = c("red", "blue"), label = FALSE, alpha
 =200)
legend("top", inset=c(0.0, -0.05), legend = c("Gravel pit", "Reforestation", "RF Topsoil recipient only","RF Woody debris", "RF Shrubs", "RF Shade shelter", "GP Topsoil recipient only",
                                               "GP Woody debris", "GP Shrubs", "GP Shade shelter"), lty = c(1, 1, NA, NA, NA, NA, NA, NA, NA, NA), pch = c(NA,NA,19,18,17,16,0,1,2,5), col = c("red", "blue", "darkolivegreen","deepskyblue3", "goldenrod", "deeppink2", "grey", "blue", "black", "orange"), bg = "white", ncol=2)
dev.off()
```

```
## png
##   2
```

Comparison of sub-plot treatments within RF sites and PE site and between the two sites.

```
#all subplots in RF (YA)
filmeta <- filter(metaYAPEst, Treat_new == "ST" | Treat_new =="SS"| Treat_new =="WD"| Treat_ne
w =="DS")
partspec <- filmeta[-c(1:8)]
comm.bc.dist <- vegdist(partspec, method = "jaccard", binary = TRUE)
ad <- adonis(comm.bc.dist ~ Treat_new, filmeta, binary = TRUE, method = "jaccard", permutation
s = 100000)
ad
```

```
##
## Call:
## adonis(formula = comm.bc.dist ~ Treat_new, data = filmeta, permutations = 1e+05,      metho
d = "jaccard", binary = TRUE)
##
## Permutation: free
## Number of permutations: 1e+05
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Treat_new  3    0.3792 0.12641 0.86049 0.06691 0.6731
## Residuals 36    5.2886 0.14691         0.93309
## Total     39    5.6678                 1.00000
```

```
bd<-betadisper(comm.bc.dist, group = filmeta$Treat_new)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df  Sum Sq   Mean Sq F value Pr(>F)
## Groups     3 0.01532 0.0051066  0.7073  0.554
## Residuals 36 0.25992 0.0072201
```

```
#all subplots in GP (PE)
filmeta <- filter(metaYAPEst, Treat_new == "PE_ST" | Treat_new =="PE_SS"| Treat_new =="PE_WD"|
 Treat_new =="PE_DS")
partspec <- filmeta[-c(1:8)]
comm.bc.dist <- vegdist(partspec, method = "jaccard", binary = TRUE)
ad <- adonis(comm.bc.dist ~ Treat_new, filmeta, binary = TRUE, method = "jaccard", permutation
s = 100000)
ad
```

```
##
## Call:
```

```
## adonis(formula = comm.bc.dist ~ Treat_new, data = filmeta, permutations = 1e+05,      metho
d = "jaccard", binary = TRUE)
##
## Permutation: free
## Number of permutations: 1e+05
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Treat_new  3    0.4165 0.13885 0.76966 0.12611 0.8223
## Residuals 16    2.8864 0.18040         0.87389
## Total     19    3.3030                 1.00000
```

```
bd<-betadisper(comm.bc.dist, group = filmeta$Treat_new)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     3 0.005642 0.0018807  0.1452 0.9313
## Residuals 16 0.207292 0.0129558
```

3.3.3.2. Summer and fall vegetation sampling results

3.3.3.2.1. Comparing summer species richness and diversity of plot-type and sites and sub-plot treatments

Comparing summer alpha species richness - poisson

```
sum_veg <- read.csv("summer_veg_data.csv")

gsum_plot_tot <- glmer(Sp_rich ~ Site_plottype + (1|Treatment) + (1|Plot), data = sum_veg, fam
ily = poisson())
sprem <- emmeans(gsum_plot_tot, list(pairwise ~ Site_plottype), adjust = "Tukey")


gall_sum <- glmer(NF_sp_rich ~ Site_plottype * Treatment + (1|Plot), data = sum_veg, family =
poisson())
```

```
## fixed-effect model matrix is rank deficient so dropping 30 columns / coefficients
```

```
## boundary (singular) fit: see ?isSingular
```

```
r.squaredGLMM(gall_sum)
```

```
## Warning: The null model is correct only if all variables used by the
## original model remain unchanged.
```

```
##                  R2m       R2c
## delta     0.8070641 0.8070641
## lognormal 0.8170104 0.8170104
## trigamma  0.7960105 0.7960105
```

```
Anova(gall_sum, type = "III")
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
## 
## Response: NF_sp_rich
##                            Chisq Df Pr(>Chisq)    
## (Intercept)             199.0934  1    < 2e-16 ***
## Site_plottype           100.1954 10    < 2e-16 ***
## Treatment                 0.8615  3    0.83471    
## Site_plottype:Treatment  17.6966 11    0.08889 .  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
gsum_plot <- glmer(NF_sp_rich ~ Site_plottype + (1|Treatment) + (1|Plot), data = sum_veg, fami
ly = poisson())
```

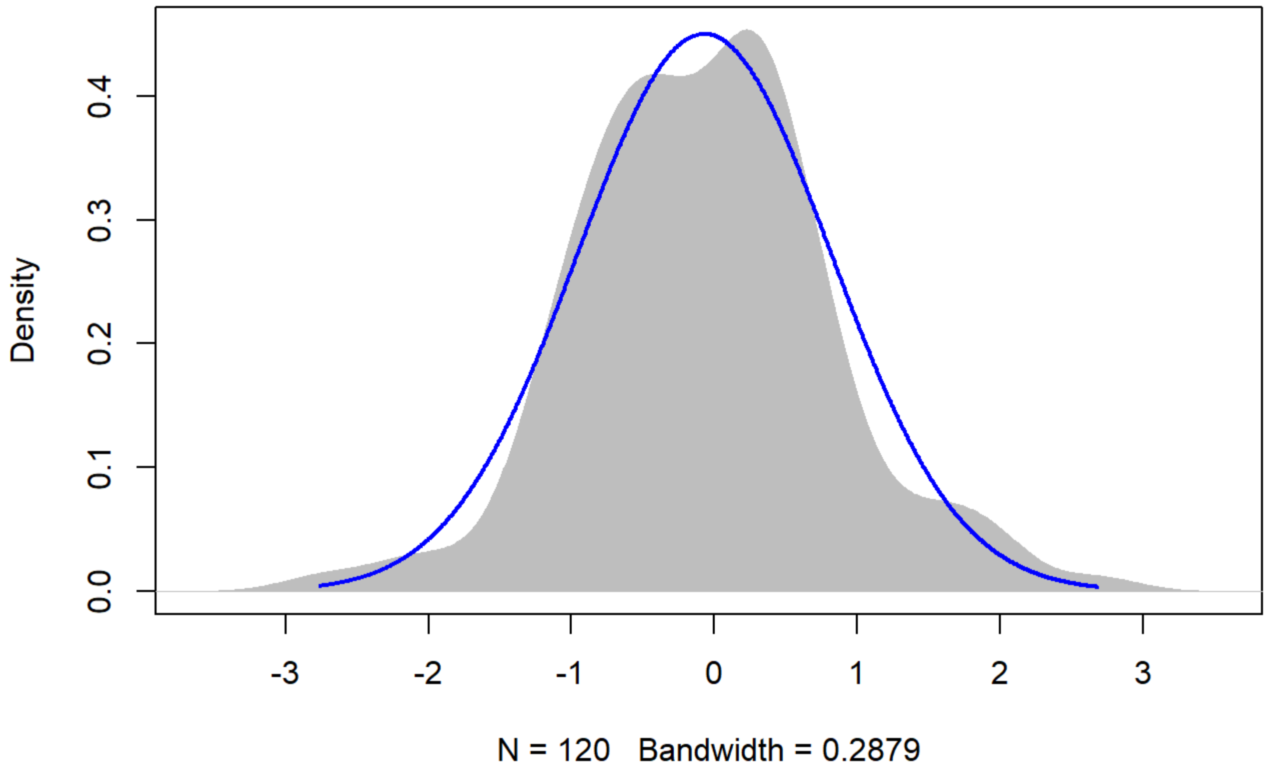
```
## boundary (singular) fit: see ?isSingular
```

```
sprem <- emmeans(gsum_plot, list(pairwise ~ Site_plottype), adjust = "Tukey")
spemm2 <- as.emmGrid(sprem$`emmeans of Site_plottype`)
CLD(spemm2)
```

```
##  Site_plottype emmean     SE  df asymp.LCL asymp.UCL .group
##  YA2016_PC      0.588 0.3333 Inf   -0.0655      1.24  1    
##  YA2015_PC      0.588 0.3333 Inf   -0.0655      1.24  1    
##  YA2015_MSC     0.642 0.1622 Inf    0.3239      0.96  1    
##  PE_PC          1.335 0.2294 Inf    0.8854      1.78  12   
##  YA2015_ST      1.908 0.0884 Inf    1.7344      2.08   23  
##  YA2016_ST      2.086 0.0788 Inf    1.9312      2.24   234 
##  NDF_PC         2.152 0.1525 Inf    1.8529      2.45   2345
##  NF_PC          2.175 0.1508 Inf    1.8793      2.47   2345
##  NF_ST          2.262 0.0833 Inf    2.0984      2.43    345
##  PE_ST          2.416 0.0668 Inf    2.2850      2.55     45
##  SDF_PC         2.625 0.1204 Inf    2.3887      2.86      5
## 
## Results are given on the log (not the response) scale. 
## Confidence level used: 0.95 
## P value adjustment: tukey method for comparing a family of 11 estimates 
## significance level used: alpha = 0.05
```

```
plotNormalDensity(resid(gall_sum))
```

```
## Warning in sqrt(object$devResid()): NaNs produced
```

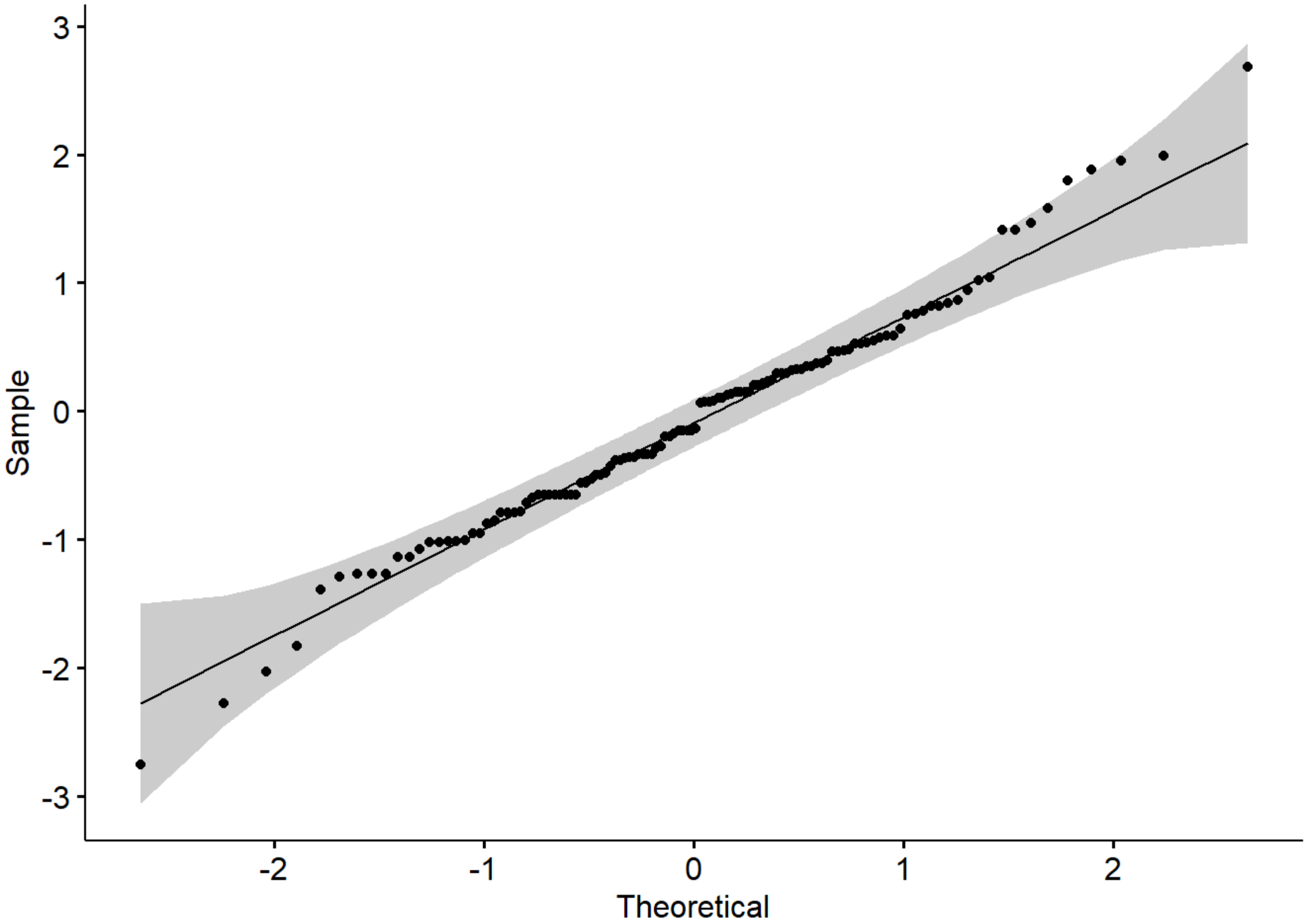


```
ggqqplot(residuals(gall_sum))
```

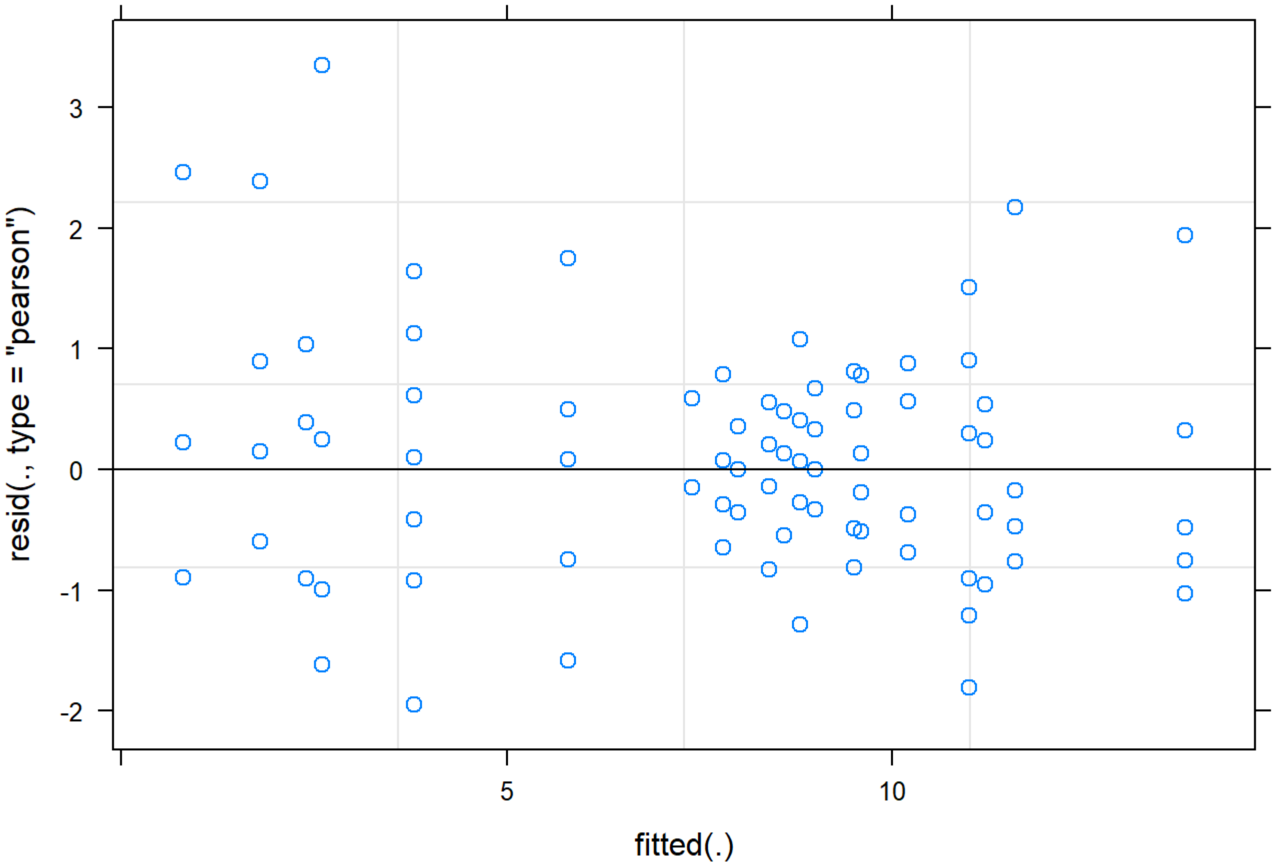
```
## Warning in sqrt(object$devResid()): NaNs produced
```

```
## Warning: Removed 4 rows containing non-finite values (stat_qq).
```

```
## Warning: Removed 4 rows containing non-finite values (stat_qq_line).

## Warning: Removed 4 rows containing non-finite values (stat_qq_line).
```

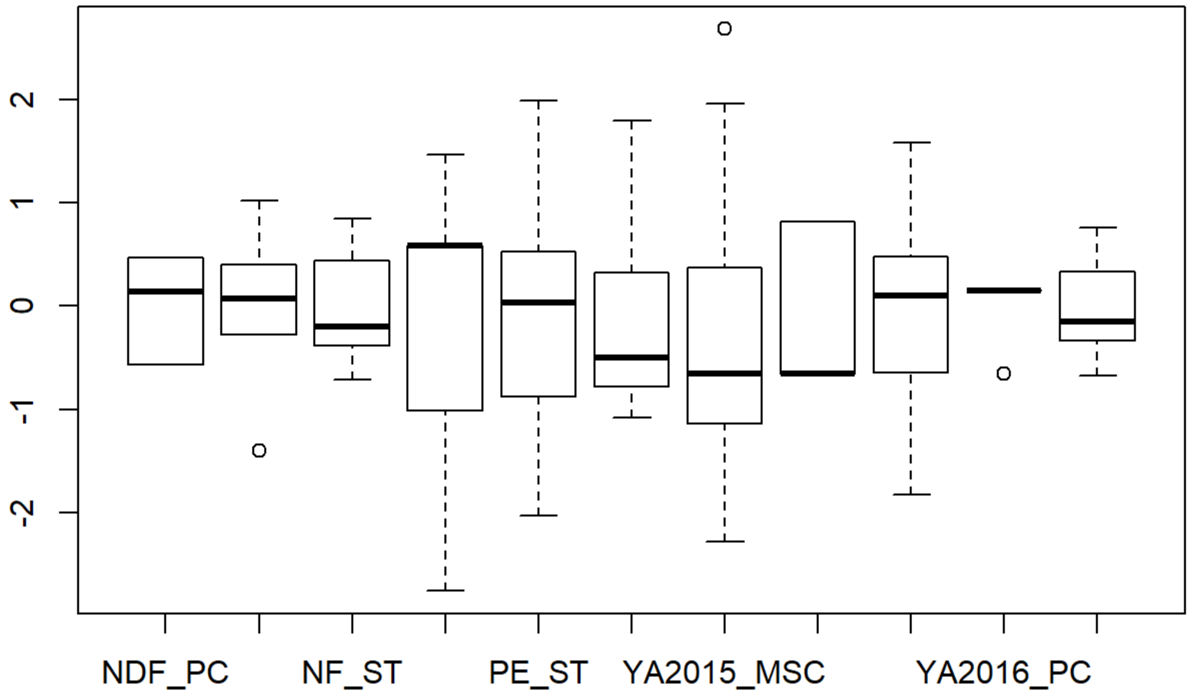


```
plot(gall_sum)
```



```
boxplot(residuals(gall_sum) ~ sum_veg$Site_plottype)
```

```
## Warning in sqrt(object$devResid()): NaNs produced
```



Non-NF species richness 2016 RF & 2015 and gravel pit

```
sum_veg <- read.csv("summer_veg_data.csv")
nonNF <- filter(sum_veg, Site == "YA2016" )
gsum_plot <- glmer(nonNF_sp ~ Site_plottype + (1|Treatment) + (1|Plot), data = nonNF, family =
 poisson())
```

```
## boundary (singular) fit: see ?isSingular
```

```
Anova(gsum_plot, type = "III")
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: nonNF_sp
##                  Chisq Df Pr(>Chisq)
## (Intercept)   655.0977  1     <2e-16 ***
## Site_plottype   0.1142  1     0.7354
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
nonNF <- filter(sum_veg, Site == "YA2015" )
gsum_plot <- glmer(nonNF_sp ~ Site_plottype + (1|Treatment) + (1|Plot), data = nonNF, family =
 poisson())
Anova(gsum_plot, type = "III")
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: nonNF_sp
##                     Chisq Df Pr(>Chisq)
## (Intercept)   1340.5055  1     <2e-16 ***
## Site_plottype    1.8072  2     0.4051
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
nonNF <- filter(sum_veg, Site == "PE" )
gsum_plot <- glmer(nonNF_sp ~ Site_plottype + (1|Treatment) + (1|Plot), data = nonNF, family =
 poisson())
r.squaredGLMM(gsum_plot)
```

```
## Warning: The null model is correct only if all variables used by the
## original model remain unchanged.
```

```
##                   R2m       R2c
## delta     0.5025162 0.5908008
## lognormal 0.5078716 0.5970971
## trigamma  0.4969933 0.5843077
```

```
Anova(gsum_plot, type = "III")
```

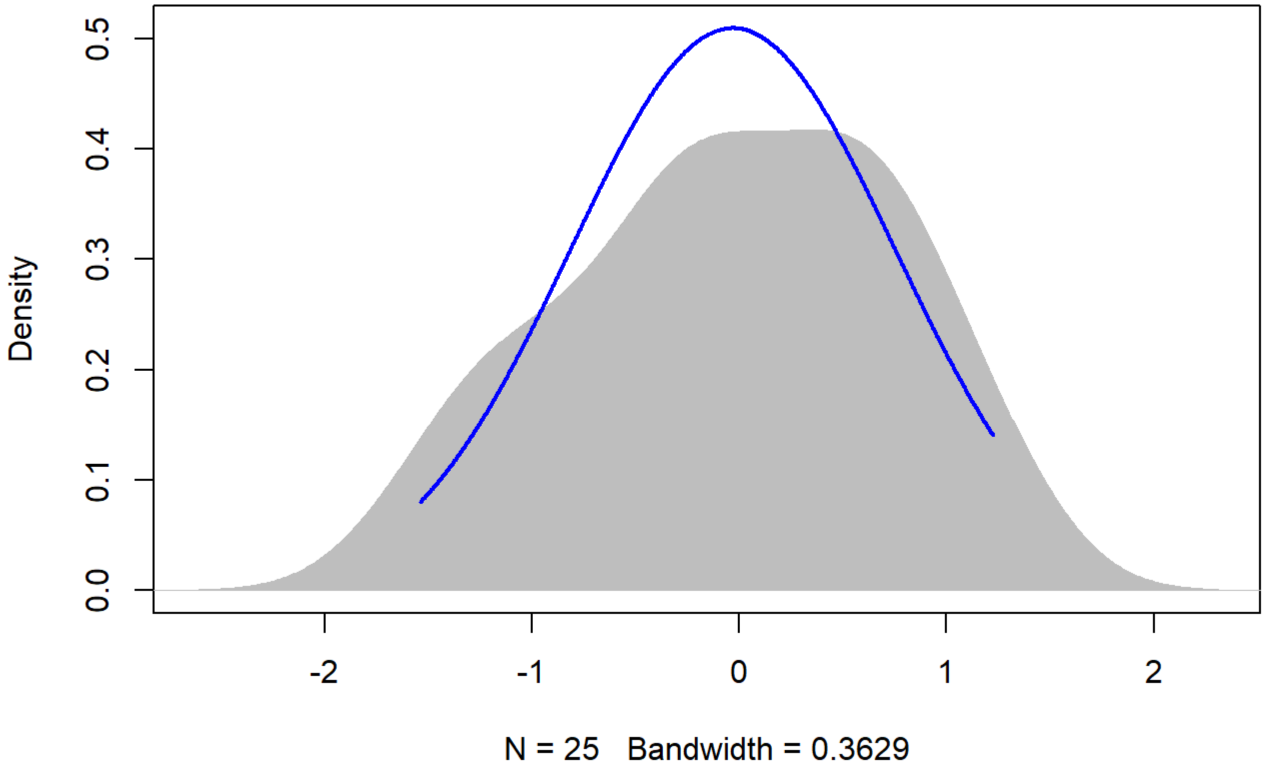
```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: nonNF_sp
##                   Chisq Df Pr(>Chisq)
## (Intercept)   240.708  1  < 2.2e-16 ***
## Site_plottype  15.289  1  9.224e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sprem <- emmeans(gsum_plot, list(pairwise ~ Site_plottype), adjust = "Tukey")
sprem
```

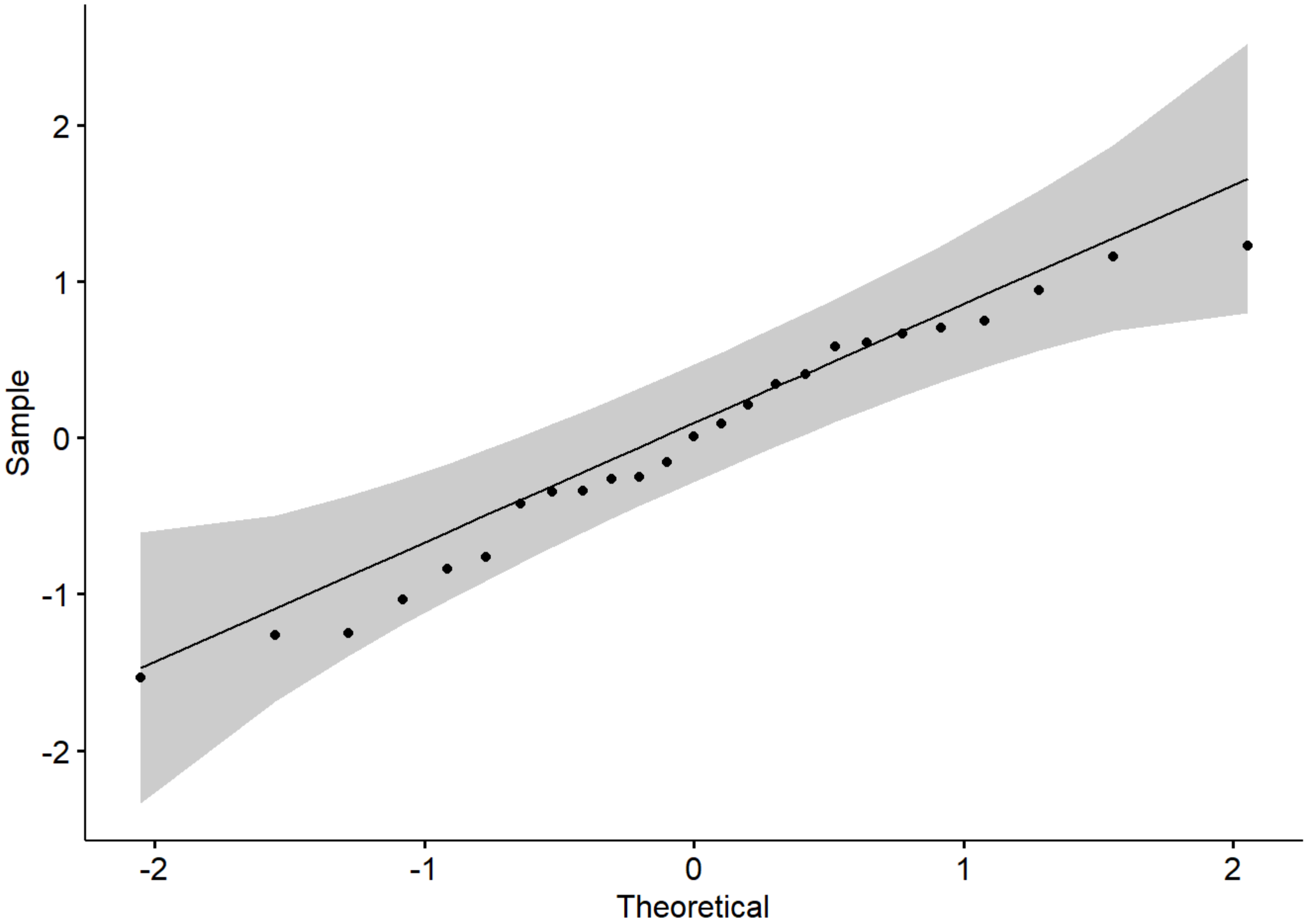
```
## $`emmeans of Site_plottype`
##  Site_plottype emmean     SE  df asymp.LCL asymp.UCL
##  PE_PC           2.39 0.1542 Inf      2.09      2.69
##  PE_ST           3.02 0.0706 Inf      2.88      3.16
##
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of Site_plottype`
##  contrast      estimate   SE  df z.ratio p.value
##  PE_PC - PE_ST   -0.627 0.16 Inf -3.910  0.0001
```

```
##
## Results are given on the log (not the response) scale.
```

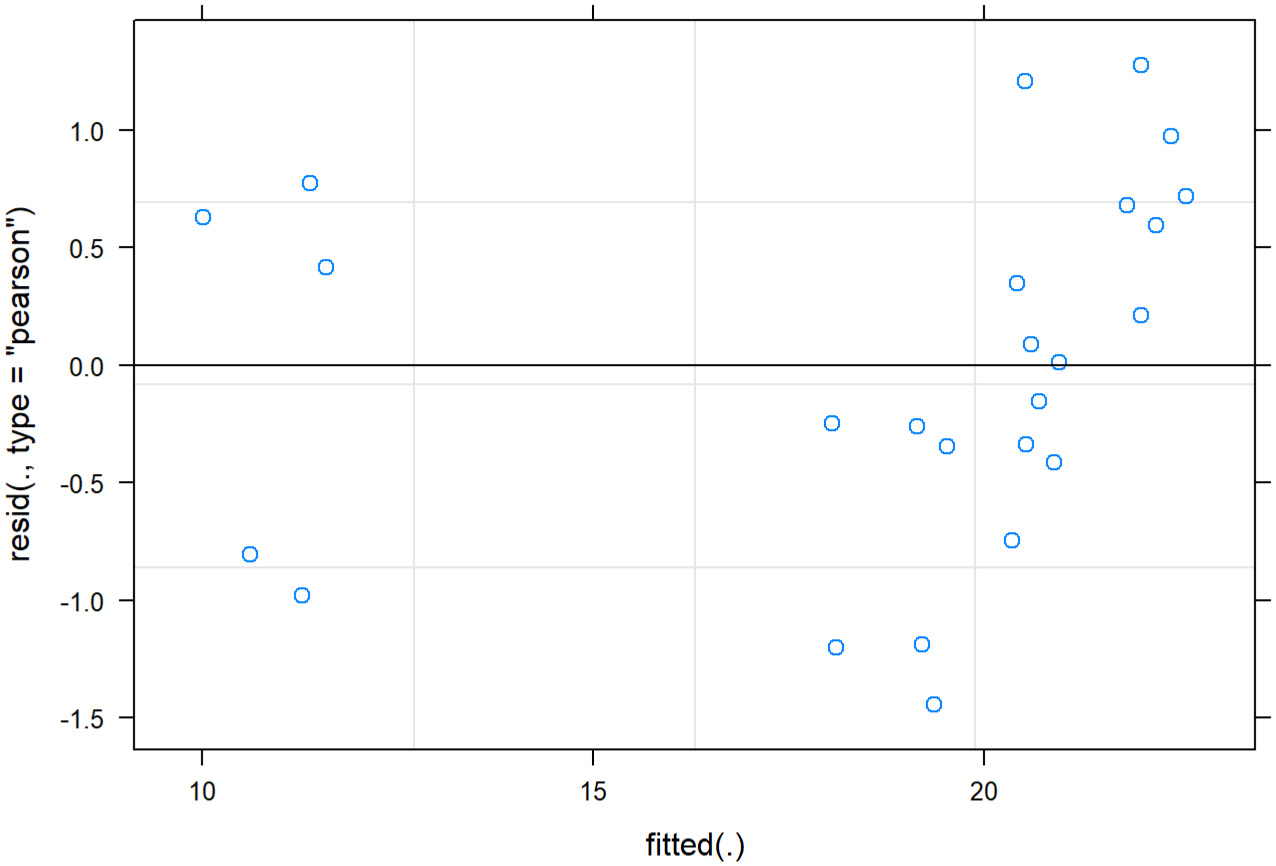
```
plotNormalDensity(resid(gsum_plot))
```



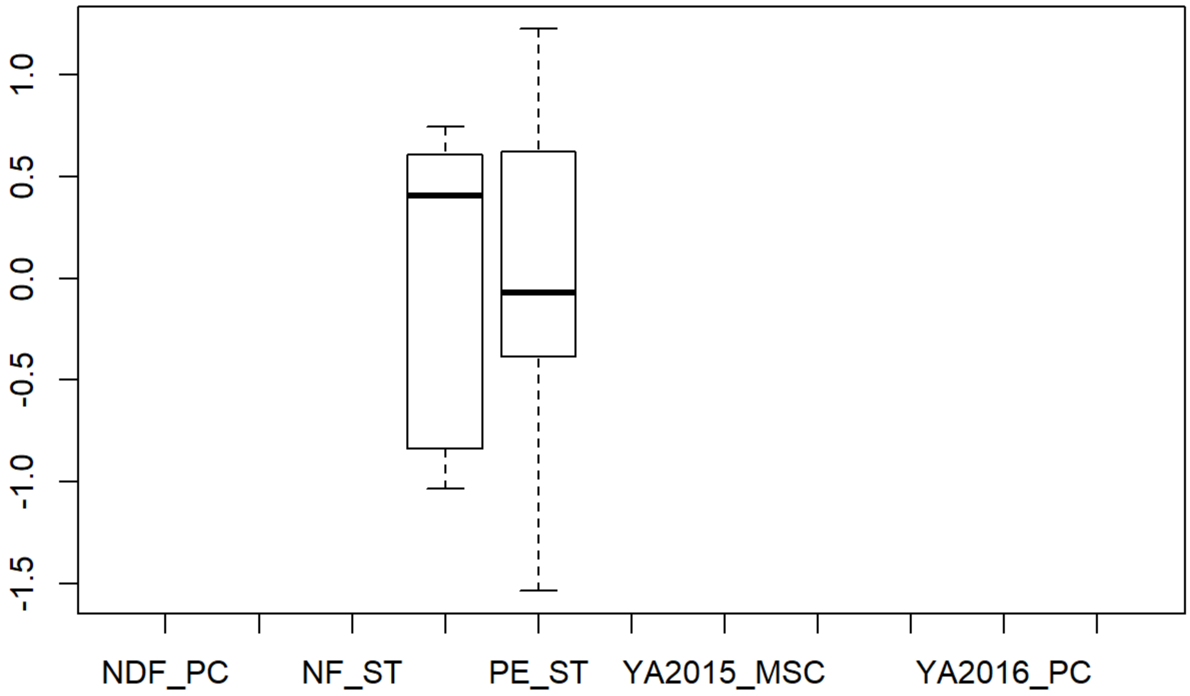
```
ggqqplot(residuals(gsum_plot))
```



```
plot(gsum_plot)
```



```
boxplot(residuals(gsum_plot) ~ nonNF$Site_plottype)
```



3.3.3.2.2. Comparing summer beta diversity of sites and plot-types and sub-plot treatment areas

Summer NMDS - plotwise

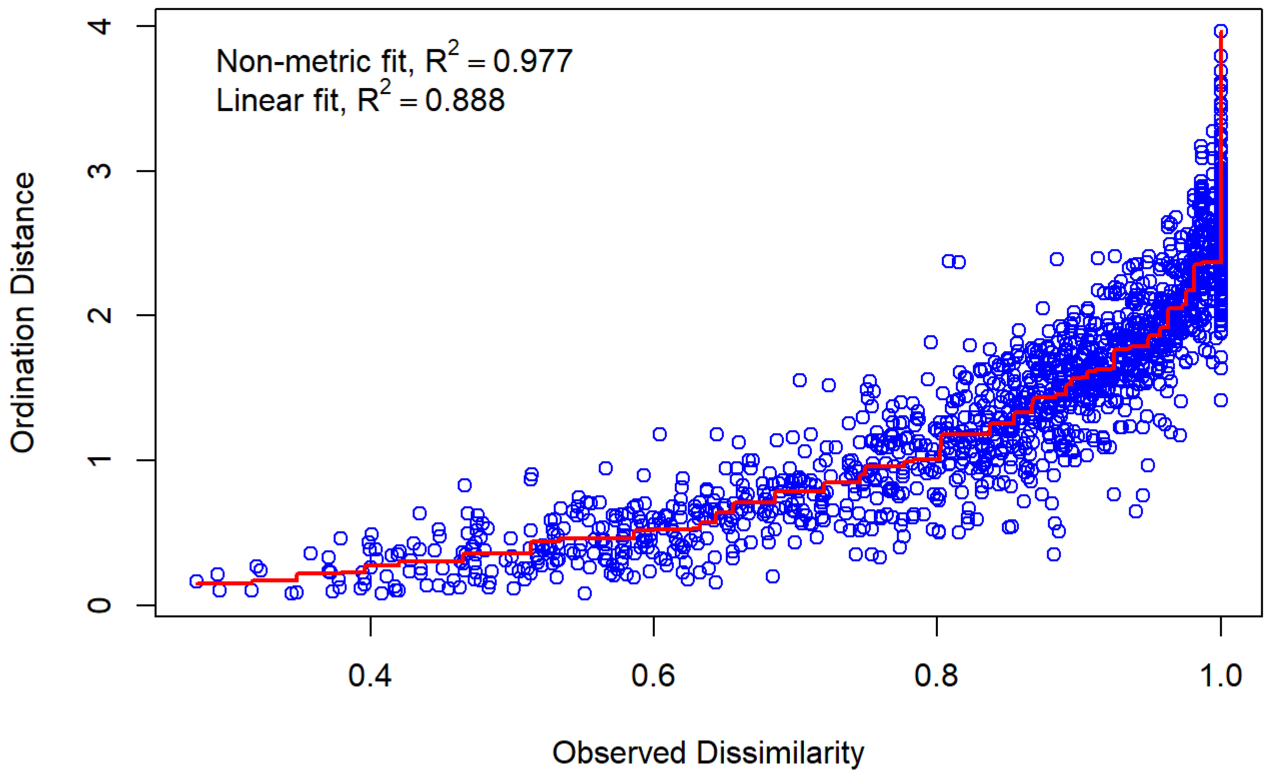
```
spec <- read.csv("freq_ST.csv", header = TRUE, row.names = 1)
meta <- read.csv("freq_ST_meta.csv")

comm.bc.dist <- vegdist(spec, method = "bray")
comm.bc.clust <- hclust(comm.bc.dist, method = "average")
comm.bc.mds <- metaMDS(spec, dist = "bray", try = 1000, trace = FALSE)

adonis2(comm.bc.dist ~ Site_plottype, meta, method = "bray")
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## adonis2(formula = comm.bc.dist ~ Site_plottype, data = meta, method = "bray")
##               Df SumOfSqs      R2      F Pr(>F)    
## Site_plottype 10   11.764 0.59899 6.5723  0.001 ***
## Residual      44    7.876 0.40101                  
## Total         54   19.640 1.00000                  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
bd<-betadisper(comm.bc.dist, group = meta$Site_plottype)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df  Sum Sq  Mean Sq F value  Pr(>F)
## Groups    10 0.29922 0.029922  2.0629 0.04898 *
## Residuals 44 0.63821 0.014505
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
stressplot(comm.bc.mds)
```



```
tiff("summer_NMDS.tiff", width = 8, height = 8, units = 'in', res = 150)
par(mar=c(2, 2, 5, 2), xpd=TRUE)

mds.fig <- ordiplot(comm.bc.mds, type = "none")
points(mds.fig, "sites", pch = 1, cex = 1.1, col = "cyan3", select = meta$Site_plottype == "ND
F_PC")
points(mds.fig, "sites", pch = 18, cex =1.1, col = "deepskyblue3", select = meta$Site_plottype
 == "NF_PC")
points(mds.fig, "sites", pch = 4, cex = 1.1, col = "blue", select = meta$Site_plottype == "SDF
```

```
_PC")
points(mds.fig, "sites", pch = 6, cex = 1.1, col = "tomato1", select = meta$Site_plottype == "PE_PC")
points(mds.fig, "sites", pch = 17, col = "goldenrod", select = meta$Site_plottype == "YA2016_PC")
points(mds.fig, "sites", pch = 16, col = "firebrick2", select = meta$Site_plottype == "YA2015_PC")
points(mds.fig, "sites", pch = 19, col = "darkolivegreen", select = meta$Site_plottype == "NF_ST")
points(mds.fig, "sites", pch = 17, cex = 1.1, col = "black", select = meta$Site_plottype == "PE_ST")
points(mds.fig, "sites", pch = 16, col = "deeppink2", select = meta$Site_plottype == "YA2016_ST")
points(mds.fig, "sites", pch = 15, col = "darkorchid2", select = meta$Site_plottype == "YA2015_MSC")
points(mds.fig, "sites", pch = 0, col = "darkorange1", select = meta$Site_plottype == "YA2015_ST")

ordihull(comm.bc.mds, meta$Site_plottype, draw = "polygon", alpha = 50, col = c("cyan3", "deepskyblue3", "darkolivegreen",  "tomato1","black", "blue", "darkorchid2","firebrick2", "darkorange1","goldenrod","deeppink2"), label = FALSE)

legend("top", inset=c(0.,-0.12), bg = "white", ncol = 2, legend = c("N. Donor Forest - Passive", "S. Donor Forest - Passive", "P. Forest - Passive" , "P. Forest - Lift-and-drop",  "Gravel Pit - Passive", "Gravel Pit - Topsoil Recipient", "RF 2016 - Passive", "RF 2016 - Topsoil Recipient", "RF 2015 - Passive", "RF 2015 - Mow-and-Spray", "RF 2015 - Topsoil Recipient"), pch = c(1,4,18,19,6,17,17,16,16,15,0),
       col = c("cyan3", "blue", "deepskyblue3","darkolivegreen", "tomato1", "black", "goldenrod","deeppink2", "firebrick2", "darkorchid2", "darkorange1"))

dev.off()
```

```
## png
##   2
```

Pairwise testing summer NMDS plot-type

```
freq <- read.csv("freq_ST_meta_g.csv")
ppsump <- read.csv("pair_perm_summer_plot.csv")

filmeta <- filter(freq, Site_plottype == "YA2015_ST" |Site_plottype =="YA2015_MSC")
partspec <- filmeta[-c(1:8)]
comm.bc.dist <- vegdist(partspec, method = "bray")
ad <- adonis(comm.bc.dist ~ Site_plottype, filmeta, method = "bray", permutations = 100000)
ppsump[1,4] <- ad$aov.tab$F.Model[1]
ppsump[1,5] <- ad$aov.tab$R2[1]
ppsump[1,6] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Site_plottype)
anova(bd)
```

```
## Analysis of Variance Table
```

```
##
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.001401 0.0014015  0.1549 0.7042
## Residuals  8 0.072398 0.0090497
```

```
filmeta <- filter(freq, Site_plottype == "YA2015_ST" |Site_plottype =="YA2015_PC")
partspec <- filmeta[-c(1:8)]
comm.bc.dist <- vegdist(partspec, method = "bray")
ad <- adonis(comm.bc.dist ~ Site_plottype, filmeta, method = "bray", permutations = 100000)
ppsump[2,4] <- ad$aov.tab$F.Model[1]
ppsump[2,5] <- ad$aov.tab$R2[1]
ppsump[2,6] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Site_plottype)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.002687 0.0026869  0.6613 0.4396
## Residuals  8 0.032505 0.0040631
```

```
filmeta <- filter(freq, Site_plottype == "YA2015_ST" |Site_plottype =="NDF_PC")
partspec <- filmeta[-c(1:8)]
comm.bc.dist <- vegdist(partspec, method = "bray")
ad <- adonis(comm.bc.dist ~ Site_plottype, filmeta, method = "bray", permutations = 100000)
ppsump[3,4] <- ad$aov.tab$F.Model[1]
ppsump[3,5] <- ad$aov.tab$R2[1]
ppsump[3,6] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Site_plottype)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.000302 0.0003016  0.0739 0.7927
## Residuals  8 0.032672 0.0040840
```

```
filmeta <- filter(freq, Site_plottype == "YA2016_ST" |Site_plottype =="YA2016_PC")
partspec <- filmeta[-c(1:8)]
comm.bc.dist <- vegdist(partspec, method = "bray")
ad <- adonis(comm.bc.dist ~ Site_plottype, filmeta, method = "bray", permutations = 100000)
ppsump[4,4] <- ad$aov.tab$F.Model[1]
ppsump[4,5] <- ad$aov.tab$R2[1]
ppsump[4,6] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Site_plottype)
```

```
anova(bd)
```

```
## Analysis of Variance Table
## 
## Response: Distances
##           Df   Sum Sq  Mean Sq F value  Pr(>F)  
## Groups     1 0.034059 0.034059  7.7726 0.02363 *
## Residuals  8 0.035055 0.004382                  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
filmeta <- filter(freq, Site_plottype == "YA2016_ST" |Site_plottype =="NDF_PC")
partspec <- filmeta[-c(1:8)]
comm.bc.dist <- vegdist(partspec, method = "bray")
ad <- adonis(comm.bc.dist ~ Site_plottype, filmeta, method = "bray", permutations = 100000)
ppsump[5,4] <- ad$aov.tab$F.Model[1]
ppsump[5,5] <- ad$aov.tab$R2[1]
ppsump[5,6] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Site_plottype)
anova(bd)
```

```
## Analysis of Variance Table
## 
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.013198 0.0131983  2.3546 0.1635
## Residuals  8 0.044843 0.0056054
```

```
filmeta <- filter(freq, Site_plottype == "PE_ST" |Site_plottype =="PE_PC")
partspec <- filmeta[-c(1:8)]
comm.bc.dist <- vegdist(partspec, method = "bray")
ad <- adonis(comm.bc.dist ~ Site_plottype, filmeta, method = "bray", permutations = 100000)
ppsump[6,4] <- ad$aov.tab$F.Model[1]
ppsump[6,5] <- ad$aov.tab$R2[1]
ppsump[6,6] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Site_plottype)
anova(bd)
```

```
## Analysis of Variance Table
## 
## Response: Distances
##           Df   Sum Sq  Mean Sq F value Pr(>F)
## Groups     1 0.012603 0.012603   0.378 0.5558
## Residuals  8 0.266749 0.033344
```

```
filmeta <- filter(freq, Site_plottype == "PE_ST" |Site_plottype =="SDF_PC")
partspec <- filmeta[-c(1:8)]
comm.bc.dist <- vegdist(partspec, method = "bray")
```

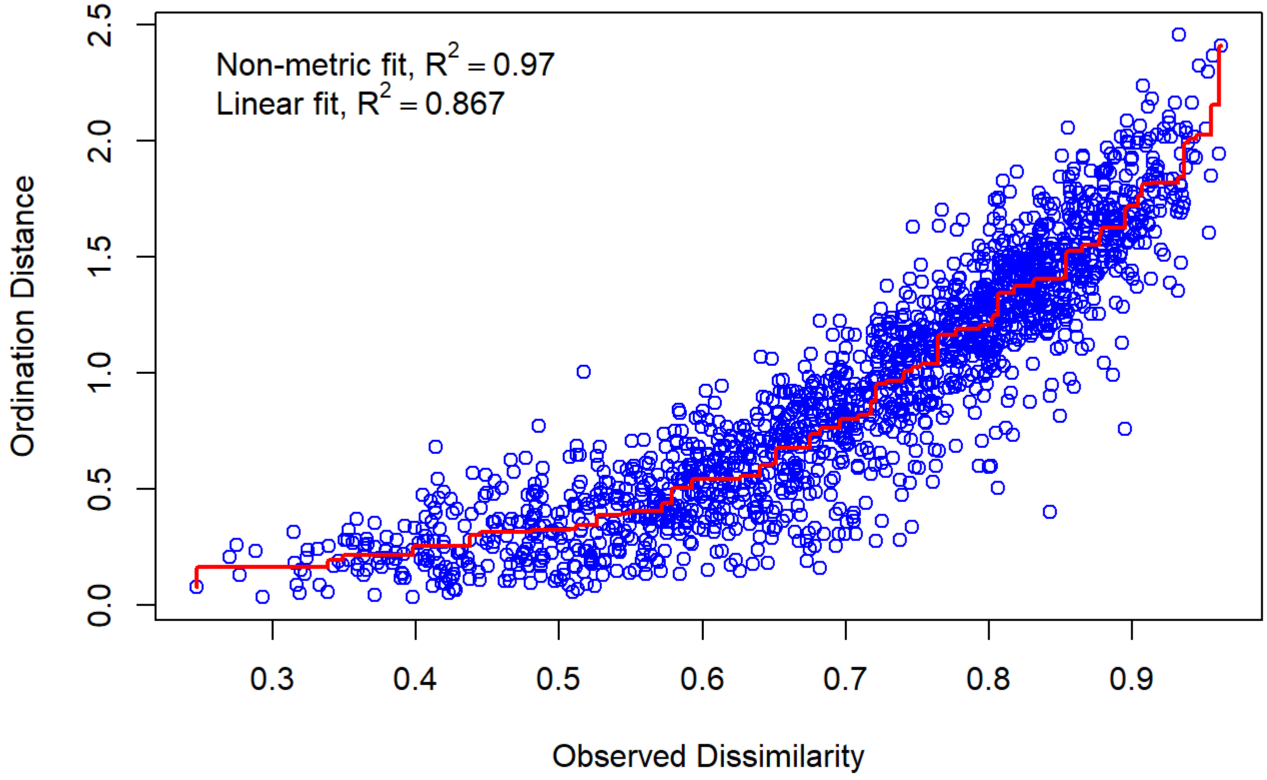
```
ad <- adonis(comm.bc.dist ~ Site_plottype, filmeta, method = "bray", permutations = 100000)
ppsump[7,4] <- ad$aov.tab$F.Model[1]
ppsump[7,5] <- ad$aov.tab$R2[1]
ppsump[7,6] <- ad$aov.tab$`Pr(>F)`[1]

bd<-betadisper(comm.bc.dist, group = filmeta$Site_plottype)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.002163 0.0021634  0.1417 0.7164
## Residuals  8 0.122155 0.0152693
```

```
ppsump[7] <-p.adjust(ppsump$p, n = 7, method = "BH")

write.csv(ppsump, "ppsumpFilled.csv")
```

Sub-plot summer NMDS

```
sub_meta <- read.csv("freq_all_meta.csv")

metaYAPEst <- sub_meta[66:124,]
spec<- metaYAPEst[,-c(1:10)]

comm.bc.dist <- vegdist(spec, method = "bray")
comm.bc.clust <- hclust(comm.bc.dist, method = "average")
comm.bc.mds <- metaMDS(spec, dist = "bray", try = 1000, trace = FALSE)

stressplot(comm.bc.mds)
```



```
tiff("summer_sub_NMDS.tiff", width = 8, height = 8, units = 'in', res = 150)

par(mar=c(2, 2, 4, 2), xpd=TRUE)
mds.fig <- ordiplot(comm.bc.mds, type = "none")
points(mds.fig, "sites", pch = 19, col = "darkolivegreen", select = metaYAPEst$Treat_new == "S
T")
points(mds.fig, "sites", pch = 18, cex =1.1, col = "deepskyblue3", select = metaYAPEst$Treat_n
ew == "WD")
points(mds.fig, "sites", pch = 17, col = "goldenrod", select = metaYAPEst$Treat_new == "DS")
points(mds.fig, "sites", pch = 16, col = "deeppink2", select = metaYAPEst$Treat_new == "SS")
points(mds.fig, "sites", pch = 0, col = "darkmagenta", select = metaYAPEst$Treat_new == "PE_ST
")
points(mds.fig, "sites", pch = 1, cex =1.1, col = "blue", select = metaYAPEst$Treat_new == "PE
_WD")
points(mds.fig, "sites", pch = 2, col = "black", select = metaYAPEst$Treat_new == "PE_DS")
points(mds.fig, "sites", pch = 5, col = "green4", select = metaYAPEst$Treat_new == "PE_SS")
ordihull(comm.bc.mds, metaYAPEst$Site_comb, draw = "lines", col = c("blue", "red"), label = FA
LSE, alpha
 =200)
legend("top", inset=c(0.0, -0.05), legend = c("Gravel pit","Reforestation", "RF Topsoil Recipi
ent only","RF Woody debris", "RF Shrubs", "RF Shade shelter", "GP Topsoil recipient only",
                                               "GP Woody debris", "GP Shrubs", "GP Shade shelt
er"), lty = c(1, 1, NA, NA, NA, NA, NA, NA, NA, NA), pch = c(NA,NA,19,18,17,16,0,1,2,5),
col = c("red", "blue", "darkolivegreen","deepskyblue3", "goldenrod", "deeppink2", "darkmagenta
", "blue", "black", "green4"), bg = "white", ncol=2)
```

```
dev.off()
```

```
## png
##   2
```

Sub-plot PERMANOVA for ST plots within Reforestation sites and the gravel pit site

```
#all subplots in RF (YA)
filmeta <- filter(metaYAPEst, Treat_new == "ST" | Treat_new =="SS"| Treat_new =="WD"| Treat_ne
w =="DS")
partspec <- filmeta[-c(1:10)]
comm.bc.dist <- vegdist(partspec, method = "bray")
ad <- adonis(comm.bc.dist ~ Treat_new, filmeta,  method = "bray", permutations = 100000)
ad
```

```
##
## Call:
## adonis(formula = comm.bc.dist ~ Treat_new, data = filmeta, permutations = 1e+05,      metho
d = "bray")
##
## Permutation: free
## Number of permutations: 1e+05
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Treat_new  3    0.7225 0.24082  1.3222 0.10179 0.1328
## Residuals 35    6.3748 0.18214         0.89821
## Total     38    7.0972                 1.00000
```

```
bd<-betadisper(comm.bc.dist, group = filmeta$Treat_new)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     3 0.011902 0.0039673  0.8655 0.4681
## Residuals 35 0.160435 0.0045839
```

```
#all subplots in GP (PE)
filmeta <- filter(metaYAPEst, Treat_new == "PE_ST" | Treat_new =="PE_SS"| Treat_new =="PE_WD"|
 Treat_new =="PE_DS")
partspec <- filmeta[-c(1:10)]
comm.bc.dist <- vegdist(partspec,  method = "bray")
ad <- adonis(comm.bc.dist ~ Treat_new, filmeta, method = "bray", permutations = 100000)
ad
```

```
##
```

```
## Call:
## adonis(formula = comm.bc.dist ~ Treat_new, data = filmeta, permutations = 1e+05,      metho
d = "bray")
##
## Permutation: free
## Number of permutations: 1e+05
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Treat_new  3    0.6100 0.20335 0.97396 0.15442 0.5014
## Residuals 16    3.3405 0.20878         0.84558
## Total     19    3.9506                 1.00000
```

```
bd<-betadisper(comm.bc.dist, group = filmeta$Treat_new)
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df   Sum Sq   Mean Sq F value Pr(>F)
## Groups     3 0.008854 0.0029512  0.2986 0.8259
## Residuals 16 0.158159 0.0098849
```