LCN: Lichen interaction network study

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Results

```
### REML

### We know from Lamit's dissertation work that lichen communities are
### heritable, largely driven by bark roughness
### Do we find similar patterns?

## Create a list to generate a results table
h2.tab <- matrix("", 10, 4)
colnames(h2.tab) <- c("Response",  "H2", "R2", "p-value")

## Total cover ~ genotype
ptc.reml <- lme4::lmer(I(PC^(1/2)) ~ (1 | geno),
                       data = na.omit(onc.dat), REML = TRUE)
ptc.reml.pval <- RLRsim::exactRLRT(ptc.reml)
ptc.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 1.6364, p-value = 0.0854
```

```
fligner.test(onc.dat$PC^(1/2), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.dat$PC^(1/2) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 13.751, df = 12, p-value =
## 0.3169
```

```
shapiro.test(residuals(ptc.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(ptc.reml)
## W = 0.93193, p-value = 0.004822
```

```
h2.tab[1, "p-value"] <- ptc.reml.pval$"p.value"
h2.tab[1, "H2"] <- H2(ptc.reml, g = onc.dat$geno)
h2.tab[1, "R2"] <- R2(ptc.reml)
R2(ptc.reml)
```

```
##       R2c
## 0.1367954
```

```r
h2.tab[1, "Response"] <- "Percent Lichen Cover"

## Species richness ~ genotype
spr.reml <- lme4::lmer(I(SR^(1/2)) ~ (1 | geno),
                       data = na.omit(onc.dat), REML = TRUE)
spr.reml.pval <- RLRsim::exactRLRT(spr.reml)
spr.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 0.080424, p-value = 0.354
```

```r
shapiro.test(residuals(spr.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(spr.reml)
## W = 0.95213, p-value = 0.03324
```

```r
fligner.test(onc.dat$SR^(1/2), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.dat$SR^(1/2) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 13.276, df = 12, p-value =
## 0.3493
```

```r
h2.tab[2, "p-value"] <- spr.reml.pval$"p.value"
h2.tab[2, "H2"] <- H2(spr.reml, g = onc.dat$geno)
h2.tab[2, "R2"] <- R2(spr.reml)
R2(spr.reml)
```

```
##        R2c
## 0.02807255
```

```r
h2.tab[2, "Response"] <- "Lichen Species Richness"


## Bark roughness REML
prb.reml <- lme4::lmer(I(BR^(1/2)) ~ (1 | geno),
                       data = na.omit(onc.dat), REML = TRUE)
prb.reml.pval <- RLRsim::exactRLRT(prb.reml)
prb.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 9.8245, p-value = 6e-04
```

```r
fligner.test(onc.dat$BR^(1/2), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.dat$BR^(1/2) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 6.1915, df = 12, p-value =
## 0.9061
```

```r
shapiro.test(residuals(prb.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(prb.reml)
## W = 0.98395, p-value = 0.6926
```

```r
h2.tab[3, "p-value"] <- prb.reml.pval$"p.value"
h2.tab[3, "H2"] <- H2(prb.reml, g = onc.dat$geno)
h2.tab[3, "R2"] <- R2(prb.reml)
R2(prb.reml)
```

```
##       R2c
## 0.3963714
```

```r
h2.tab[3, "Response"] <- "Percent Rough Bark"

## pH ~ genotype
ph.reml <- lme4::lmer(I(pH^(1/2)) ~ (1 | geno),
                      data = na.omit(onc.dat), REML = TRUE)
ph.reml.pval <- RLRsim::exactRLRT(ph.reml)
ph.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 0.52364, p-value = 0.2049
```

```r
fligner.test(log(onc.dat$pH), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  log(onc.dat$pH) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 22.971, df = 12, p-value =
## 0.02797
```

```r
shapiro.test(residuals(ph.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(ph.reml)
## W = 0.76737, p-value = 9.03e-08
```

```
# h2.tab[1, "p-value"] <- ph.reml.pval$"p.value"
# h2.tab[1, "H2"] <- H2(ph.reml, g = onc.dat$geno)
# h2.tab[1, "R2"] <- R2(ph.reml)
R2(ph.reml)
```

```
##       R2c
## 0.1404423
```

```
# h2.tab[1, "Response"] <- "Percent Lichen Cover"

## condensed tannins  REML
ct.reml <- lme4::lmer(I(CT^(1/4)) ~ (1 | geno),
                      data = na.omit(onc.dat), REML = TRUE)
ct.reml.pval <- RLRsim::exactRLRT(ct.reml)
ct.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 4.0284, p-value = 0.0186
```

```
fligner.test(onc.dat$CT^(1/4), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.dat$CT^(1/4) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 7.8941, df = 12, p-value =
## 0.7933
```

```
shapiro.test(residuals(ct.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(ct.reml)
## W = 0.75061, p-value = 4.002e-08
```

```
## CN ratio REML
cnr.reml <- lme4::lmer(I(CN^(1)) ~ (1 | geno),
                       data = na.omit(onc.dat), REML = TRUE)
```

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

```
cnr.reml.pval <- RLRsim::exactRLRT(cnr.reml)
cnr.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 5.6843e-14, p-value = 0.4598
```

```r
fligner.test(onc.dat$CN^(1/1), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.dat$CN^(1/1) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 8.1116, df = 12, p-value =
## 0.7763
```

```r
shapiro.test(residuals(cnr.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(cnr.reml)
## W = 0.92434, p-value = 0.002442
```

```r
## Bark roughness PCA

####### This is a rough draft of chem data analysis with new pH #######
pca.onc <- princomp(na.omit(onc.dat[, c("pH", "CT", "CN")]))
cumsum(pca.onc[["sdev"]] / sum(pca.onc[["sdev"]]))
```

```
##    Comp.1    Comp.2    Comp.3
## 0.7652602 0.9986463 1.0000000
```

```r
tpc.onc <- pca.onc[["scores"]][, 1:2]
onc.dat.test <- cbind(onc.dat,
                      tpc.onc[match(rownames(onc.dat), rownames(tpc.onc)), ])

pc1.reml <- lme4::lmer(I(Comp.1^(1/1)) ~ (1 | geno),
                       data = onc.dat.test, REML = TRUE)
RLRsim::exactRLRT(pc1.reml)
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 0.68862, p-value = 0.1779
```

```r
pc2.reml <- lme4::lmer(I(Comp.2^(1/1)) ~ (1 | geno),
                       data = onc.dat.test, REML = TRUE)
RLRsim::exactRLRT(pc2.reml)
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 0.22788, p-value = 0.2861
```

```r
cn.d.onc.test <- distNet(cn.onc[as.character(onc.dat.test[!is.na(onc.dat.test[, "Comp.1"]), "tree.id"])]
adonis2(cn.d.onc.test ~ Comp.1 * Comp.2, data = onc.dat.test)
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## adonis2(formula = cn.d.onc.test ~ Comp.1 * Comp.2, data = onc.dat.test)
##               Df SumOfSqs      R2      F Pr(>F)
## Comp.1         1    26.78 0.01962 1.0763  0.269
## Comp.2         1    10.07 0.00738 0.4049  0.541
## Comp.1:Comp.2  1   108.89 0.07978 4.3767  0.035 *
## Residual      49  1219.08 0.89322
## Total         52  1364.81 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mantel(cn.d.onc.test ~ dist(na.omit(onc.dat[, c("pH", "CN", "CT")])))
```

```
##     mantelr       pval1       pval2       pval3   llim.2.5%  ulim.97.5%
##  0.15698039  0.09200000  0.90900000  0.09200000 -0.06340377  0.25347788
```

```
## Is species richness correlated with percent cover?
cor.test(onc.dat[, "SR"], onc.dat[, "PC"], data = onc.dat)
```

```
##
##  Pearson's product-moment correlation
##
## data:  onc.dat[, "SR"] and onc.dat[, "PC"]
## t = 8.3456, df = 55, p-value = 2.393e-11
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.6047186 0.8437321
## sample estimates:
##       cor
## 0.7475023
```

```
## Were these correlated with bark roughness?
ptc.prb.lm <- lm(I(PC^(1/2)) ~ I(BR^(1/2)), data = onc.dat)
summary(ptc.prb.lm)
```

```
##
## Call:
## lm(formula = I(PC^(1/2)) ~ I(BR^(1/2)), data = onc.dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.9770 -1.6378  0.6333  1.9603  3.4658
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   4.4142     1.0901   4.049 0.000162 ***
## I(BR^(1/2))   0.4942     0.1896   2.607 0.011730 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.485 on 55 degrees of freedom
## Multiple R-squared:   0.11,  Adjusted R-squared:  0.09381
```

```
## F-statistic: 6.797 on 1 and 55 DF,  p-value: 0.01173
```

```
fligner.test(onc.dat$PC, onc.dat$BR)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.dat$PC and onc.dat$BR
## Fligner-Killeen:med chi-squared = 27.401, df = 24, p-value =
## 0.2861
```

```
shapiro.test(residuals(ptc.prb.lm))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(ptc.prb.lm)
## W = 0.95045, p-value = 0.02061
```

```
spr.prb.lm <- lm(I(SR^(1)) ~ I(BR^(1/2)), data = onc.dat)
summary(spr.prb.lm)
```

```
##
## Call:
## lm(formula = I(SR^(1)) ~ I(BR^(1/2)), data = onc.dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.0420 -1.3123 -0.1178  1.2308  4.3519
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.5015     0.8002   3.126  0.00283 **
## I(BR^(1/2))   0.1709     0.1392   1.228  0.22456
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.824 on 55 degrees of freedom
## Multiple R-squared:  0.0267, Adjusted R-squared:  0.009003
## F-statistic: 1.509 on 1 and 55 DF,  p-value: 0.2246
```

```
fligner.test(onc.dat$SR^(1), onc.dat$BR)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.dat$SR^(1) and onc.dat$BR
## Fligner-Killeen:med chi-squared = 26.046, df = 24, p-value =
## 0.3508
```

```
shapiro.test(residuals(spr.prb.lm))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(spr.prb.lm)
## W = 0.97168, p-value = 0.2008
```

```r
## COM ~ genotype + Bark roughness + PTC + SPR
set.seed(2)
rcom.ng.perm <- vegan::adonis2(onc.com.rel^(1/1) ~ BR + PC + SR,
                               data = onc.dat, perm = 10000, mrank = TRUE)
set.seed(2)
rcom.perm <- vegan::adonis2(onc.com.rel^(1/1) ~ geno + BR + PC + SR,
                            data = onc.dat, perm = 10000, mrank = TRUE)
set.seed(2)
com.ng.perm <- vegan::adonis2(onc.com^(1/1) ~ BR + PC + SR,
                              data = onc.dat, perm = 10000, mrank = TRUE)
set.seed(2)
com.perm <- vegan::adonis2(onc.com^(1/1) ~ geno + BR + PC + SR,
                           data = onc.dat, perm = 10000, mrank = TRUE)
rcom.ng.perm
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 10000
##
## vegan::adonis2(formula = onc.com.rel^(1/1) ~ BR + PC + SR, data = onc.dat, permutations = 10000, mra
##          Df SumOfSqs      R2       F    Pr(>F)
## BR        1   0.4398 0.03889  3.7408  0.008799 **
## PC        1   3.8618 0.34151 32.8482 9.999e-05 ***
## SR        1   0.7754 0.06857  6.5958 9.999e-05 ***
## Residual 53   6.2309 0.55102
## Total    56  11.3079 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
rcom.perm
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 10000
##
## vegan::adonis2(formula = onc.com.rel^(1/1) ~ geno + BR + PC + SR, data = onc.dat, permutations = 100
##          Df SumOfSqs      R2       F    Pr(>F)
## geno     12   2.7463 0.24287  1.8221 0.0031997 **
## BR        1   0.1248 0.01104  0.9938 0.3900610
## PC        1   2.6711 0.23622 21.2661 9.999e-05 ***
## SR        1   0.6159 0.05447  4.9036 0.0009999 ***
## Residual 41   5.1498 0.45541
## Total    56  11.3079 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
h2.tab[4, "p-value"] <- unlist(rcom.perm)["Pr(>F)1"]
h2.tab[4, "H2"] <- H2(rcom.perm, g = onc.dat$geno)
h2.tab[4, "R2"] <- R2(rcom.perm)
h2.tab[4, "Response"] <- "Lichen Community Composition"

## Is network similarity correlated with community composition?
ecodist::mantel(cn.d.onc ~ vegdist(onc.com.rel), mrank = TRUE)
```

```
##    mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## 0.09198784 0.07200000 0.92900000 0.12000000 0.05120132 0.13656424
```

```
spr.d <- dist(onc.dat$SR)
ptc.d <- dist(onc.dat$PC)
prb.d <- dist(onc.dat$BR)
### rough -> cover -> rich -> net
ecodist::mantel(cn.d.onc ~ vegdist(onc.com.rel) + spr.d + ptc.d + prb.d, mrank = TRUE)
```

```
##    mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## 0.06853395 0.15400000 0.84700000 0.31300000 0.02256902 0.13046001
```

```
## Partial Mantels using RFLP distance
ecodist::mantel(cn.mu.d.onc ~ rflp.d)
```

```
##     mantelr       pval1       pval2       pval3   llim.2.5%  ulim.97.5%
## -0.00603936  0.54500000  0.45600000  0.96700000 -0.15782909  0.18127044
```

```
ecodist::mantel(onc.com.mu.d ~ rflp.d)
```

```
##    mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
##  0.1179051  0.2830000  0.7180000  0.4830000 -0.2789494  0.2435282
```

```
ecodist::mantel(cn.mu.d.onc ~ onc.com.mu.d)
```

```
##     mantelr       pval1       pval2       pval3   llim.2.5%  ulim.97.5%
##  0.29000439  0.08800000  0.91300000  0.08800000 -0.02360565  0.42465976
```

```
## Was lichen network similarity determined by genotype?
set.seed(1234)
cn.perm <- vegan::adonis2(cn.d.onc.na ~ geno +
                            BR + pH + CN + CT +
                            PC + SR + SE,
                          by = "term",
                          data = na.omit(onc.dat),
                          permutations = 10000, mrank = FALSE)

cn.perm.ng <- vegan::adonis2(cn.d.onc ~ BR + PC  + SR,
               data = onc.dat, permutations = 10000, mrank = TRUE)
cn.perm.ng
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 10000
##
## vegan::adonis2(formula = cn.d.onc ~ BR + PC + SR, data = onc.dat, permutations = 10000, mrank = TRUE
##          Df SumOfSqs      R2       F    Pr(>F)
## BR        1    61.42 0.03968  4.1680   0.04020 *
## PC        1    49.47 0.03197  3.3573   0.06839 .
## SR        1   655.76 0.42373 44.5034 9.999e-05 ***
## Residual 53   780.96 0.50462
## Total    56  1547.61 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cn.perm
```

```
## Permutation test for adonis under reduced model
```

```
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 10000
##
## vegan::adonis2(formula = cn.d.onc.na ~ geno + BR + pH + CN + CT + PC + SR + SE, data = na.omit(onc.da
##          Df SumOfSqs      R2       F    Pr(>F)
## geno     12   367.65 0.26937  2.3065   0.02860 *
## BR        1    23.63 0.01732  1.7792   0.18828
## pH        1     8.96 0.00656  0.6745   0.41866
## CN        1    37.70 0.02762  2.8379   0.08849 .
## CT        1    76.22 0.05585  5.7383   0.03310 *
## PC        1    28.50 0.02088  2.1458   0.14349
## SR        1   332.23 0.24342 25.0117 9.999e-05 ***
## SE        1    51.59 0.03780  3.8843   0.04470 *
## Residual 33   438.33 0.32117
## Total    52  1364.81 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
h2.tab[5, "p-value"] <- as.matrix(cn.perm)[1, "Pr(>F)"]
h2.tab[5, "H2"] <- H2(cn.perm, g = onc.dat[, "geno"], perm =10000)
h2.tab[5, "R2"] <- R2(cn.perm)
h2.tab[5, "Response"] <- "Lichen Network"
                                        # db rda for network similarity
dbr.cn.geno <- vegan::dbrda(cn.d.onc ~ geno, data = onc.dat, distance = "bray")
anova(dbr.cn.geno, permutations = 5000)
```

```
## Permutation test for dbrda under reduced model
## Permutation: free
## Number of permutations: 5000
##
## Model: vegan::dbrda(formula = cn.d.onc ~ geno, data = onc.dat, distance = "bray")
##          Df Variance      F Pr(>F)
## Model    12    8.045 1.5057  0.146
## Residual 44   19.591
```

```
H2(dbr.cn.geno)
```

```
## [1] 0.2911089
```

```
## What aspects of networks explained the similiarity?
## L = number of edges, LD = link density, C = connectivity,
## dcen = degree centrality
link.reml <- lme4::lmer(I(log(L + 0.00000001) ) ~ (1 | geno),
                        data = onc.dat, REML = TRUE)
link.reml.pval <- RLRsim::exactRLRT(link.reml, nsim = 50000)
link.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 50000 simulated values)
##
## data:
## RLRT = 2.0484, p-value = 0.06674
```

```r
fligner.test(log(onc.dat$L + 0.0000001), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  log(onc.dat$L + 1e-07) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 11.991, df = 12, p-value =
## 0.4464
```

```r
shapiro.test(residuals(link.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(link.reml)
## W = 0.83643, p-value = 2.036e-06
```

```r
h2.tab[6, "p-value"] <- link.reml.pval$"p.value"
h2.tab[6, "H2"] <- H2(link.reml, g = onc.dat$geno)
h2.tab[6, "R2"] <- R2(link.reml)
R2(link.reml)
```

```
##       R2c
## 0.1701568
```

```r
h2.tab[6, "Response"] <- "Number of Network Links"


                                        # network centrality
cen.reml <- lme4::lmer(I(Cen^(1/2))  ~ (1 | geno),
                       data = onc.dat, REML = TRUE)
cen.reml.pval <- RLRsim::exactRLRT(cen.reml, nsim = 50000)
cen.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 50000 simulated values)
##
## data:
## RLRT = 2.7801, p-value = 0.03958
```

```r
fligner.test(onc.dat$L^(1/1), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.dat$L^(1/1) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 14.241, df = 12, p-value =
## 0.2856
```

```r
shapiro.test(residuals(cen.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(cen.reml)
## W = 0.90072, p-value = 0.0002041
```

```
h2.tab[7, "p-value"] <- cen.reml.pval$"p.value"
h2.tab[7, "H2"] <- H2(cen.reml, g = onc.dat$geno)
h2.tab[7, "R2"] <- R2(cen.reml)
R2(cen.reml)
```

```
##       R2c
## 0.2016649
```

```
h2.tab[7, "Response"] <- "Network Centrality"

                                        # network modularity
mod.reml <- lme4::lmer(I(onc.ns[, "mod.lik"]^(1/4)) ~ (1 | geno),
                       data = onc.dat, REML = TRUE)
mod.reml.pval <- RLRsim::exactRLRT(mod.reml)
mod.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 0.23363, p-value = 0.267
```

```
fligner.test(onc.ns[, "mod.lik"]^(1/4), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.ns[, "mod.lik"]^(1/4) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 13.439, df = 12, p-value =
## 0.3379
```

```
shapiro.test(residuals(mod.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(mod.reml)
## W = 0.54001, p-value = 4.252e-12
```

```
h2.tab[8, "p-value"] <- mod.reml.pval$"p.value"
h2.tab[8, "H2"] <- H2(mod.reml, g = onc.dat$geno)
h2.tab[8, "R2"] <- R2(mod.reml)
h2.tab[8, "Response"] <- "Network Modularity"

## Added diversity and evenness

## Species diversity ~ genotype
spd.reml <- lme4::lmer(I(SD^(1/2)) ~ (1 | geno),
                       data = na.omit(onc.dat), REML = TRUE)
spd.reml.pval <- RLRsim::exactRLRT(spd.reml)
spd.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
```

```
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 0.078644, p-value = 0.3532
```

```
shapiro.test(residuals(spd.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(spd.reml)
## W = 0.89237, p-value = 0.0001793
```

```
fligner.test(onc.dat$SD^(1/2), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  onc.dat$SD^(1/2) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 17.299, df = 12, p-value =
## 0.1387
```

```
h2.tab[9, "p-value"] <- spd.reml.pval$"p.value"
h2.tab[9, "H2"] <- H2(spd.reml, g = onc.dat$geno)
h2.tab[9, "R2"] <- R2(spd.reml)
R2(spd.reml)
```

```
##        R2c
## 0.02907546
```

```
h2.tab[9, "Response"] <- "Lichen Species Diversity"

## Species diversity ~ genotype
spe.reml <- lme4::lmer(I(SE^(1/4)) ~ (1 | geno),
                       data = na.omit(onc.dat), REML = TRUE)
spe.reml.pval <- RLRsim::exactRLRT(spe.reml)
spe.reml.pval
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 0.35064, p-value = 0.2461
```

```
shapiro.test(residuals(spe.reml))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(spe.reml)
## W = 0.67851, p-value = 1.705e-09
```

```
fligner.test(onc.dat$SD^(1/2), onc.dat$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
```

```
##
## data:  onc.dat$SD^(1/2) and onc.dat$geno
## Fligner-Killeen:med chi-squared = 17.299, df = 12, p-value =
## 0.1387
```

```
h2.tab[10, "p-value"] <- spe.reml.pval$"p.value"
h2.tab[10, "H2"] <- H2(spe.reml, g = onc.dat$geno)
h2.tab[10, "R2"] <- R2(spe.reml)
R2(spe.reml)
```

```
##        R2c
## 0.05732341
```

```
h2.tab[10, "Response"] <- "Lichen Species Evenness"

                                    # network stats in relation to other variables
L.aov <- aov(I(log(L + 0.000001)) ~ BR + PC + SR, data = onc.dat)
summary(L.aov)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## BR           1  102.3   102.3   2.776   0.1016
## PC           1  239.6   239.6   6.504   0.0137 *
## SR           1  957.0   957.0  25.980 4.71e-06 ***
## Residuals   53 1952.2    36.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
shapiro.test(residuals(L.aov))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(L.aov)
## W = 0.9629, p-value = 0.07794
```

```
cen.aov <- aov(I(Cen^(1/2)) ~ BR + PC + SR, data = onc.dat)
summary(cen.aov)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## BR           1   3.77    3.77   2.174    0.146
## PC           1   6.46    6.46   3.724    0.059 .
## SR           1  56.48   56.48  32.552 5.31e-07 ***
## Residuals   53  91.95    1.73
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
shapiro.test(residuals(cen.aov))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(cen.aov)
## W = 0.97222, p-value = 0.2126
```

```
mod.aov <- aov(I(onc.ns[, "mod.lik"]^(1/4)) ~ BR + PC + SR, data = onc.dat)
summary(mod.aov)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
```

```
## BR           1 0.0442  0.0442   0.787    0.379
## PC           1 0.0879  0.0879   1.564    0.217
## SR           1 1.3799  1.3799  24.558 7.76e-06 ***
## Residuals   53 2.9781  0.0562
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
shapiro.test(residuals((mod.aov)))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals((mod.aov))
## W = 0.9201, p-value = 0.001078
```

```
##
cor.test(onc.ns[, "L"], onc.ns[, "Cen"])
```

```
##
##  Pearson's product-moment correlation
##
## data:  onc.ns[, "L"] and onc.ns[, "Cen"]
## t = 13.37, df = 55, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.7950728 0.9244074
## sample estimates:
##       cor
## 0.8744752
```

```
                                        # are these metrics correlated with network similarity
L.d <- dist(onc.dat$L)
cen.d <- dist(onc.dat$Cen)
mod.d <- dist(cn.mod.onc)
cn.L.cen.perm <- adonis2(cn.d.onc ~ L + Cen, data = onc.dat, mrank = TRUE)

## So, are there patterns in the centrality of individual lichen species?
sppcen.test <- apply(cen.spp[, apply(cen.spp, 2, sum) >= 2], 2, function(x)
    lme4::lmer(I(x^(1/2)) ~ (1 | geno), data = na.omit(onc.dat), REML = TRUE))
```

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

```
sppcen.pval <- lapply(sppcen.test, RLRsim::exactRLRT)
sppcen.tab <- do.call(rbind, lapply(sppcen.pval, function(x)
    c(x[["statistic"]], x[["p.value"]])))
sppcen.h2 <- round(unlist(lapply(sppcen.test, H2)), 3)
sppcen.h2
```

```
##    Xg    Cs    Ls    Ch    Xm    Pm    Rs
## 0.000 0.076 0.000 0.152 0.190 0.000 0.000
```

```
## Mean centrality of species
sort(apply(cen.spp, 2, mean), decreasing = TRUE)
```

```
##         Cs         Ch         Ls         Rs         Xg         Pm
```

```
## 0.73023360 0.51060368 0.41242791 0.19765745 0.15651469 0.08511420
##         Xm         Pu         Pa
## 0.06858041 0.02264151 0.00000000
```

```
summary(aov(value ~ X2, data = melt(cen.spp)))
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## X2            8  27.04   3.380   8.086  3e-10 ***
## Residuals   468 195.63   0.418
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(aov(value ~ X2, data = melt(cen.spp)))
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = value ~ X2, data = melt(cen.spp))
##
## $X2
##              diff        lwr          upr     p adj
## Cs-Ch  0.21962992 -0.1717750  0.611034785 0.7158140
## Ls-Ch -0.09817577 -0.4895806  0.293229097 0.9973174
## Pa-Ch -0.51060368 -0.9020086 -0.119198814 0.0018322
## Pm-Ch -0.42548948 -0.8168944 -0.034084614 0.0215980
## Pu-Ch -0.48796217 -0.8793670 -0.096557305 0.0037079
## Rs-Ch -0.31294623 -0.7043511  0.078458638 0.2386358
## Xg-Ch -0.35408900 -0.7454939  0.037315874 0.1124897
## Xm-Ch -0.44202327 -0.8334281 -0.050618401 0.0139219
## Ls-Cs -0.31780569 -0.7092106  0.073599181 0.2201386
## Pa-Cs -0.73023360 -1.1216385 -0.338828730 0.0000004
## Pm-Cs -0.64511940 -1.0365243 -0.253714530 0.0000145
## Pu-Cs -0.70759209 -1.0989970 -0.316187221 0.0000011
## Rs-Cs -0.53257615 -0.9239810 -0.141171278 0.0008956
## Xg-Cs -0.57371891 -0.9651238 -0.182314042 0.0002163
## Xm-Cs -0.66165319 -1.0530581 -0.270248317 0.0000075
## Pa-Ls -0.41242791 -0.8038328 -0.021023042 0.0301134
## Pm-Ls -0.32731371 -0.7187186  0.064091158 0.1867880
## Pu-Ls -0.38978640 -0.7811913  0.001618467 0.0519144
## Rs-Ls -0.21477046 -0.6061753  0.176634410 0.7402505
## Xg-Ls -0.25591322 -0.6473181  0.135491646 0.5178196
## Xm-Ls -0.34384750 -0.7352524  0.047557371 0.1376135
## Pm-Pa  0.08511420 -0.3062907  0.476519070 0.9990336
## Pu-Pa  0.02264151 -0.3687634  0.414046379 1.0000000
## Rs-Pa  0.19765745 -0.1937474  0.589062322 0.8187315
## Xg-Pa  0.15651469 -0.2348902  0.547919558 0.9456749
## Xm-Pa  0.06858041 -0.3228245  0.459985283 0.9998045
## Pu-Pm -0.06247269 -0.4538776  0.328932178 0.9999034
## Rs-Pm  0.11254325 -0.2788616  0.503948121 0.9931235
## Xg-Pm  0.07140049 -0.3200044  0.462805357 0.9997355
## Xm-Pm -0.01653379 -0.4079387  0.374871082 1.0000000
## Rs-Pu  0.17501594 -0.2163889  0.566420812 0.9000620
## Xg-Pu  0.13387318 -0.2575317  0.525278048 0.9786988
## Xm-Pu  0.04593890 -0.3454660  0.437343773 0.9999909
## Xg-Rs -0.04114276 -0.4325476  0.350262105 0.9999962
```

```
## Xm-Rs -0.12907704 -0.5204819  0.262327830 0.9830852
## Xm-Xg -0.08793428 -0.4793391  0.303470594 0.9987764
```

```
apply(cen.spp, 2, sd) / sqrt(nrow(cen.spp))
```

```
##         Xg         Cs         Ls         Ch         Xm         Pm
## 0.05925513 0.14349031 0.13434259 0.12920446 0.04002923 0.04918653
##         Pa         Pu         Rs
## 0.00000000 0.02264151 0.08722534
```

```
## Lichen size distribution
## X. gallericulata thalli are about 0.22 +/- 0.003 cm^2 on average
## with an average median size of 0.12 +/- 0.001 cm^2
## and, size does not vary significantly with genotype.
xgs.reml <- lme4::lmer(I(mean.thallus) ~ (1 | geno),
                       data = xgs.data[xgs.data$geno %in%
                                       names(which(table(xgs.data$geno) > 2)), ],
                       REML = TRUE)
xgs.median.reml <- lme4::lmer(median.thallus ~ (1 | geno),
                       data = xgs.data[xgs.data$geno %in%
                                       names(which(table(xgs.data$geno) > 2)), ],
                       REML = TRUE)
RLRsim::exactRLRT(xgs.reml)
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 2.4792, p-value = 0.0473
```

```
RLRsim::exactRLRT(xgs.median.reml)
```

```
##
##  simulated finite sample distribution of RLRT.
##
##  (p-value based on 10000 simulated values)
##
## data:
## RLRT = 0.092023, p-value = 0.3389
```

```
fligner.test(xgs.data$mean.thallus, xgs.data$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  xgs.data$mean.thallus and xgs.data$geno
## Fligner-Killeen:med chi-squared = 13.244, df = 17, p-value =
## 0.7197
```

```
fligner.test(xgs.data$median.thallus, xgs.data$geno)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  xgs.data$median.thallus and xgs.data$geno
## Fligner-Killeen:med chi-squared = 19.374, df = 17, p-value =
```

```
## 0.3075
```

```
mean(xgs.data$mean.thallus)
```

```
## [1] 0.1808442
```

```
sd(xgs.data$mean.thallus) / (length(xgs.data$mean.thallus) - 1)
```

```
## [1] 0.001845945
```

```
mean(xgs.data$median.thallus)
```

```
## [1] 0.1170852
```

```
sd(xgs.data$median.thallus) / (length(xgs.data$median.thallus) - 1)
```

```
## [1] 0.001223999
```

```
                                        # ONC and Wild Stand (Uintah)
all.dat <- rbind(wild.dat[, c("BR", "PC", "SR", "L", "Cen")],
                 onc.dat[, c("BR", "PC", "SR", "L", "Cen")])
                                        # Network distances
cn.all <- cn.wild
for (i in 1:length(cn.wild)){
    cn.all[[i]] <- cn.wild[[i]][match(rownames(cn.onc[[1]]), rownames(cn.wild[[i]])),
                                match(colnames(cn.onc[[1]]), colnames(cn.wild[[i]]))]
}
cn.all <- append(cn.all, cn.onc)
cn.d.all <- distNet(cn.all, method = "bc")
cn.nms.geno <- c(rep("wild", length(cn.wild)), onc.geno)
if (!exists("cn.nms.all")){
    set.seed(12345)
    cn.nms.all <- nmds.min(nmds(cn.d.all, 2, 2))
    vec.all <- envfit(cn.nms.all, all.dat)
                                        # jitter identical points
    cn.nms.all[cn.nms.geno == "H10", ] <- cn.nms.all[cn.nms.geno == "H10", ] - 0.2
}
```

Tables

```
h2.tab[, "H2"] <- round(as.numeric(h2.tab[, "H2"]), digits = 5)
h2.tab[, "R2"] <- round(as.numeric(h2.tab[, "R2"]), digits = 5)
h2.tab[, "p-value"] <- round(as.numeric(h2.tab[, "p-value"]), digits = 5)
h2.tab <- h2.tab[order(h2.tab[, "H2"], decreasing = TRUE), ]
h2.xtab <- xtable::xtable(h2.tab, caption =
    "Genotypic effects of cottonwood trees on the associated lichen community.",
                          label = "tab:h2_table")
print(h2.xtab,
      type = "latex",
      include.rownames = FALSE,
      include.colnames = TRUE
)
```

% latex table generated in R 3.6.1 by xtable 1.8-4 package % Wed Oct 9 16:53:22 2019

Response	H2	R2	p-value
Percent Rough Bark	0.39637	0.39637	6e-04
Network Centrality	0.20166	0.20166	0.03958
Number of Network Links	0.17016	0.17016	0.06674
Lichen Community Composition	0.16093	0.24287	0.0032
Percent Lichen Cover	0.1368	0.1368	0.0854
Lichen Network	0.06385	0.26937	0.0286
Lichen Species Evenness	0.05732	0.05732	0.2461
Network Modularity	0.05731	0.05731	0.267
Lichen Species Diversity	0.02908	0.02908	0.3532
Lichen Species Richness	0.02807	0.02807	0.354

Table 1: Genotypic effects of cottonwood trees on the associated lichen community.

```
                                    # community permanova
rcom.ng.perm.xtab <- xtable::xtable(rcom.ng.perm, caption =
    "PerMANOVA Pseudo-F Table showing the predictors of community similarity.",
                          label = "tab:com_ng_perm")
print(rcom.ng.perm.xtab,
      type = "latex",
      include.rownames = TRUE,
      include.colnames = TRUE
)
```

% latex table generated in R 3.6.1 by xtable 1.8-4 package % Wed Oct 9 16:53:22 2019

	Df	SumOfSqs	R2	F	Pr(>F)
BR	1	0.44	0.04	3.74	0.0088
PC	1	3.86	0.34	32.85	0.0001
SR	1	0.78	0.07	6.60	0.0001
Residual	53	6.23	0.55		
Total	56	11.31	1.00		

Table 2: PerMANOVA Pseudo-F Table showing the predictors of community similarity.

```
rcom.perm.xtab <- xtable::xtable(rcom.perm, caption =
    "PerMANOVA Pseudo-F Table showing the predictors of community similarity.",
                          label = "tab:rcom_perm")
print(rcom.perm.xtab,
      type = "latex",
      include.rownames = TRUE,
      include.colnames = TRUE
)
```

% latex table generated in R 3.6.1 by xtable 1.8-4 package % Wed Oct 9 16:53:22 2019

```
                                    # network permanova
cn.perm.ng.xtab <- xtable::xtable(cn.perm.ng, caption =
    "PerMANOVA Pseudo-F Table showing the predictors of network similarity.",
                          label = "tab:cn_perm_ng")
print(cn.perm.ng.xtab,
      type = "latex",
      include.rownames = TRUE,
      include.colnames = TRUE
)
```

	Df	SumOfSqs	R2	F	Pr(>F)
geno	12	2.75	0.24	1.82	0.0032
BR	1	0.12	0.01	0.99	0.3901
PC	1	2.67	0.24	21.27	0.0001
SR	1	0.62	0.05	4.90	0.0010
Residual	41	5.15	0.46		
Total	56	11.31	1.00		

Table 3: PerMANOVA Pseudo-F Table showing the predictors of community similarity.

% latex table generated in R 3.6.1 by xtable 1.8-4 package % Wed Oct 9 16:53:22 2019

	Df	SumOfSqs	R2	F	Pr(>F)
BR	1	61.42	0.04	4.17	0.0402
PC	1	49.47	0.03	3.36	0.0684
SR	1	655.76	0.42	44.50	0.0001
Residual	53	780.96	0.50		
Total	56	1547.61	1.00		

Table 4: PerMANOVA Pseudo-F Table showing the predictors of network similarity.

```
cn.perm.xtab <- xtable::xtable(cn.perm, caption =
    "PerMANOVA Pseudo-F Table showing the predictors of network similarity.",
                          label = "tab:cn_perm")
print(cn.perm.xtab,
      type = "latex",
      include.rownames = TRUE,
      include.colnames = TRUE
)
```

% latex table generated in R 3.6.1 by xtable 1.8-4 package % Wed Oct 9 16:53:22 2019

	Df	SumOfSqs	R2	F	Pr(>F)
geno	12	367.65	0.27	2.31	0.0286
BR	1	23.63	0.02	1.78	0.1883
pH	1	8.96	0.01	0.67	0.4187
CN	1	37.70	0.03	2.84	0.0885
CT	1	76.22	0.06	5.74	0.0331
PC	1	28.50	0.02	2.15	0.1435
SR	1	332.23	0.24	25.01	0.0001
SE	1	51.59	0.04	3.88	0.0447
Residual	33	438.33	0.32		
Total	52	1364.81	1.00		

Table 5: PerMANOVA Pseudo-F Table showing the predictors of network similarity.

```
                                    # network metrics anova
L.aov.xtab <- xtable::xtable(L.aov, caption =
    "ANOVA F Table showing the predictors of the number of network links.",
                          label = "tab:L_aov")
print(L.aov.xtab,
      type = "latex",
      include.rownames = TRUE,
      include.colnames = TRUE
)
```

% latex table generated in R 3.6.1 by xtable 1.8-4 package % Wed Oct 9 16:53:22 2019

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
BR	1	102.25	102.25	2.78	0.1016
PC	1	239.57	239.57	6.50	0.0137
SR	1	956.96	956.96	25.98	0.0000
Residuals	53	1952.23	36.83		

Table 6: ANOVA F Table showing the predictors of the number of network links.

```
cen.aov.xtab <- xtable::xtable(cen.aov, caption =
    "ANOVA F Table showing the predictors of network centralization.",
                           label = "tab:cen_aov")
print(cen.aov.xtab,
      type = "latex",
      include.rownames = TRUE,
      include.colnames = TRUE
)
```

% latex table generated in R 3.6.1 by xtable 1.8-4 package % Wed Oct 9 16:53:22 2019

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
BR	1	3.77	3.77	2.17	0.1463
PC	1	6.46	6.46	3.72	0.0590
SR	1	56.48	56.48	32.55	0.0000
Residuals	53	91.95	1.73		

Table 7: ANOVA F Table showing the predictors of network centralization.

```
                                    # networks and network metrics
                                    # permanova
cn.L.cen.perm.xtab <- xtable::xtable(cn.L.cen.perm, caption =
    "PerMANOVA Pseudo-F Table showing the predictors of network similarity.",
                           label = "tab:cn_L_cen_perm")
print(cn.L.cen.perm.xtab,
      type = "latex",
      include.rownames = TRUE,
      include.colnames = TRUE
)
```

% latex table generated in R 3.6.1 by xtable 1.8-4 package % Wed Oct 9 16:53:22 2019

	Df	SumOfSqs	R2	F	Pr(>F)
L	1	1330.80	0.86	734.67	0.0010
Cen	1	118.99	0.08	65.69	0.0010
Residual	54	97.82	0.06		
Total	56	1547.61	1.00		

Table 8: PerMANOVA Pseudo-F Table showing the predictors of network similarity.

Plots

Figure: Genotype barplots Community composition NMDS with vectors

```
par(mfrow = c(1, 1), mar = c(5.1, 4.1, 4.1, 2.1) / 1)
chp.coord <- ch.plot(ord.com[, 1:2], onc.geno,
                     cex = 2, mu.pch = 19,
                     pt.col = "white",
                     bar.col = "darkgrey")
text(chp.coord, labels = rownames(chp.coord))
plot(vec.com, col = "black", lwd = 7)
```

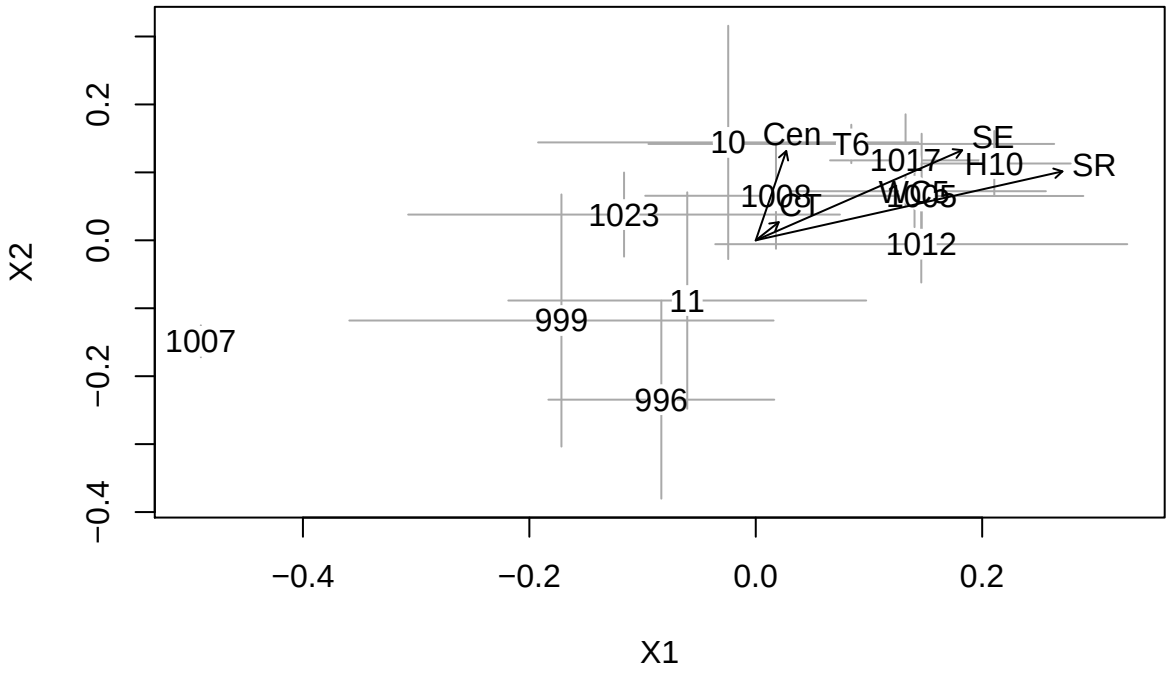


Figure: Lichen networks

```
par(mfrow = c(2, 2), mar = c(0, 0.1, 1.0, 0.1))
set.seed(123)
net.col <- sign(meanNet(cn.mu.onc))
net.col[net.col == -1] <- 2
net.col[net.col == 1] <- 1
net.elwd <- (abs(meanNet(cn.mu.onc)) * 10)^2
coord <- gplot(abs(meanNet(cn.mu.onc)), gmode = "digraph",
      displaylabels = TRUE,
      edge.lwd = net.elwd,
      edge.col = net.col,
      vertex.col = "black",
      vertex.cex = 0.5,
      arrowhead.cex = 0.5,
      label.cex = 1,
      main = "All Genotypes")
cn.mu.plot <- cn.mu.onc[names(cn.mu.onc) %in%
```

```
                        c("996", "WC5", "1008")]
cn.mu.plot <- cn.mu.plot[
  order(unlist(lapply(cn.mu.plot,
                      function(x) sum(abs(sign(x))))))]
for (i in 1:length(cn.mu.plot)){
        net.col <- sign(cn.mu.plot[[i]])
        net.col[net.col == -1] <- 2
        net.col[net.col == 1] <- 1
        net.elwd <- (abs(cn.mu.plot[[i]]) * 10)^2
        set.seed(123)
        gplot(abs(cn.mu.plot[[i]]), gmode = "digraph",
              displaylabels = TRUE,
              coord = coord,
              edge.lwd = net.elwd,
              edge.col = net.col,
              vertex.col = "black",
              vertex.cex = 0.5,
              arrowhead.cex = 0.5,
              label.cex = 1,
              main = names(cn.mu.plot)[i])
}
```

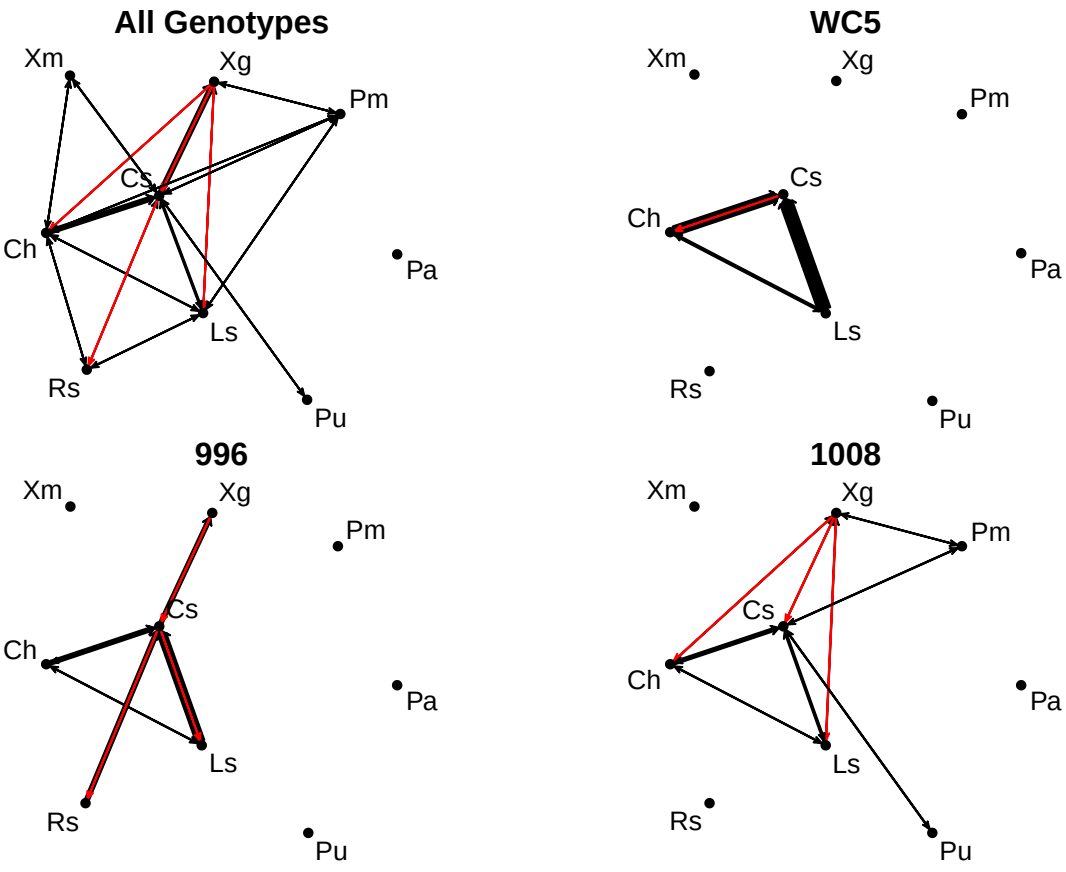


Figure: Genotype network similarity by genotype

```
par(mfrow = c(1, 1), mar = c(5.1, 4.1, 4.1, 2.1))
chp.coord <- ch.plot(cn.nms.onc, onc.geno,
                     cex = 2.65, lwd = 2.5, mu.pch = 15,
                     pt.col = "white",
                     bar.col = "darkgrey")
text(chp.coord, labels = rownames(chp.coord), cex = 0.65)
plot(vec.cn, col = "black", lwd = 5)
```

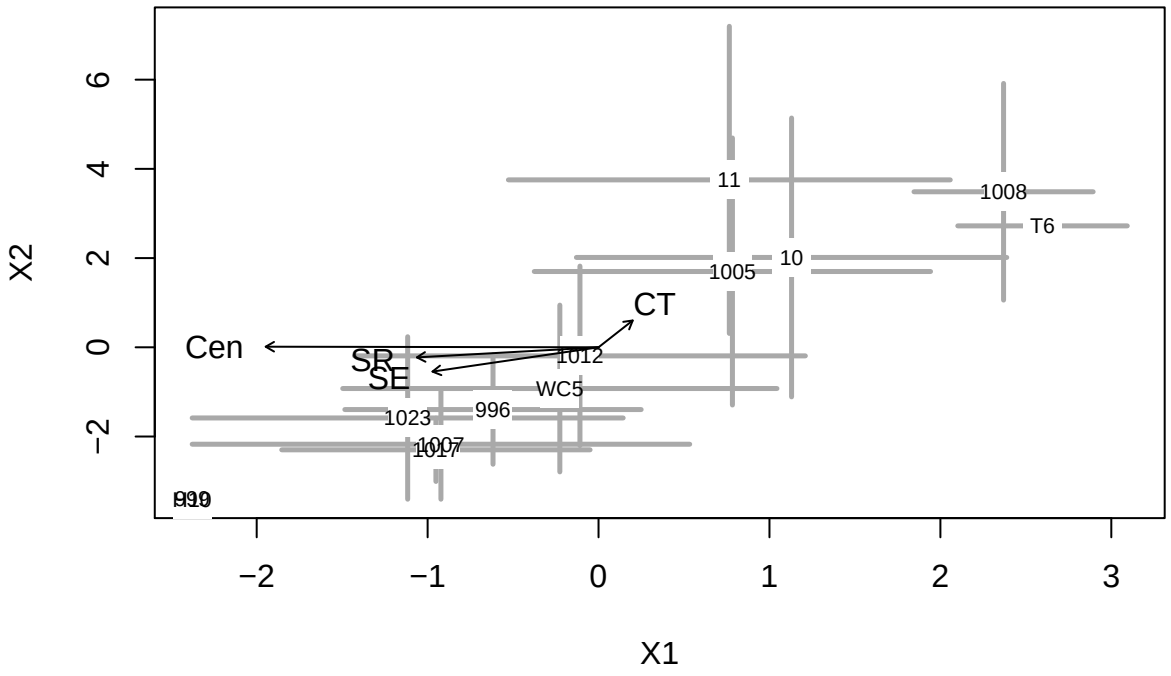
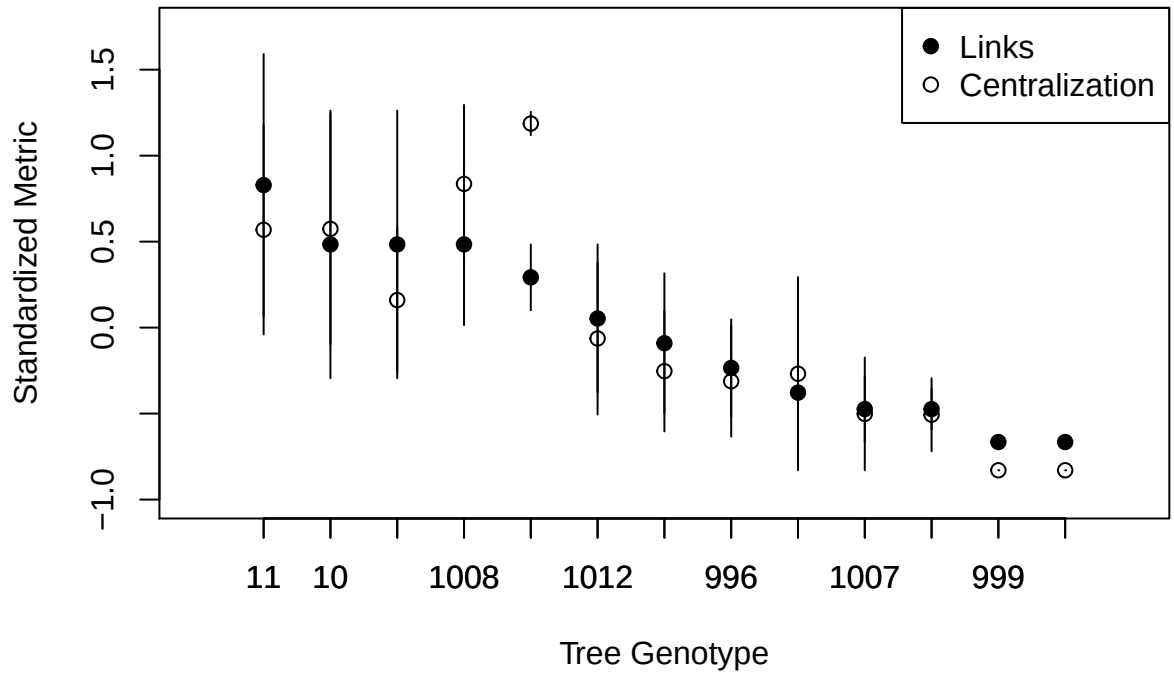


Figure: A) Lichen networks

Figure: (A) Linkage and centrality by genotype and (B) Total cover and species richness predict L and Cen

```
mdc.plot(onc.dat[, "geno"], onc.dat[, "L"], ylim = c(-1, 1.75),
         xlab = "Tree Genotype", ylab = "Standardized Metric",
         ord = order(tapply(onc.dat[, "L"], onc.dat[, "geno"], mean), decreasing = TRUE))
mdc.plot(onc.dat[, "geno"], onc.dat[, "Cen"], add = TRUE, pch = 1,
         ord = order(tapply(onc.dat[, "L"], onc.dat[, "geno"], mean), decreasing = TRUE))
legend("topright", legend = c("Links", "Centralization"), pch = c(19, 1), bty = "none")
```



Supplementary Figure: Lichen size distribution

```
plot(density(xgs.data$median.thallus),
     xlab = "Median Lichen Thallus Area (cm^2)",
     main = "")
abline(v = median(xgs.data$median.thallus, na.rm = TRUE), lty = 2)
```

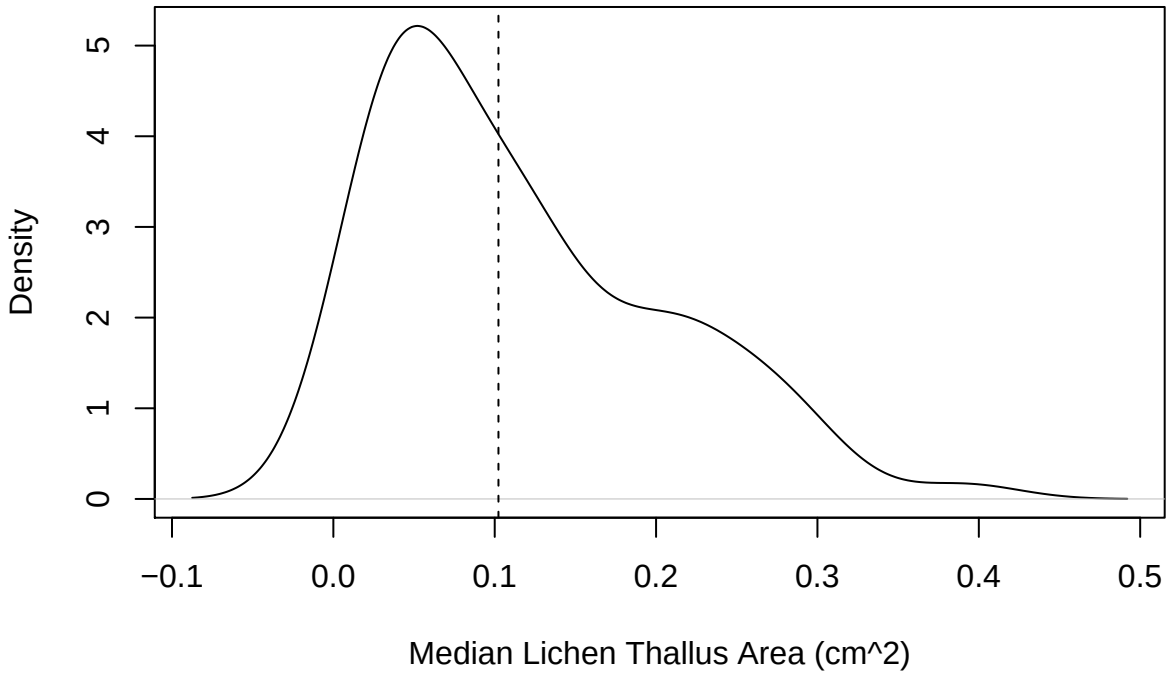
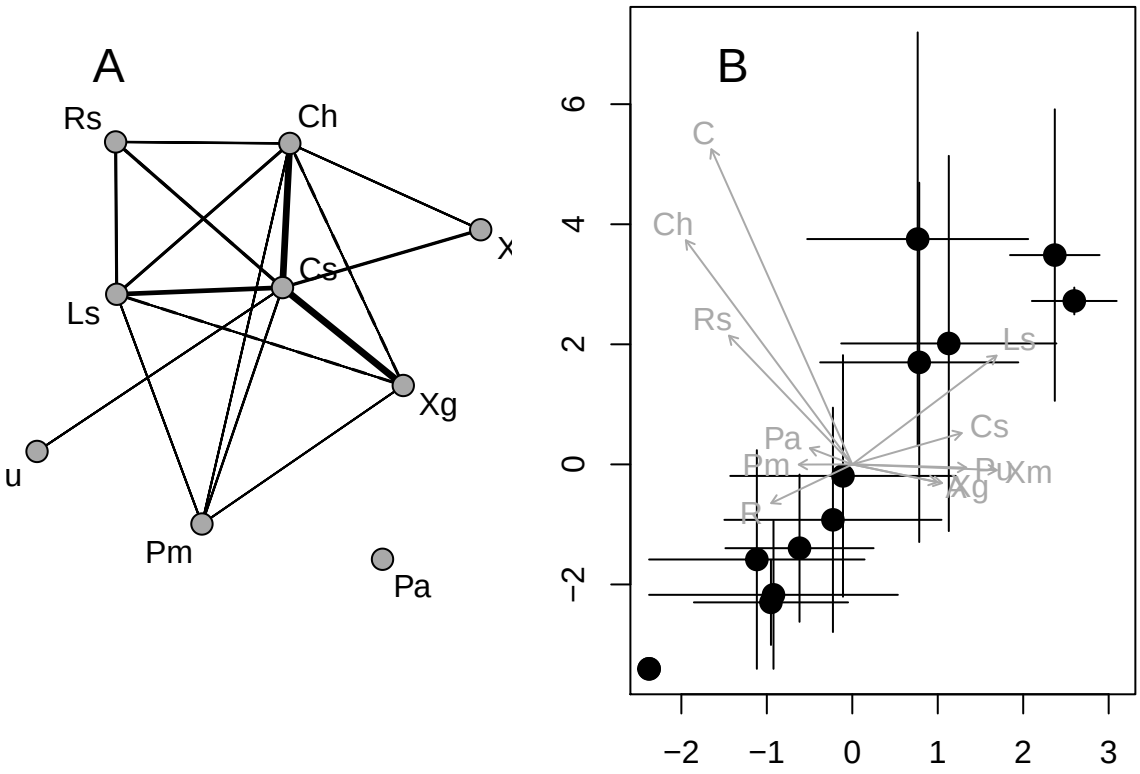
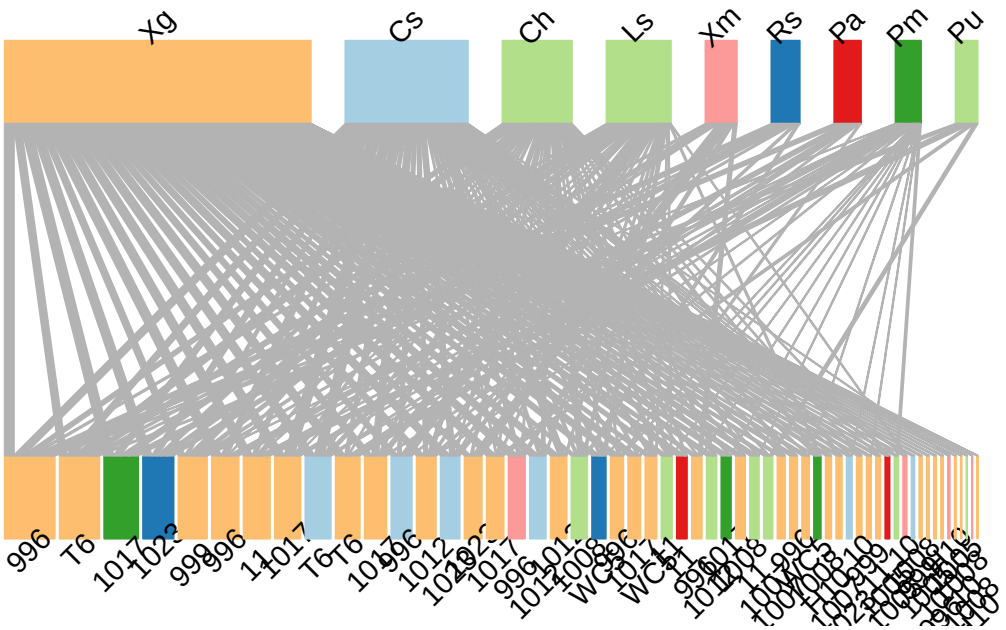


Figure 2

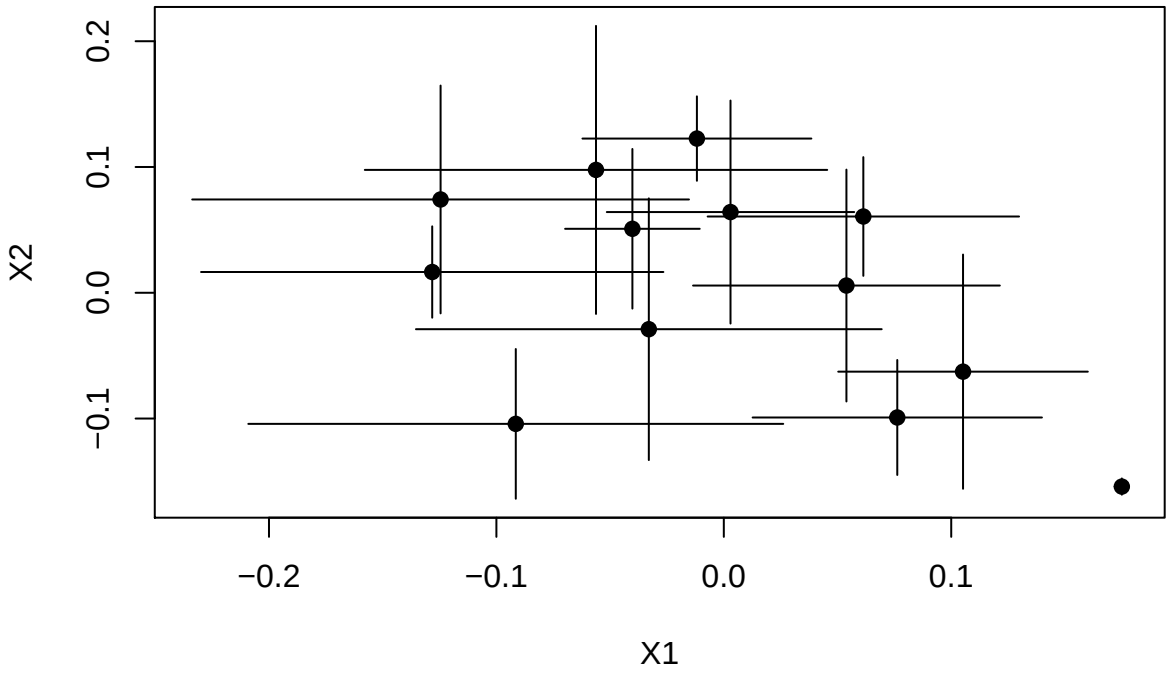
```
par(mfrow = c(1, 2), mar = c(5.1, 4.1, 4.1, 2.1) / 2)
gplot(meanNet(cn.mu.onc), gmode = "graph",
      displaylabels = TRUE,
      edge.lwd = meanNet(cn.mu.onc) * 20,
      vertex.col = "darkgrey")
legend("topleft", legend = "A", bty = "n", cex = 1.5)
chp.coord <- ch.plot(cn.nms.onc, onc.geno, cex = 1.5)
plot(nv.onc, col = "darkgrey")
legend("topleft", legend = "B", bty = "n", cex = 1.5)
```




```
par(mfrow = c(1, 1), mar = c(5.1, 4.1, 4.1, 2.1))
bipartite::plotweb(pw.onc, method = "normal",
                   text.rot = 45,
                   col.low = col.pal[mods.onc$tree],
                   col.high = col.pal[mods.onc$sp],
                   bor.col.low = col.pal[mods.onc$tree],
                   bor.col.high = col.pal[mods.onc$sp],
                   col.interaction = "grey70",
                   bor.col.interaction = "grey70",
                   labsize = 1.5)
```




```
ch.plot(nms.onc, onc.geno)
```

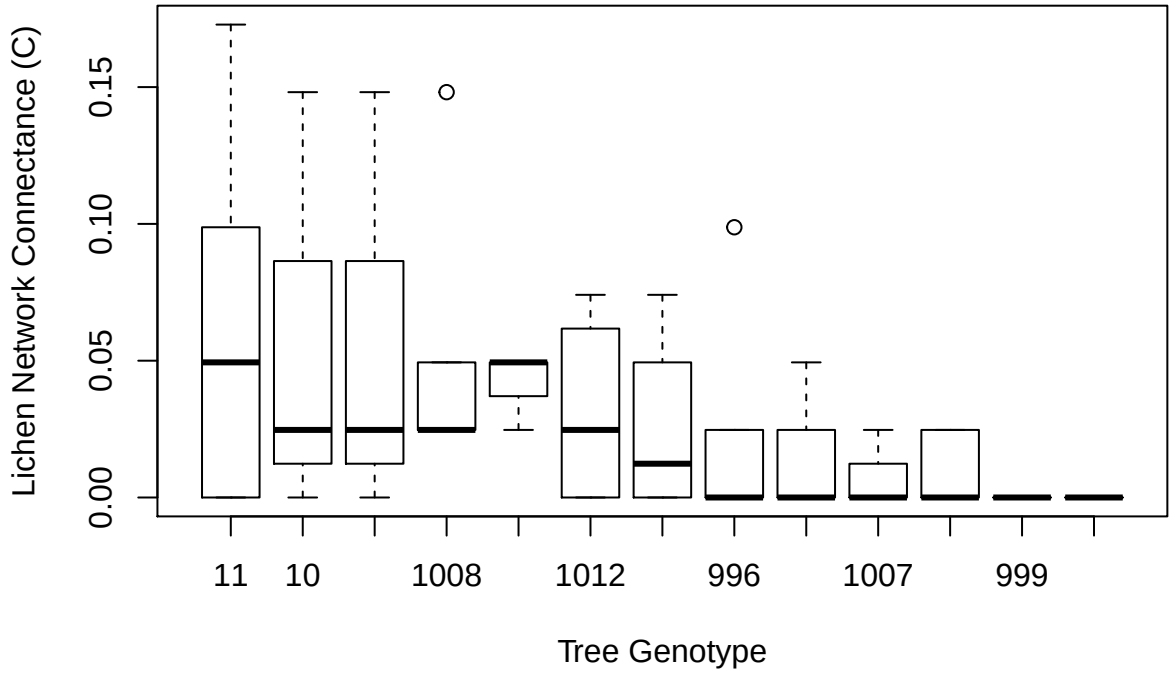



```
##                X1          X2
## 10   -0.091479884 -0.104244255
## 1005 -0.124540472  0.074171596
## 1007  0.175012652 -0.154102531
## 1008  0.061349598  0.060637950
## 1012 -0.056201035  0.097682862
## 1017 -0.040197275  0.050863036
## 1023  0.053916695  0.005735269
## 11   -0.032978298 -0.028980365
## 996   0.076271011 -0.099167595
## 999   0.105185439 -0.062733516
```

```
## H10  -0.011830997  0.122603983
## T6    0.002941633  0.064173827
## WC5  -0.128224482  0.016507373
```

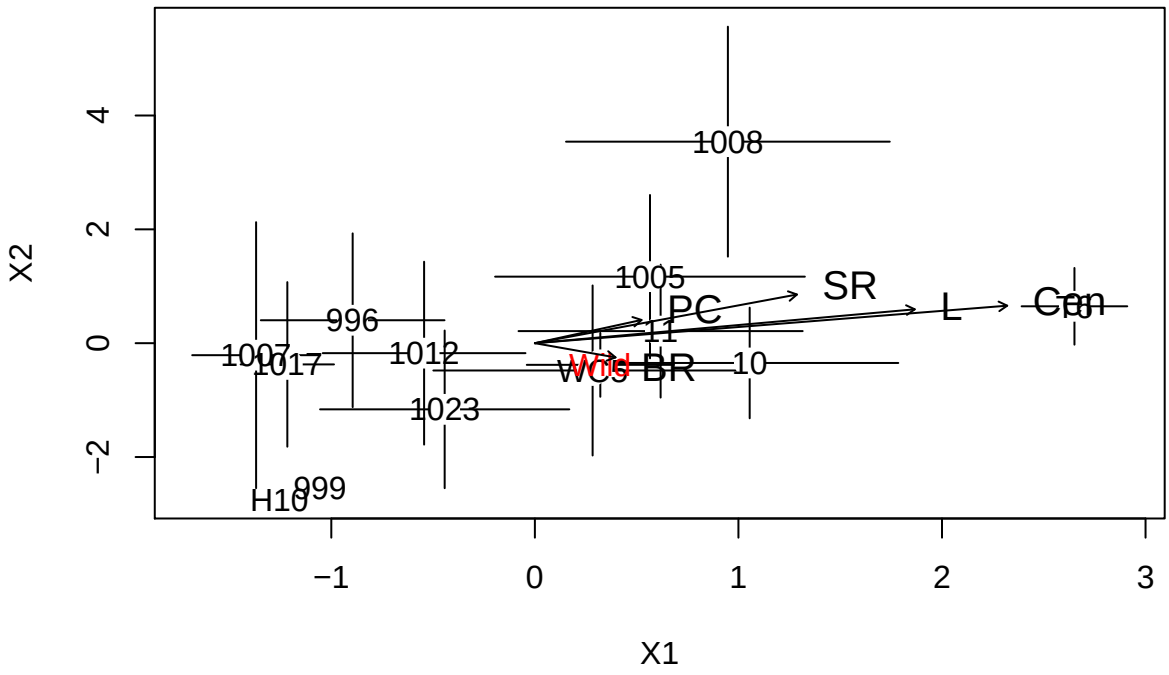
```
## plot(cv.onc, col = "grey30")
## legend("topleft", legend = "A")
```

```
g.order <- tapply(ns.onc[, "C"], onc.geno, mean)
g.order <- names(g.order)[order(g.order, decreasing = TRUE)]
onc.g <- factor(onc.geno, levels = g.order)
plot(ns.onc[, "C"] ~ onc.g, xlab = "Tree Genotype", ylab = "Lichen Network Connectance (C)")
```



Which wild uintah trees are similar to garden trees?

```
coords <- ch.plot(cn.nms.all, cn.nms.geno, mu.pch = "", cex = 2)
points(coords, pch = 19, col = "white", cex = 2)
text(coords[!grepl("wild", rownames(coords)), ],
     labels = rownames(coords)[!grepl("wild", rownames(coords))],
     col = "black")
text(coords[grep("wild", rownames(coords)), 1],
     coords[grep("wild", rownames(coords)), 2],
     labels = "Wild", col = "red")
plot(vec.all, col = "black", cex = 1.23)
```



Send results to manuscript

```
manuscript.dir <- "../../lcn_manuscript"
### Send tables and figures to manuscript directory
if (exists("manuscript.dir")){
    tabs.figs <- dir(manuscript.dir)
    tab.fig.update <- dir("../results/lcn_notebook_files/figure-latex/",
                          full.names = TRUE)[
                              dir("../results/lcn_notebook_files/figure-latex/") %in% tabs.figs]
    tab.fig.update <- c(tab.fig.update,
                        dir("../docs", full.names = TRUE)[dir("../docs") %in% tabs.figs])
    sapply(tab.fig.update, file.copy, to = manuscript.dir, overwrite = TRUE)
                                        # supplementary figures
    si.dir <- paste0(manuscript.dir, "/supplement")
    si <- dir(si.dir)
    si.update <- dir("../results/lcn_notebook_files/figure-latex/",
                     full.names = TRUE)[
                         dir("../results/lcn_notebook_files/figure-latex/") %in% si]
    si.update <- c(si.update, dir("../docs", full.names = TRUE)[dir("../docs") %in% si])
    sapply(si.update, file.copy, to = si.dir,
           overwrite = TRUE)
}
```

```
## named list()
```

Loading and pre-processing data

```
## This is a place-holder for the echoing the data loading code.
```