

Rock Lichen data from Sunset Crater

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Data Summary

- This is an analysis of the effect of Pinyon Pine tree traits on the saxicole (lichen and moss) community on rocks under the canopy of the trees.
- Trees were sampled in a pairwise design in which pairs were comprised of one tree that is susceptible to the herbivory of a stem boring moth (*Diorictria abietella*) and an adjacent tree that is resistant to the moth.
- As tree resistance to the moth is genetically based, pairwise sampling was conducted in order to isolate this genetic effect.
- Some trees that were sampled were dead, these trees were removed from the analysis.
- Plant data were observed by R. Michalet
 - Vegetation.xlsx
 - Light penetration.xls
 - light_&_litter(1).xls

Main Results

- Rock epiphyte communities were adequately sampled, based on species accumulation curves, with moth resistant trees accumulating slightly more lichen species.
- Several tree variables, including light availability, leaf litter abundance and rock abundance, were impacted by moth susceptibility, creating strong differences in sub-canopy conditions.
- Saxicole community abundance, richness, diversity, composition were significantly, generally negatively, affected by moth herbivory.
- Correlation analysis supported an indirect link between genetically based moth susceptibility and impacts on lichen communities via decreasing rock (i.e. habitat) availability through increased leaf abscission and accumulation on rocks under trees.

Analysis and Results

Analyses were conducted in the **R** statistical programming language. The following section loads dependencies and custom functions used in the analysis.

Dependencies

```
cran.pkgs <- c("reshape2", "vegan", "ecodist", "xtable", "knitr")

## install packages that are not installed
if (any(!(cran.pkgs %in% installed.packages()[, 1]))){
  apply(cran.pkgs[which(!(cran.pkgs %in%
    installed.packages()[, 1]))],
    install.packages,
    dependencies = TRUE,
```

```

      repos = 'http://cran.us.r-project.org')
}

## Load libraries
sapply(cran.pkgs, library, quietly = TRUE, character.only = TRUE)

## Custom Functions

## se: Calculate the standard error of a variable.
se <- function(x){sd(x) / sqrt(length(x))}

```

Load Data

The following are variable descriptions (Variable, Type, Range, Definition):

- Moth,categorical,0 or 1,Was the tree susceptible (0) or resistant (1) to moth attack
- Live/Dead,categorical,0 or 1,Was the tree dead (0) or alive (1)
- Litter %,continuous,0 to 100,Percent cover inside quadrat
- Rocks > 3cm %,continuous,0 to 100,Percent cover of rocks > 3cm? inside quadrat
- Rocks < 3cm %,continuous,0 to 100,Percent cover of rocks < 3cm? inside quadrat
- Shrubs %,continuous,0 to 100,Percent cover of shrubs inside quadrat
- Grass %,continuous,0 to 100,Percent cover of grass inside quadrat
- Branches %,continuous,0 to 100,Percent cover of branches on ground inside quadrat
- Distance,continuous,0 to 100,“Distance from main trunk, converted to percent of crown radius at that azimuth”
- Azimuth,continuous,0 to 360,Compass direction from main trunk
- Slope,continuous,0 to 90,Topographical steepness
- Aspect,continuous,0 to 360,Compass direction of slope
- Light,continuous,,Amount of light available to epiliths

```

## Data are in ../data/scrl
l.dat <- read.csv("../data/spp_env_combined.csv")

## Fix species names
colnames(l.dat)[colnames(l.dat) == "Acasup"] <- "Acaame"

## Summary of data
summary(l.dat)

## remove dead trees
l.dat <- l.dat[l.dat[, "Live.Dead"] != 0, ]

## Lichen species list
spp.l <- c("Acacon", "Acaame", "Acaobp", "Sterile.sp", "Brown.cr",
"Lobalp", "Canros", "Calare", "Phydub", "Rhichr", "Xanlin", "Xanpli",
"Xanele", "GrBr.cr", "Gray.cr")
spp.moss <- c("Synrur", "Cerpur.Bryarg")

## Create a community matrix
com <- l.dat[, colnames(l.dat) %in% c(spp.l, spp.moss)]
com.moss <- l.dat[, colnames(l.dat) %in% spp.moss]

## Add the tree labels to the rownames
rownames(com) <- paste(l.dat[, "Moth"], l.dat[, "Tree.pairs"], sep = "_")

```

```

rownames(com.moss) <- paste(l.dat[, "Moth"], l.dat[, "Tree.pairs"], sep = "_")
rownames(l.dat) <- paste(l.dat[, "Moth"], l.dat[, "Tree.pairs"], sep = "_")

## Paired environmental differences
total.rocks <- apply(l.dat[, c("Big.rocks..", "Small.rocks..")], 1, sum)
env <- l.dat[, c("Litter..", "Big.rocks..", "Small.rocks..",
               "Shrubs..", "Grass..", "Branches..",
               "Light...N", "Light...S", "Light...average")]
env <- cbind(env, total.rocks)
env.dif <- apply(env, 2, function(x, p) tapply(x, p, diff), p = l.dat[, "Tree.pairs"])

```

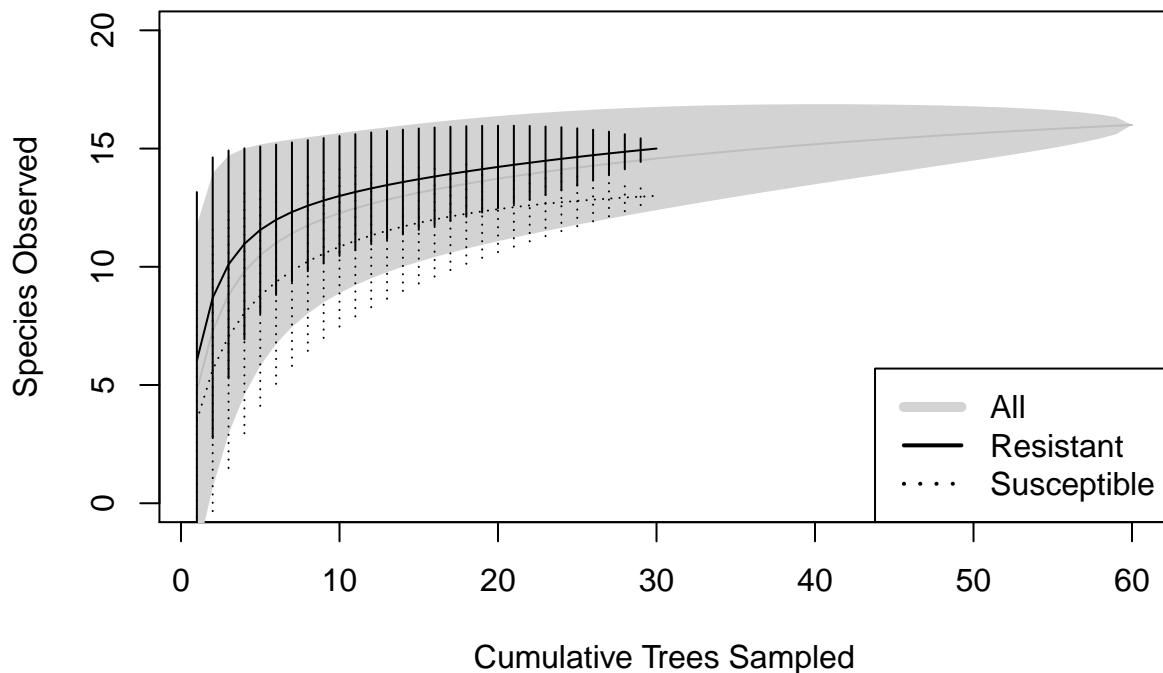
Saxicole communities were sufficiently sampled

```

spa.all <- specaccum(com, method = "exact")
spa.res <- specaccum(com[l.dat[, "Moth"] == 1, ], method = "exact")
spa.sus <- specaccum(com[l.dat[, "Moth"] == 0, ], method = "exact")

plot(spa.all,
     ylim = c(0, 20),
     xlab = "Cumulative Trees Sampled",
     ylab = "Species Observed",
     col = "grey", ci.col = 'lightgrey', ci.type = "poly", ci.lty = 0)
plot(spa.res, ci.col = "black", ci.type = "bar", lty = 1, add = TRUE, ci.lty = 1)
plot(spa.sus, ci.col = "black", ci.type = "bar", lty = 3, add = TRUE, ci.lty = 3)
legend("bottomright",
     legend = c("All", "Resistant", "Susceptible"),
     lty = c(1, 1, 3), lwd = c(5, 2, 2), col = c("lightgrey", "black", "black"))

```



```

pdf("../results/scrl_spp-accum.pdf", width = 5, height = 5)
plot(spa.all,
     ylim = c(0, 20),

```

```

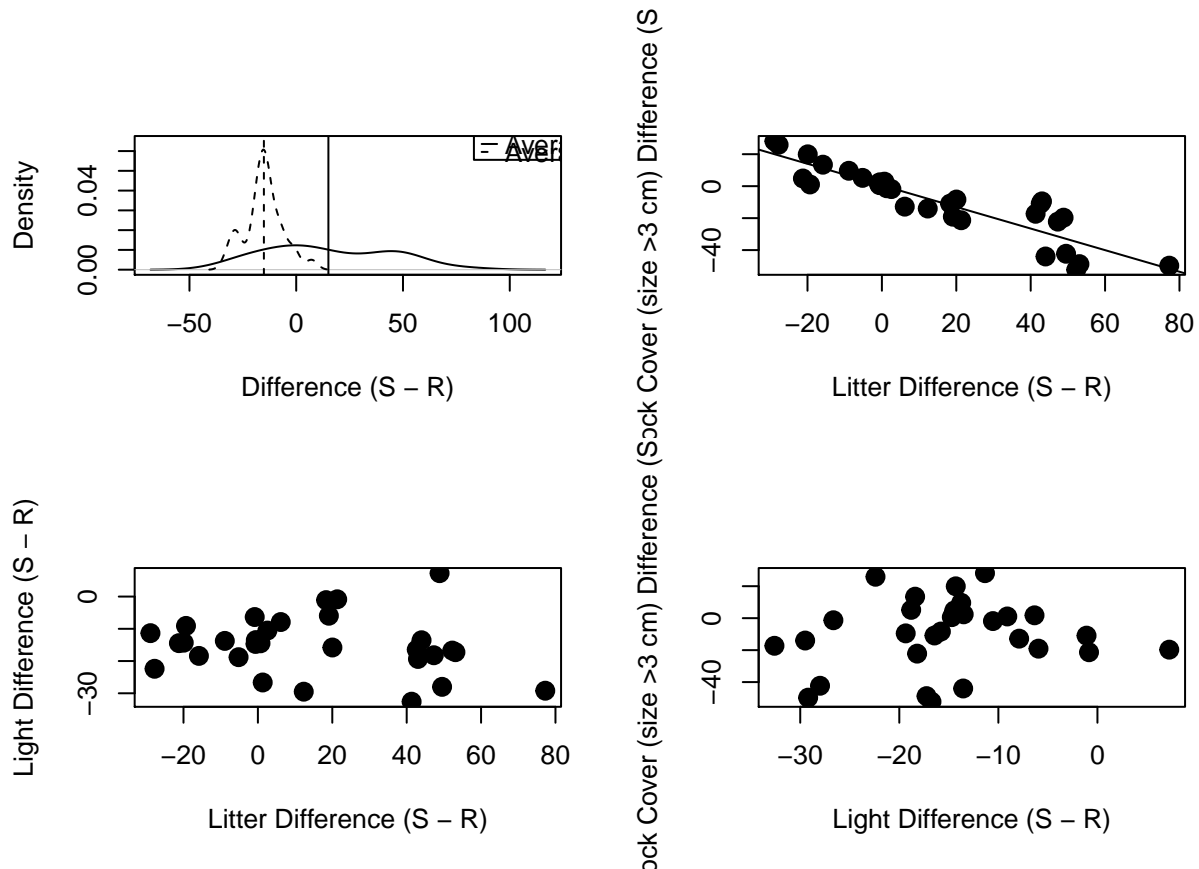
xlab = "Cumulative Trees Sampled",
ylab = "Species Observed",
col = "grey", ci.col = 'lightgrey', ci.type = "poly", ci.lty = 0)
plot(spa.res, ci.col = "black", ci.type = "bar", lty = 1, add = TRUE, ci.lty = 1)
plot(spa.sus, ci.col = "black", ci.type = "bar", lty = 3, add = TRUE, ci.lty = 3)
legend("bottomright",
      legend = c("All", "Resistant", "Susceptible"),
      lty = c(1, 1, 3), lwd = c(5, 2, 2), col = c("lightgrey", "black", "black"))
dev.off()

```

```

## X11cairo
##      2

```



Moth trees have different microenvironments

```

env.test.l <- apply(env.dif, 2, t.test)
env.test.l <- lapply(env.test.l, unlist)
env.test.tab <- do.call(rbind, env.test.l)
env.test.tab <- env.test.tab[, c(1, 2, 3, 6, 4, 5)]
env.test.tab <- apply(env.test.tab, 2, as.numeric)
rownames(env.test.tab) <- names(env.test.l)
colnames(env.test.tab) <- c("t", "df", "p-value", "Mean Difference", "Lower CI 95%", "Upper CI 95%")
kable(env.test.tab, digits = 4)

```

| | t | df | p-value | Mean Difference | Lower CI 95% | Upper CI 95% |
|----------|--------|----|---------|-----------------|--------------|--------------|
| Litter.. | 2.8665 | 29 | 0.0077 | 15.0700 | 4.3178 | 25.8222 |

| | t | df | p-value | Mean Difference | Lower CI 95% | Upper CI 95% |
|-----------------|---------|----|---------|-----------------|--------------|--------------|
| Big.rocks.. | -2.4617 | 29 | 0.0200 | -9.6837 | -17.7289 | -1.6384 |
| Small.rocks.. | -2.0792 | 29 | 0.0466 | -4.9750 | -9.8688 | -0.0812 |
| Shrubs.. | -1.7605 | 29 | 0.0889 | -0.5147 | -1.1126 | 0.0832 |
| Grass.. | -1.0000 | 29 | 0.3256 | -0.0493 | -0.1502 | 0.0516 |
| Branches.. | 1.0000 | 29 | 0.3256 | 0.1420 | -0.1484 | 0.4324 |
| Light...N | -8.0191 | 29 | 0.0000 | -15.9767 | -20.0514 | -11.9019 |
| Light...S | -7.5187 | 29 | 0.0000 | -14.2900 | -18.1772 | -10.4028 |
| Light...average | -9.2728 | 29 | 0.0000 | -15.1333 | -18.4712 | -11.7955 |
| total.rocks | -2.8178 | 29 | 0.0086 | -14.6587 | -25.2983 | -4.0190 |

Moth trees have different lichen communities

```
abun <- apply(com, 1, sum)
rich <- apply(com, 1, function(x) sum(sign(x)))
shan <- apply(com, 1, diversity, index = "shannon")
tt.a <- t.test(tapply(abun, l.dat[, "Tree.pairs"], diff))
tt.r <- t.test(tapply(rich, l.dat[, "Tree.pairs"], diff))
tt.h <- t.test(tapply(shan, l.dat[, "Tree.pairs"], diff))
tt.arh <- do.call(rbind,
  list(a = unlist(tt.a), r = unlist(tt.r), h = unlist(tt.h)))
data.frame(tt.arh)
```

```
##          statistic.t parameter.df          p.value          conf.int1
## a -2.24872719194069          29  0.0322967805096532 -2.94827641857598
## r -2.95490149904486          29  0.00615219062629224 -4.2867753443144
## h -2.44676815758056          29  0.0207112921139992 -0.802255887812151
##          conf.int2 estimate.mean.of.x null.value.mean          stderr
## a -0.139723581424019          -1.544          0 0.686610632687508
## r -0.779891322352267 -2.53333333333333          0 0.857332582541993
## h -0.0717134452340905 -0.436984666523121          0 0.17859667871239
## alternative          method          data.name
## a two.sided One Sample t-test tapply(abun, l.dat[, "Tree.pairs"], diff)
## r two.sided One Sample t-test tapply(rich, l.dat[, "Tree.pairs"], diff)
## h two.sided One Sample t-test tapply(shan, l.dat[, "Tree.pairs"], diff)
```

composition is different (PERMANOVA, in text and supplement)

```
com.ds <- cbind(com, ds = rep(0.0001, nrow(com)))
com.ds.rel <- apply(com, 2, function(x) x/max(x))
com.ds.rel <- cbind(com.ds.rel, ds = rep(0.0001, nrow(com)))
com.ds.rel[is.na(com.ds.rel)] <- 0

set.seed(123)
ptab.moth <- adonis2(com.ds ~ Moth, data = l.dat,
  strata = l.dat[, "Tree.pairs"],
  by = "margin", nperm = 100000)

set.seed(123)
ptab.moth.rel <- adonis2(com.ds.rel ~ Moth, data = l.dat,
  strata = l.dat[, "Tree.pairs"],
  by = "margin", nperm = 100000)

kable(ptab.moth)
```

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|----------|----|------------|-----------|----------|--------|
| Moth | 1 | 0.8329281 | 0.0389768 | 2.352343 | 0.023 |
| Residual | 58 | 20.5368939 | 0.9610232 | NA | NA |
| Total | 59 | 21.3698219 | 1.0000000 | NA | NA |

```
kable(ptab.moth.rel)
```

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|----------|----|------------|-----------|----------|--------|
| Moth | 1 | 0.8791695 | 0.0405034 | 2.448363 | 0.021 |
| Residual | 58 | 20.8269063 | 0.9594966 | NA | NA |
| Total | 59 | 21.7060758 | 1.0000000 | NA | NA |

three main species were reduced by moths (FDR paired t-tests, in text + supplement)

```
ind.spp <- apply(com, 2, function(x, p) t.test(tapply(x, p, diff)), p = 1.dat[, "Tree.pairs"])
isp <- apply(do.call(rbind, lapply(ind.spp, unlist)), 2, as.numeric)
```

```
## Warning in apply(do.call(rbind, lapply(ind.spp, unlist)), 2, as.numeric): NAs
## introduced by coercion
```

```
## Warning in apply(do.call(rbind, lapply(ind.spp, unlist)), 2, as.numeric): NAs
## introduced by coercion
```

```
## Warning in apply(do.call(rbind, lapply(ind.spp, unlist)), 2, as.numeric): NAs
## introduced by coercion
```

```
rownames(isp) <- names(ind.spp)
isp[, "p.value"] <- p.adjust(isp[, "p.value"], method = "fdr")
isp.all <- isp[, !(apply(isp, 2, function(x) all(is.na(x))))]
isp <- isp[order(isp[, "p.value"]), ]
```

```
isp.all <- isp.all[, c(1, 2, 3, 6, 4, 5)]
colnames(isp.all) <- c("t", "df", "p-value", "Mean Difference", "Lower CI 95%", "Upper CI 95%")
kable(isp.all, digits = 4)
```

| | t | df | p-value | Mean Difference | Lower CI 95% | Upper CI 95% |
|------------|---------|----|---------|-----------------|--------------|--------------|
| Aacon | -3.3776 | 29 | 0.0159 | -0.0447 | -0.0717 | -0.0176 |
| Acaame | -3.2421 | 29 | 0.0159 | -0.1607 | -0.2620 | -0.0593 |
| Acaobp | -1.0747 | 29 | 0.4341 | -0.2860 | -0.8303 | 0.2583 |
| Sterile.sp | -1.0000 | 29 | 0.4341 | -0.0020 | -0.0061 | 0.0021 |
| Brown.cr | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Lobalp | -2.0414 | 29 | 0.2016 | -0.0047 | -0.0093 | 0.0000 |
| Canros | -3.5819 | 29 | 0.0159 | -0.3837 | -0.6027 | -0.1646 |
| Calare | -1.6076 | 29 | 0.2563 | -0.0307 | -0.0697 | 0.0083 |
| Phydub | -1.9226 | 29 | 0.2061 | -0.1053 | -0.2174 | 0.0067 |
| Rhichr | -1.5803 | 29 | 0.2563 | -0.2310 | -0.5300 | 0.0680 |
| Xanlin | -0.6170 | 29 | 0.6672 | -0.2267 | -0.9781 | 0.5247 |
| Xanpli | -0.2598 | 29 | 0.8500 | -0.0277 | -0.2455 | 0.1901 |
| Xanele | -1.5662 | 29 | 0.2563 | -0.0473 | -0.1091 | 0.0145 |
| GrBr.cr | 1.0000 | 29 | 0.4341 | 0.0013 | -0.0014 | 0.0041 |
| Gray.cr | 0.1093 | 29 | 0.9137 | 0.0003 | -0.0059 | 0.0066 |
| Synrur | 0.3628 | 29 | 0.8221 | 0.0220 | -0.1020 | 0.1460 |

| | t | df | p-value | Mean Difference | Lower CI 95% | Upper CI 95% |
|---------------|---------|----|---------|-----------------|--------------|--------------|
| Cerpur.Bryarg | -1.2357 | 29 | 0.4027 | -0.0173 | -0.0460 | 0.0114 |

```
write.csv(round(isp.all, 5), file = "results/scrl_isp_table.csv")
```

Calculate the average abundances of the indicators

```
isp.names <- as.character(na.omit(rownames(isp[isp[, "p.value"] < 0.05, ])))
isp.com <- com[,colnames(com) %in% isp.names]
isp.dif <- apply(isp.com, 2, function(x,y) tapply(x, y, diff), y = l.dat[, "Tree.pairs"])
```

Create a multi-bar plot figure for the community.

```
isp.dat <- melt(isp.dif)
colnames(isp.dat) <- c("Tree.pairs", "Species", "diff")
isp.mu <- tapply(isp.dat[, "diff"], isp.dat[, "Species"], mean)
isp.se <- tapply(isp.dat[, "diff"], isp.dat[, "Species"], se)
ard.dif <- cbind(tapply(abun, l.dat[, "Tree.pairs"], diff),
                tapply(rich, l.dat[, "Tree.pairs"], diff),
                tapply(shan, l.dat[, "Tree.pairs"], diff))
colnames(ard.dif) <- c("Abundance", "Richness", "Diversity")
ard.dat <- melt(ard.dif)
colnames(ard.dat) <- c("Tree.pairs", "Stat", "diff")
ard.mu <- tapply(ard.dat[, "diff"], ard.dat[, "Stat"], mean)
ard.se <- tapply(ard.dat[, "diff"], ard.dat[, "Stat"], se)

pdf(file = "./results/scrl_isp_ard.pdf", width = 9, height = 5)

par(mfrow = c(1,2))
bp.out <- barplot(ard.mu, col = "darkgrey", ylim = c(-5, 0),
                 ylab = "Difference (S - R)", border = "NA")
segments(bp.out[, 1], ard.mu + ard.se,
         bp.out[, 1], ard.mu - ard.se,
         lwd = 1.5)
bp.out <- barplot(isp.mu, col = "darkgrey", ylim = c(-0.5, 0),
                 ylab = "Difference (S - R)", border = "NA",
                 axisnames = TRUE,
                 names.arg = sapply(names(isp.mu),
                                     function(x)
                                         paste(c(substr(x, 1, 1),
                                                substr(x, 4, 4)), collapse = "")))
segments(bp.out[, 1], isp.mu + isp.se,
         bp.out[, 1], isp.mu - isp.se,
         lwd = 1.5)
dev.off()

## X11cairo
##      2
```

Create a plot of the two most indicative species

```
pdf(file = "./results/scrl_complot.pdf", width = 7, height = 7)
plot(com[, c("Acaame", "Canros")], pch = l.dat[, "Moth"] + 1, cex = 3, col = l.dat[, "Moth"] + 1)
legend("topleft", title = "Tree Type", legend = c("Resistant", "Susceptible"), pch = c(2, 1), col = c(2, 1))
dev.off()
```

```
## X11cairo
##      2
```

Create plot with indicator taxa

```
pdf(file = "./results/scrl_pdif.pdf", width = 7, height = 7)
plot(melt(isp.dif)[-1], xlab = "Species", ylab = "Abundance Reduction")
dev.off()
```

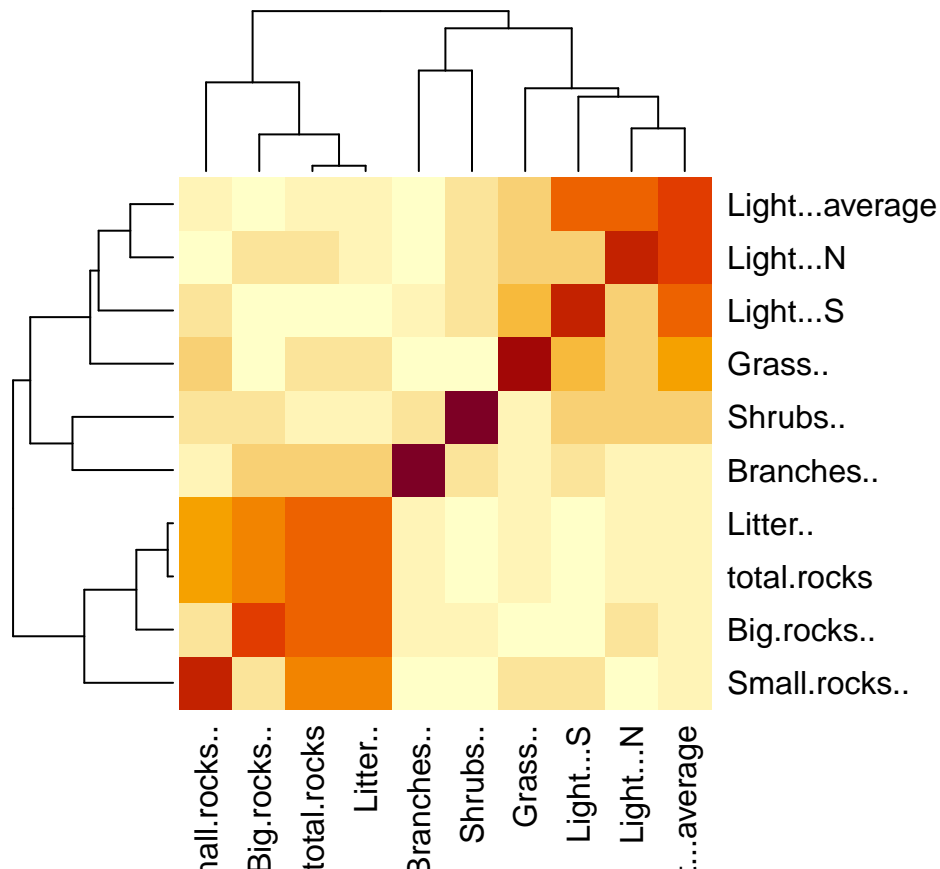
```
## X11cairo
##      2
```

Litter covering rocks was the main driver

Although light did significantly explain variation in the lichen community, this was not significant once the variation in litter was controlled for.

There was high correlation among environmental variables.

```
heatmap(abs(round(cor(env.dif), 3)))
```



```
set.seed(123)
ptab.env <- adonis2(com.ds ~ Litter.. + Light...average, data = l.dat,
  strata = l.dat[, "Tree.pairs"],
  by = "margin", nperm = 100000)
kable(ptab.env)
```

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|----------|----|-----------|-----------|----------|--------|
| Litter.. | 1 | 1.0035484 | 0.0469610 | 2.972456 | 0.007 |

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|-----------------|----|------------|-----------|----------|--------|
| Light...average | 1 | 0.4114619 | 0.0192543 | 1.218728 | 0.243 |
| Residual | 57 | 19.2441042 | 0.9005271 | NA | NA |
| Total | 59 | 21.3698219 | 1.0000000 | NA | NA |

```
set.seed(123)
ptab.env <- adonis2(com.ds ~ Light...average + Litter.. , data = l.dat,
  strata = l.dat[, "Tree.pairs"],
  by = "margin", nperm = 100000)
kable(ptab.env)
```

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|-----------------|----|------------|-----------|----------|--------|
| Light...average | 1 | 0.4114619 | 0.0192543 | 1.218728 | 0.243 |
| Litter.. | 1 | 1.0035484 | 0.0469610 | 2.972456 | 0.007 |
| Residual | 57 | 19.2441042 | 0.9005271 | NA | NA |
| Total | 59 | 21.3698219 | 1.0000000 | NA | NA |

```
set.seed(123)
ptab.env <- adonis2(com.ds ~ total.rocks ,
  strata = l.dat[, "Tree.pairs"],
  by = "term", nperm = 100000)
kable(ptab.env)
```

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|-------------|----|-----------|-----------|----------|--------|
| total.rocks | 1 | 1.664876 | 0.0779078 | 4.900435 | 0.002 |
| Residual | 58 | 19.704946 | 0.9220922 | NA | NA |
| Total | 59 | 21.369822 | 1.0000000 | NA | NA |

```
set.seed(123)
ptab.env <- adonis2(com.ds ~ Big.rocks.. , data = l.dat,
  strata = l.dat[, "Tree.pairs"],
  by = "term", nperm = 100000)
kable(ptab.env)
```

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|-------------|----|-----------|-----------|----------|--------|
| Big.rocks.. | 1 | 2.428473 | 0.1136403 | 7.436188 | 0.001 |
| Residual | 58 | 18.941349 | 0.8863597 | NA | NA |
| Total | 59 | 21.369822 | 1.0000000 | NA | NA |

```
set.seed(123)
ptab.env <- adonis2(com.ds ~ Small.rocks.. , data = l.dat,
  strata = l.dat[, "Tree.pairs"],
  by = "term", nperm = 100000)
kable(ptab.env)
```

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|---------------|----|------------|-----------|----------|--------|
| Small.rocks.. | 1 | 0.2204425 | 0.0103156 | 0.604541 | 0.782 |
| Residual | 58 | 21.1493794 | 0.9896844 | NA | NA |
| Total | 59 | 21.3698219 | 1.0000000 | NA | NA |

```
set.seed(123)
ptab.env <- adonis2(com.ds ~ Litter.. , data = l.dat,
  strata = l.dat[, "Tree.pairs"],
  by = "term", nperm = 100000)
kable(ptab.env)
```

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|----------|----|-----------|-----------|----------|--------|
| Litter.. | 1 | 1.714256 | 0.0802185 | 5.058457 | 0.002 |
| Residual | 58 | 19.655566 | 0.9197815 | NA | NA |
| Total | 59 | 21.369822 | 1.0000000 | NA | NA |

Because light was significantly, negatively correlated with litter and large rocks.

```
cor.test(env.dif[, "Big.rocks.."], env.dif[, "Litter.."])
```

```
##
## Pearson's product-moment correlation
##
## data: env.dif[, "Big.rocks.."] and env.dif[, "Litter.."]
## t = -11.106, df = 28, p-value = 9.054e-12
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.9530598 -0.8039735
## sample estimates:
## cor
## -0.9027609
```

```
pdf("./results/scrl_litterVbigrocks.pdf", width = 5, height = 5)
dev.off()
```

```
## pdf
## 2
```

Although there was a correlation between the differences in big rocks and litter, there were no significant correlations between the differences in light average and either the differences in litter or the differences in big rocks.

```
summary(lm(Big.rocks.. ~ Litter.., data = data.frame(env.dif)))
```

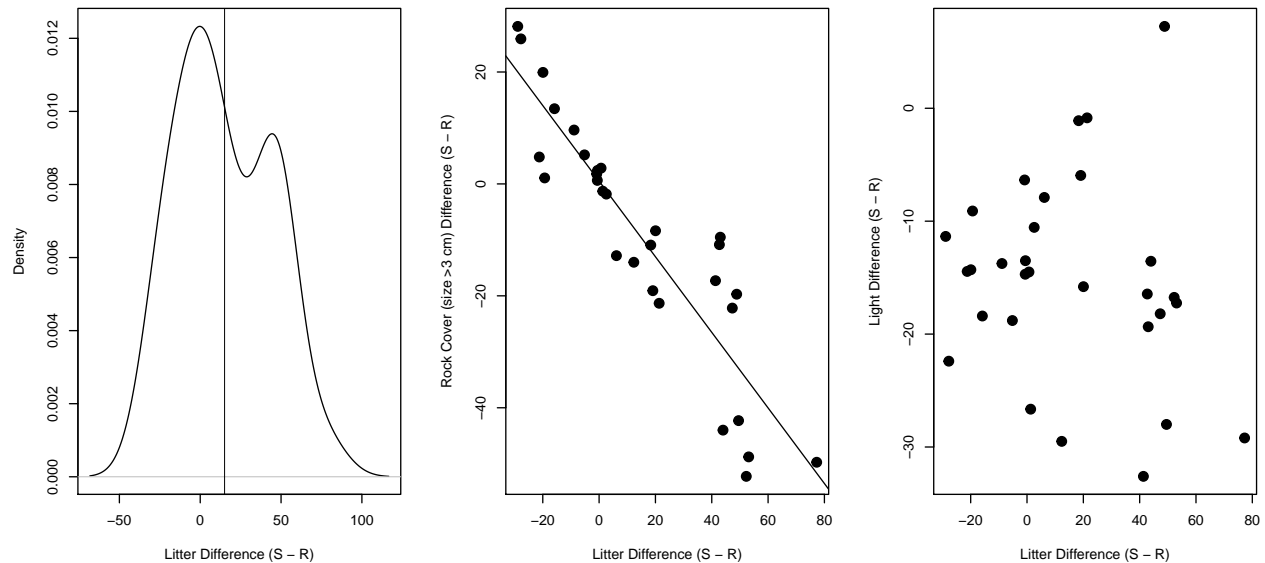
```
##
## Call:
## lm(formula = Big.rocks.. ~ Litter.., data = data.frame(env.dif))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.455  -7.235   1.075   5.646  19.057
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept) 0.49589 1.95076 0.254 0.801
## Litter.. -0.67548 0.06082 -11.106 9.05e-12 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.432 on 28 degrees of freedom
## Multiple R-squared: 0.815, Adjusted R-squared: 0.8084
## F-statistic: 123.3 on 1 and 28 DF, p-value: 9.054e-12
summary(lm(Light...average ~ Litter.., data = data.frame(env.dif)))

##
## Call:
## lm(formula = Light...average ~ Litter.., data = data.frame(env.dif))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -16.070  -4.241  -0.112   3.719  24.181
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -14.33153    1.85372  -7.731 2.02e-08 ***
## Litter..    -0.05321    0.05780  -0.921  0.365
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.963 on 28 degrees of freedom
## Multiple R-squared: 0.02937, Adjusted R-squared: -0.005291
## F-statistic: 0.8474 on 1 and 28 DF, p-value: 0.3652
summary(lm(Light...average ~ Big.rocks.., data = data.frame(env.dif)))

##
## Call:
## lm(formula = Light...average ~ Big.rocks.., data = data.frame(env.dif))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.0434  -4.4272  -0.0929   3.9825  22.9413
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -14.59444    1.80972  -8.064 8.82e-09 ***
## Big.rocks..  0.05565    0.07770   0.716  0.48
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.015 on 28 degrees of freedom
## Multiple R-squared: 0.01799, Adjusted R-squared: -0.01708
## F-statistic: 0.513 on 1 and 28 DF, p-value: 0.4798
par(mfrow = c(1,3))
plot(density(tapply(1.dat[, "Litter.."], 1.dat[, "Tree.pairs"], diff)),
     main = "", xlab = "Litter Difference (S - R)")
abline(v = mean(tapply(1.dat[, "Litter.."], 1.dat[, "Tree.pairs"], diff)),
       lwd = 0.5)
```

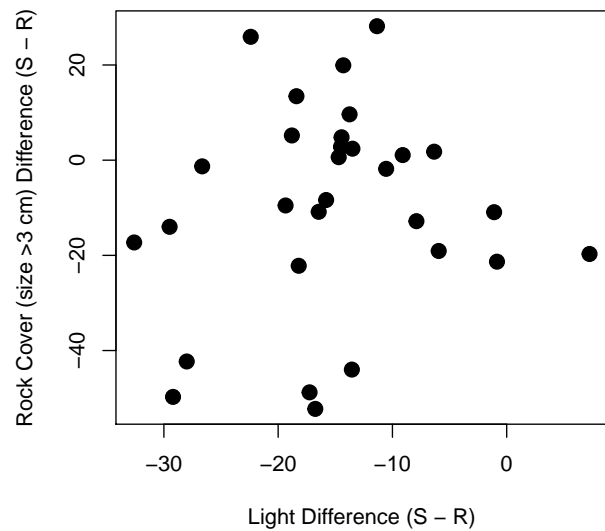
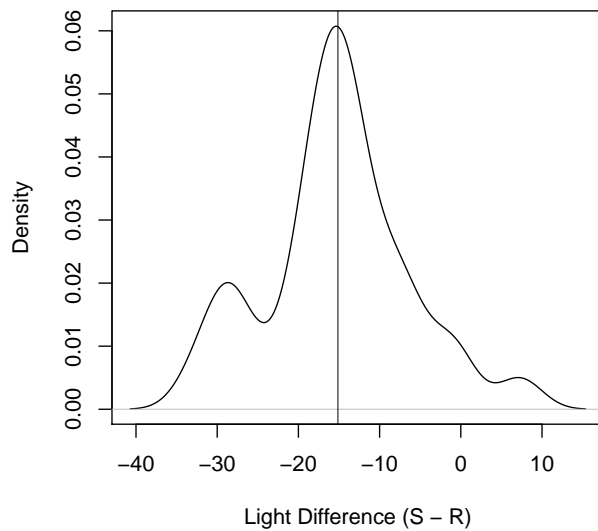
```
plot(env.dif[, "Big.rock.."] ~ env.dif[, "Litter.."],
     xlab = "Litter Difference (S - R)", ylab = "Rock Cover (size >3 cm) Difference (S - R)",
     pch = 19, cex = 1.5)
abline(lm(env.dif[, "Big.rock.."] ~ env.dif[, "Litter.."]))
plot(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff),
     tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff),
     xlab = "Litter Difference (S - R)", ylab = "Light Difference (S - R)",
     pch = 19, cex = 1.5)
```



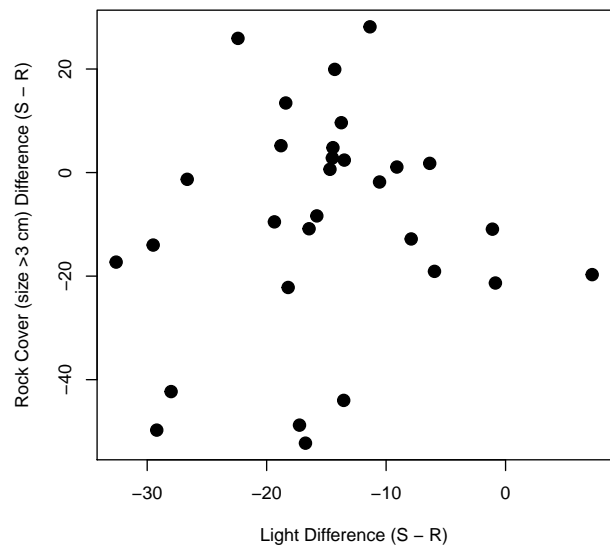
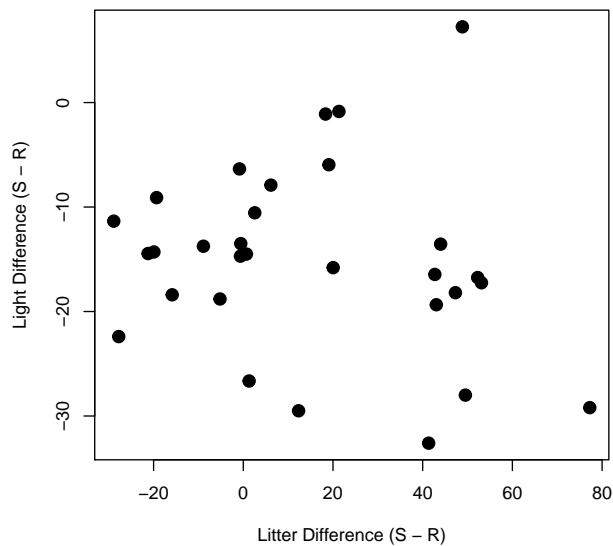
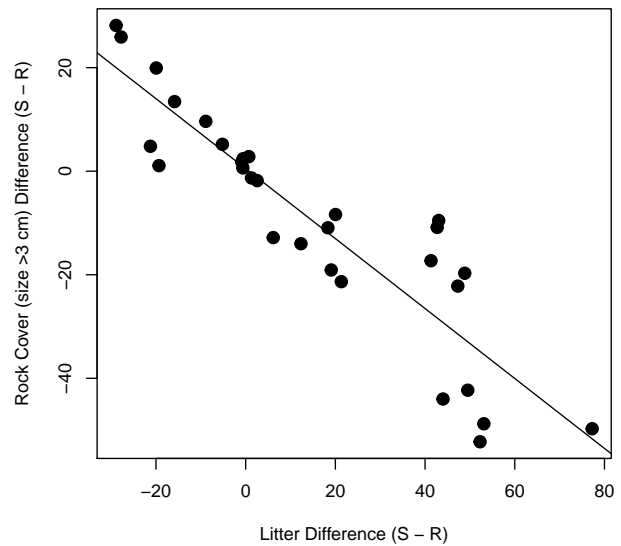
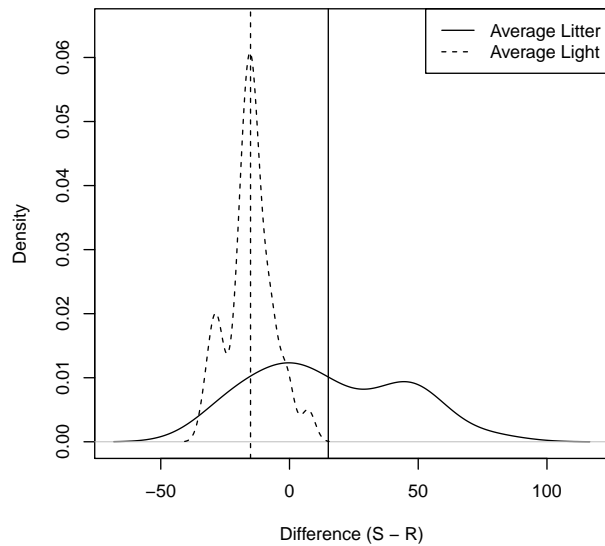
```
pdf("./results/scrl_moth_effects_1x3.pdf", width = 10, height = 5)
par(mfrow = c(1,3))
plot(density(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)),
     main = "", xlab = "Litter Difference (S - R)")
abline(v = mean(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)),
       lwd = 0.5)
plot(env.dif[, "Big.rock.."] ~ env.dif[, "Litter.."],
     xlab = "Litter Difference (S - R)", ylab = "Rock Cover (size >3 cm) Difference (S - R)",
     pch = 19, cex = 1.5)
abline(lm(env.dif[, "Big.rock.."] ~ env.dif[, "Litter.."]))
plot(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff),
     tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff),
     xlab = "Litter Difference (S - R)", ylab = "Light Difference (S - R)",
     pch = 19, cex = 1.5)
dev.off()
```

```
## X11cairo
##      2
```

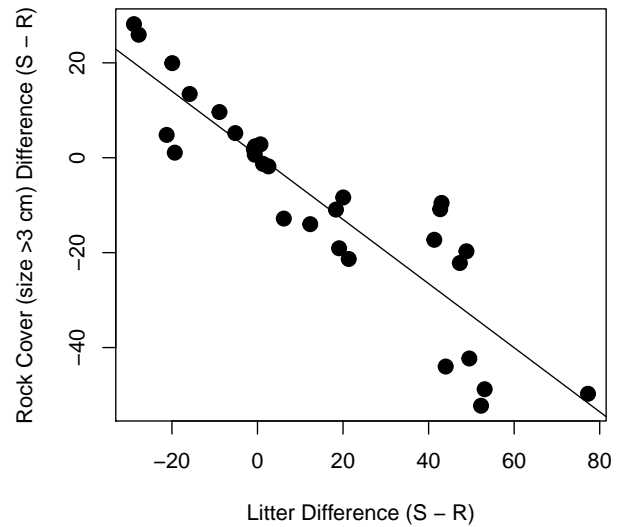
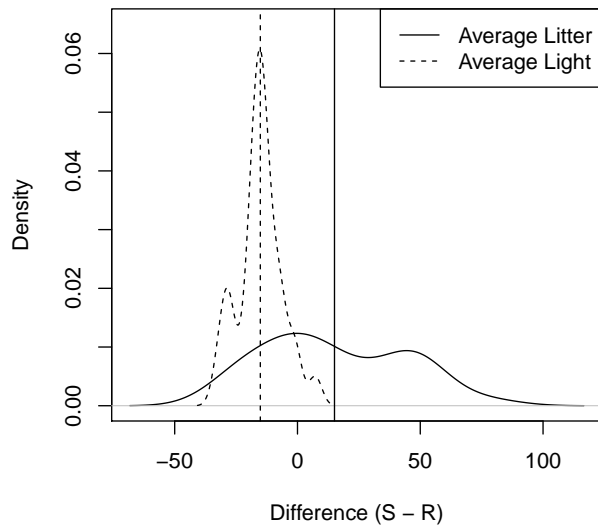
```
par(mfrow = c(1,2))
plot(density(tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff)),
     main = "", xlab = "Light Difference (S - R)")
abline(v = mean(tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff)),
       lwd = 0.5)
plot(env.dif[, "Big.rock.."] ~ env.dif[, "Light...average"],
     xlab = "Light Difference (S - R)", ylab = "Rock Cover (size >3 cm) Difference (S - R)",
     pch = 19, cex = 1.5)
```



```
par(mfrow = c(2,2))
plot(density(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)),
     main = "", xlab = "Difference (S - R)", ylim = c(0, 0.065))
lines(density(tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff)), lty = 2)
abline(v = mean(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)),
       lwd = 1)
abline(v = mean(tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff)),
       lwd = 1, lty = 2)
legend("topright", legend = c("Average Litter", "Average Light"), lty = c(1, 2))
plot(env.dif[, "Big.rock.."] ~ env.dif[, "Litter.."],
     xlab = "Litter Difference (S - R)", ylab = "Rock Cover (size >3 cm) Difference (S - R)",
     pch = 19, cex = 1.5)
abline(lm(env.dif[, "Big.rock.."] ~ env.dif[, "Litter.."]))
plot(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff),
     tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff),
     xlab = "Litter Difference (S - R)", ylab = "Light Difference (S - R)",
     pch = 19, cex = 1.5)
plot(env.dif[, "Big.rock.."] ~ env.dif[, "Light...average"],
     xlab = "Light Difference (S - R)", ylab = "Rock Cover (size >3 cm) Difference (S - R)",
     pch = 19, cex = 1.5)
```



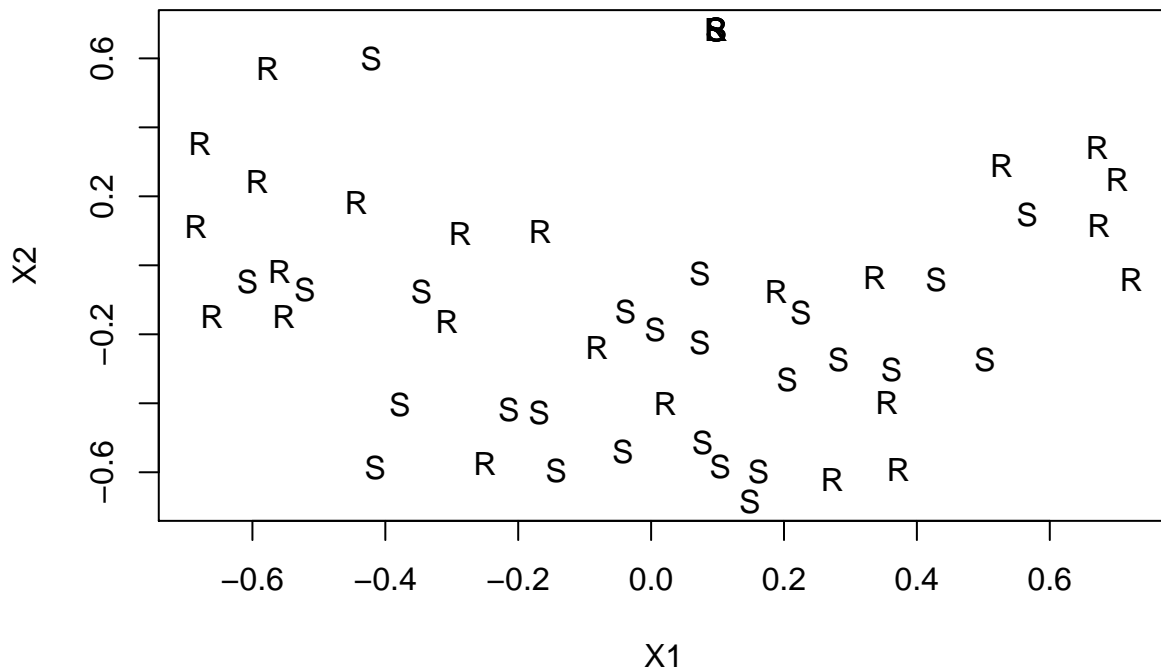
```
par(mfrow = c(1,2))
plot(density(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)),
     main = "", xlab = "Difference (S - R)", ylim = c(0, 0.065))
lines(density(tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff)), lty = 2)
abline(v = mean(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)),
       lwd = 1)
abline(v = mean(tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff)),
       lwd = 1, lty = 2)
legend("topright", legend = c("Average Litter", "Average Light"), lty = c(1, 2))
plot(env.dif[, "Big.rock.."] ~ env.dif[, "Litter.."],
     xlab = "Litter Difference (S - R)", ylab = "Rock Cover (size >3 cm) Difference (S - R)",
     pch = 19, cex = 1.5)
abline(lm(env.dif[, "Big.rock.."] ~ env.dif[, "Litter.."]))
```



```
nmds.out <- nmds(vegdist(com.ds), 2, 2)
ord <- nmds.min(nmds.out, dims = 2)

## Minimum stress for given dimensionality: 0.2169355
## r^2 for minimum stress configuration: 0.6416469

ord.pch <- c("R", "S")[(l.dat[, "Moth"] + 1)]
plot(X2~ X1, data = ord, pch = ord.pch)
```



Litter not light was correlated with large rocks (dist cor, in text). Thus, higher amounts of litter under trees was not related to the penetration of light under the tree canopy.

```
cor.test(tapply(l.dat[, "Big.rock.."], l.dat[, "Tree.pairs"], diff),
         tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff))
```

```
##
## Pearson's product-moment correlation
```

```

##
## data:  tapply(l.dat[, "Big.rocks.."], l.dat[, "Tree.pairs"], diff) and tapply(l.dat[, "Litter.."], l
## t = -11.106, df = 28, p-value = 9.054e-12
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.9530598 -0.8039735
## sample estimates:
##      cor
## -0.9027609
cor.test(tapply(l.dat[, "Big.rocks.."], l.dat[, "Tree.pairs"], diff),
         tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff))

##
## Pearson's product-moment correlation
##
## data:  tapply(l.dat[, "Big.rocks.."], l.dat[, "Tree.pairs"], diff) and tapply(l.dat[, "Light...average"], l
## t = 0.71624, df = 28, p-value = 0.4798
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.2376184  0.4716125
## sample estimates:
##      cor
## 0.1341335
cor.test(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff),
         tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff))

##
## Pearson's product-moment correlation
##
## data:  tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff) and tapply(l.dat[, "Light...average"], l
## t = -0.92053, df = 28, p-value = 0.3652
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.5007401  0.2013096
## sample estimates:
##      cor
## -0.1713898
cor.test(tapply(l.dat[, "Small.rocks.."], l.dat[, "Tree.pairs"], diff),
         tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff))

##
## Pearson's product-moment correlation
##
## data:  tapply(l.dat[, "Small.rocks.."], l.dat[, "Tree.pairs"], diff) and tapply(l.dat[, "Litter.."], l
## t = -4.994, df = 28, p-value = 2.819e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.8391386 -0.4332285
## sample estimates:
##      cor
## -0.6863699

```


Vegetation Analysis

Results Summary

- Both vegetation and light from the plant dataset respond to moth susceptibility (see t-tests below)
- Plant cover, richness and Shannon's diversity respond to moth susceptibility (see t-tests below)
- Plant community composition using Bray-Curtis dissimilarity and a PERMANOVA model that accounts for tree pairs is significantly affected by moth susceptibility (Tables 11-12)
- Using the light, litter and rock cover from the saxicole dataset, plant community composition is significantly correlated with light and litter but not rock cover. Light has a strong effect but the effect of litter is weak and is non-significant after controlling for the effect of light, suggesting that the effect of litter is due to the covariance between light and litter (Tables 13-16)
- Two main species of plant were indicators of moth susceptibility: Apache plume and *Asteraceae ovals*. Both showed reduced cover under moth susceptible trees (Table 17)
- Saxicole and plant communities were not multivariately correlated based on Mantel Tests on both un-relativized and species max relativized cover (see Mantel Test below)

From Richard Michalet

First sheet is the vegetation matrix with all relevés.

Second sheet are values of vegetation cover, rock cover and species richness in all replicates of all treatments + mean values of treatments and corresponding graphs.

From what I remember the methods were simple, quadrats of 1square meter in four treatments with a full factorial design, exposure (north and south of the tree), mortality (alive vs dead shrubs), tree susceptibility (resistant vs susceptible) and tree presence (below the canopy or outside the canopy in open conditions at the close vicinity of the trees).

You can see that without stats results are obvious: strong effect of tree susceptibility only below the tree and in both exposure for both alive and dead trees.

```
library(readxl)

veg <- readxl::read_xlsx("data/Vegetation.xlsx")
veg <- as.data.frame(veg)
l.raw <- read.csv("data/rawdata Sunset Crater for Matt.csv")
l.raw <- l.raw[!(grepl("cover", l.raw[,1])),]
le.raw <- read.csv("data/rawdata Sunset Crater for Matt_env.csv")
le.raw <- le.raw[!(grepl("cover", le.raw[,1])),]
le.raw <- na.omit(le.raw)
```

Observation checks

Do the saxicole community and environment data match?

```
## [1] TRUE
```

Are all of the trees in the saxicole dataset represented in the veg dataset?

```
## [1] TRUE
```

Coalesce datasets

```
l.d <- data.frame(le.raw[, -2:-3], l.raw[, -1:-3])
l.d <- split(l.d, l.d[, "Tree.ID"])
l.d <- l.d[names(l.d) %in% le.raw[, "Tree.ID"]]
l.d <- lapply(l.d, function(x) x[, -1])
```

```

l.d <- lapply(l.d, apply, 2, mean)
l.df <- do.call(rbind, l.d)
trt <- strsplit(rownames(l.df), "")
moth.alive <- lapply(trt, function(x) x[x %in% c(letters, LETTERS)][1:2])
moth.alive <- do.call(rbind, moth.alive)
tree <- lapply(trt, function(x) x[x %in% 0:9])
tree <- as.numeric(unlist(lapply(tree, paste, collapse = "")))
l.df <- data.frame(Tree.pairs = tree,
                  Moth = moth.alive[, 1],
                  Live.Dead = moth.alive[, 2],
                  l.df)
l.df <- l.df[l.df[, "Live.Dead"] == "A", ]
l.df[, "Moth"] <- as.character(l.df[, "Moth"])
l.df[l.df[, "Moth"] == "R", "Moth"] <- 1
l.df[l.df[, "Moth"] == "S", "Moth"] <- 0
moth.tree <- paste(l.df[, "Moth"], l.df[, "Tree.pairs"], sep = "_")
l.df <- l.df[match(rownames(l.dat), moth.tree), ]

```

Check that l.dat and l.df are correctly coalesced:

```

## [1] TRUE

## [1] TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE TRUE FALSE TRUE
## [13] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [25] TRUE TRUE

```

Check that the values of the variables match, excluding light:

The following vector should work to match-up the saxicoles with the veg data:

Checking the vegetation and rock cover correlations. We find that vegetation cover is significantly, but not strongly correlated with rock cover. Large rock cover measurements in the saxicole dataset is strongly correlated with total rock cover in the plant dataset.

Both vegetation and rock cover are strongly affected by moth susceptibility.

```
cor.test(v.dat[, "Vegetation.cover"], v.dat[, "Rock.cover"], alt = "greater")
```

```

##
## Pearson's product-moment correlation
##
## data: v.dat[, "Vegetation.cover"] and v.dat[, "Rock.cover"]
## t = 1.8835, df = 58, p-value = 0.03233
## alternative hypothesis: true correlation is greater than 0
## 95 percent confidence interval:
## 0.0269872 1.0000000
## sample estimates:
## cor
## 0.2400809

```

```
cor.test(l.dat[, "Big.rock.."], v.dat[, "Rock.cover"], alt = "greater")
```

```

##
## Pearson's product-moment correlation
##
## data: l.dat[, "Big.rock.."] and v.dat[, "Rock.cover"]
## t = 9.5342, df = 58, p-value = 8.816e-14
## alternative hypothesis: true correlation is greater than 0

```

```
## 95 percent confidence interval:
## 0.6809688 1.0000000
## sample estimates:
## cor
## 0.7813334

t.test(tapply(v.dat[, "Rock.cover"], v.dat[, "Tree.Pair"], diff))

##
## One Sample t-test
##
## data: tapply(v.dat[, "Rock.cover"], v.dat[, "Tree.Pair"], diff)
## t = -3.3582, df = 29, p-value = 0.002208
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## -27.621617 -6.711716
## sample estimates:
## mean of x
## -17.16667

t.test(tapply(v.dat[, "Vegetation.cover"], v.dat[, "Tree.Pair"], diff))

##
## One Sample t-test
##
## data: tapply(v.dat[, "Vegetation.cover"], v.dat[, "Tree.Pair"], diff)
## t = -7.2026, df = 29, p-value = 6.269e-08
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## -28.67505 -15.99162
## sample estimates:
## mean of x
## -22.33333
```

Both plant richness and Shannon's Diversity index were significantly affected by moth susceptibility.

```
v.rich <- apply(v.com, 1, function(x) sum(sign(x)))
v.shan <- apply(v.com, 1, diversity)

t.test(tapply(v.rich, l.dat[, "Tree.pairs"], diff))

##
## One Sample t-test
##
## data: tapply(v.rich, l.dat[, "Tree.pairs"], diff)
## t = -7.477, df = 29, p-value = 3.062e-08
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## -1.6555988 -0.9444012
## sample estimates:
## mean of x
## -1.3

t.test(tapply(v.shan, l.dat[, "Tree.pairs"], diff))

##
## One Sample t-test
```

```
##
## data:  tapply(v.shan, l.dat[, "Tree.pairs"], diff)
## t = -4.2192, df = 29, p-value = 0.00022
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.4386895 -0.1522394
## sample estimates:
##  mean of x
## -0.2954645
```

This is a multivariate analysis of the plant community response to moth susceptibility (PERMANOVA). This analysis uses a modified Bray-Curtis Dissimilarity metric, which permits the inclusion of quadrats that had no plants in them. The analysis also accounts for the paired structure of the data (i.e. pairs of moth susceptible and resistant trees).

```
set.seed(123)
ptab.v.moth <- adonis2(v.com.ds ~ Moth, data = l.dat,
                      strata = v.dat[, "Tree.pairs"],
                      by = "margin", nperm = 100000)

set.seed(123)
ptab.v.moth.rel <- adonis2(v.com.ds.rel ~ Moth, data = l.dat,
                          strata = v.dat[, "Tree.pairs"],
                          by = "margin", nperm = 100000)
```

Here are the results of the multivariate plant community response.

Table 11: PERMANOVA of plant community response to moth.

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|----------|----|-----------|-----------|----------|--------|
| Moth | 1 | 5.174376 | 0.3081168 | 25.82917 | 0.001 |
| Residual | 58 | 11.619181 | 0.6918832 | NA | NA |
| Total | 59 | 16.793557 | 1.0000000 | NA | NA |

Here are the results of the multivariate plant community response after relativizing by species max.

Table 12: PERMANOVA of relativized plant community response to moth.

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|----------|----|-----------|----------|----------|--------|
| Moth | 1 | 5.989174 | 0.288048 | 23.46617 | 0.001 |
| Residual | 58 | 14.803100 | 0.711952 | NA | NA |
| Total | 59 | 20.792275 | 1.000000 | NA | NA |

Do light, litter or rock cover influence plant communities?

```
set.seed(123)
ptab.v.env <- adonis2(v.com.ds ~ Light...average + Litter.. + Big.rock...,
                    data = l.dat,
                    strata = l.dat[, "Tree.pairs"],
                    by = "margin", nperm = 100000)

set.seed(123)
ptab.v.env.rel <- adonis2(v.com.ds.rel ~ Light...average + Litter.. + Big.rock...,
                        data = l.dat,
```

```
strata = l.dat[, "Tree.pairs"],
by = "margin", nperm = 100000)
```

Light has a strong effect on the plant community. Litter also has an effect but it is small and marginally significant, either un-relativized or relativized, respectively.

Table 13: PERMANOVA of plant community response to several environmental variables.

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|-----------------|----|------------|-----------|-----------|--------|
| Light...average | 1 | 2.8692870 | 0.1708564 | 12.696810 | 0.001 |
| Litter.. | 1 | 0.6890028 | 0.0410278 | 3.048889 | 0.049 |
| Big.rocks.. | 1 | 0.3621592 | 0.0215654 | 1.602582 | 0.189 |
| Residual | 56 | 12.6551530 | 0.7535719 | NA | NA |
| Total | 59 | 16.7935571 | 1.0000000 | NA | NA |

Table 14: PERMANOVA of relativized plant community response to several environmental variables.

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|-----------------|----|------------|-----------|-----------|--------|
| Light...average | 1 | 3.2173963 | 0.1547400 | 11.469106 | 0.001 |
| Litter.. | 1 | 0.7307945 | 0.0351474 | 2.605075 | 0.061 |
| Big.rocks.. | 1 | 0.5197916 | 0.0249993 | 1.852910 | 0.138 |
| Residual | 56 | 15.7095234 | 0.7555462 | NA | NA |
| Total | 59 | 20.7922745 | 1.0000000 | NA | NA |

```
set.seed(123)
ptab.v.env.seq <- adonis2(v.com.ds ~ Light...average + Litter.. + Big.rocks...,
  data = l.dat,
  strata = l.dat[, "Tree.pairs"],
  by = "term", nperm = 100000)

set.seed(123)
ptab.v.env.rel.seq <- adonis2(v.com.ds.rel ~ Light...average + Litter.. + Big.rocks...,
  data = l.dat,
  strata = l.dat[, "Tree.pairs"],
  by = "term", nperm = 100000)
```

After controlling for the effect of light, the effect of litter is no longer significant, un-relativized or relativized, respectively.

Table 15: Sequential PERMANOVA of plant community response to several environmental variables. Variance is explained sequentially by factors entered into the model from top to bottom.

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|-----------------|----|------------|-----------|-----------|--------|
| Light...average | 1 | 3.2765116 | 0.1951053 | 14.498809 | 0.001 |
| Litter.. | 1 | 0.4997333 | 0.0297574 | 2.211358 | 0.103 |
| Big.rocks.. | 1 | 0.3621592 | 0.0215654 | 1.602582 | 0.189 |
| Residual | 56 | 12.6551530 | 0.7535719 | NA | NA |
| Total | 59 | 16.7935571 | 1.0000000 | NA | NA |

Table 16: Sequential PERMANOVA of relativized plant community response to several environmental variables. Variance is explained sequentially by factors entered into the model from top to bottom.

| | Df | SumOfSqs | R2 | F | Pr(>F) |
|-----------------|----|------------|-----------|----------|--------|
| Light...average | 1 | 3.8762571 | 0.1864278 | 13.81776 | 0.001 |
| Litter.. | 1 | 0.6867025 | 0.0330268 | 2.44790 | 0.059 |
| Big.rocks.. | 1 | 0.5197916 | 0.0249993 | 1.85291 | 0.138 |
| Residual | 56 | 15.7095234 | 0.7555462 | NA | NA |
| Total | 59 | 20.7922745 | 1.0000000 | NA | NA |

- Indicator species

```
## Warning in apply(do.call(rbind, lapply(ind.spp.v, unlist))), 2, as.numeric): NAs
## introduced by coercion
```

```
## Warning in apply(do.call(rbind, lapply(ind.spp.v, unlist))), 2, as.numeric): NAs
## introduced by coercion
```

```
## Warning in apply(do.call(rbind, lapply(ind.spp.v, unlist))), 2, as.numeric): NAs
## introduced by coercion
```

There are two species that are responding to moth susceptibility, Apache plume and *Asteraceae ovaes*.

Table 17: Indicator Species Analysis using False Discovery Rate (FDR) adjusted p-values from t-tests of paired differences between resistant and susceptible trees (Resistant - Susceptible).

| | t | df | p-value | Mean Difference | Lower CI 95% | Upper CI 95% |
|---------------------------|---------|----|---------|-----------------|--------------|--------------|
| Apache.plume | -4.6010 | 29 | 0.0007 | -10.2667 | -14.8304 | -5.7029 |
| Asteraceae.ovaes | -3.9581 | 29 | 0.0020 | -8.1333 | -12.3360 | -3.9307 |
| Rhus.trilobata | -1.8410 | 29 | 0.1869 | -3.1667 | -6.6847 | 0.3514 |
| Avena | -1.7951 | 29 | 0.1869 | -0.2000 | -0.4279 | 0.0279 |
| Juniperus.monosperma | -1.0000 | 29 | 0.3256 | -0.1667 | -0.5075 | 0.1742 |
| Pinus.edulis.R | 1.0000 | 29 | 0.3256 | 0.3333 | -0.3484 | 1.0151 |
| Rabbit.brush | -1.0000 | 29 | 0.3256 | -0.6667 | -2.0302 | 0.6968 |
| Plante.grise.allongée | -1.0000 | 29 | 0.3256 | -0.1000 | -0.3045 | 0.1045 |
| Scarlet.glia | -1.0000 | 29 | 0.3256 | -0.0667 | -0.2030 | 0.0697 |
| Bouteloua.gracilis | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Pinus.edulis.S | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Stipa.A | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Stipa.B | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Stipa.très.grand | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Ephedra | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Grande.grass.corymbe | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Boraginacée.rosette.grise | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Grass.à.nœud | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Brachypode | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Carex | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Cactus | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Hordeum | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Chenopodiaceae | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Ribes | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Aster.grise | NaN | 29 | NaN | 0.0000 | NaN | NaN |

| | t | df | p-value | Mean Difference | Lower CI 95% | Upper CI 95% |
|------------------|-----|----|---------|-----------------|--------------|--------------|
| Rosette.frisée | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Chamaephyte.gris | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Castilleja | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Opuntia | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Rubiaceae | NaN | 29 | NaN | 0.0000 | NaN | NaN |
| Andropogon | NaN | 29 | NaN | 0.0000 | NaN | NaN |

Univariate response of plants to moth susceptibility

Abundance, richness and evenness of the plant community were significantly different between moth resistant and susceptible trees. All were reduced by moth susceptibility.

```
abun.v <- apply(v.com, 1, sum)
rich.v <- apply(v.com, 1, function(x) sum(sign(x)))
shan.v <- apply(v.com, 1, diversity, index = "shannon")
tt.a.v <- t.test(tapply(abun.v, l.dat[, "Tree.pairs"], diff))
tt.r.v <- t.test(tapply(rich.v, l.dat[, "Tree.pairs"], diff))
tt.h.v <- t.test(tapply(shan.v, l.dat[, "Tree.pairs"], diff))
tt.arh.v <- do.call(rbind,
                    list(a = unlist(tt.a.v), r = unlist(tt.r.v), h = unlist(tt.h.v)))
data.frame(tt.arh.v)
```

```
##      statistic.t parameter.df      p.value      conf.int1
## a -7.13460124102881      29 7.49696694770826e-08 -28.8641508037377
## r -7.47696081076927      29 3.06180988056911e-08 -1.65559883247522
## h -4.21918281746198      29 0.00021997569844751 -0.438689517413495
##      conf.int2 estimate.mean.of.x null.value.mean      stderr
## a -16.0025158629289 -22.4333333333333      0 3.14430093224081
## r -0.944401167524782      -1.3      0 0.173867435299056
## h -0.152239411998494 -0.295464464705995      0 0.0700288367413597
## alternative      method      data.name
## a two.sided One Sample t-test tapply(abun.v, l.dat[, "Tree.pairs"], diff)
## r two.sided One Sample t-test tapply(rich.v, l.dat[, "Tree.pairs"], diff)
## h two.sided One Sample t-test tapply(shan.v, l.dat[, "Tree.pairs"], diff)
```

The differences in richness and diversity are significant but small. Given how divergent the species accumulation curves are for resistant and susceptible plant communities, I parsed out how many unique species total occur under each tree type. It turns out that, as shown in the species accumulation curves, there are a total of 8 unique species that were found under resistant trees, but just 3 unique species found under susceptible trees.

```
r.com.v <- v.com[v.dat[, "data"] == "R", ]
s.com.v <- v.com[v.dat[, "data"] == "S", ]
r.us.v <- sum(sign(apply(sign(r.com.v), 2, sum)))
s.us.v <- sum(sign(apply(sign(s.com.v), 2, sum)))
r.us.v
```

```
## [1] 8
```

```
s.us.v
```

```
## [1] 3
```

Multivariate Correlation of Plants and Saxicoles

There is no significant multivariate correlation between the veg and saxicole communities, regardless of whether the community data are relativized. This is likely a result of the two communities responded to

different variables with low correlation (i.e. rocks = saxicoles and light = plants). This was true either without or with relativization by species max.

```
v.d <- vegdist(v.com.ds)
l.d <- vegdist(com.ds)

mantel(v.d ~ l.d)

##      mantelr      pval1      pval2      pval3      llim.2.5%      ulim.97.5%
## -0.002762319  0.513000000  0.488000000  0.914000000 -0.034504235  0.032707393

v.d <- vegdist(v.com.ds.rel)
l.d <- vegdist(com.ds.rel)

mantel(v.d ~ l.d)

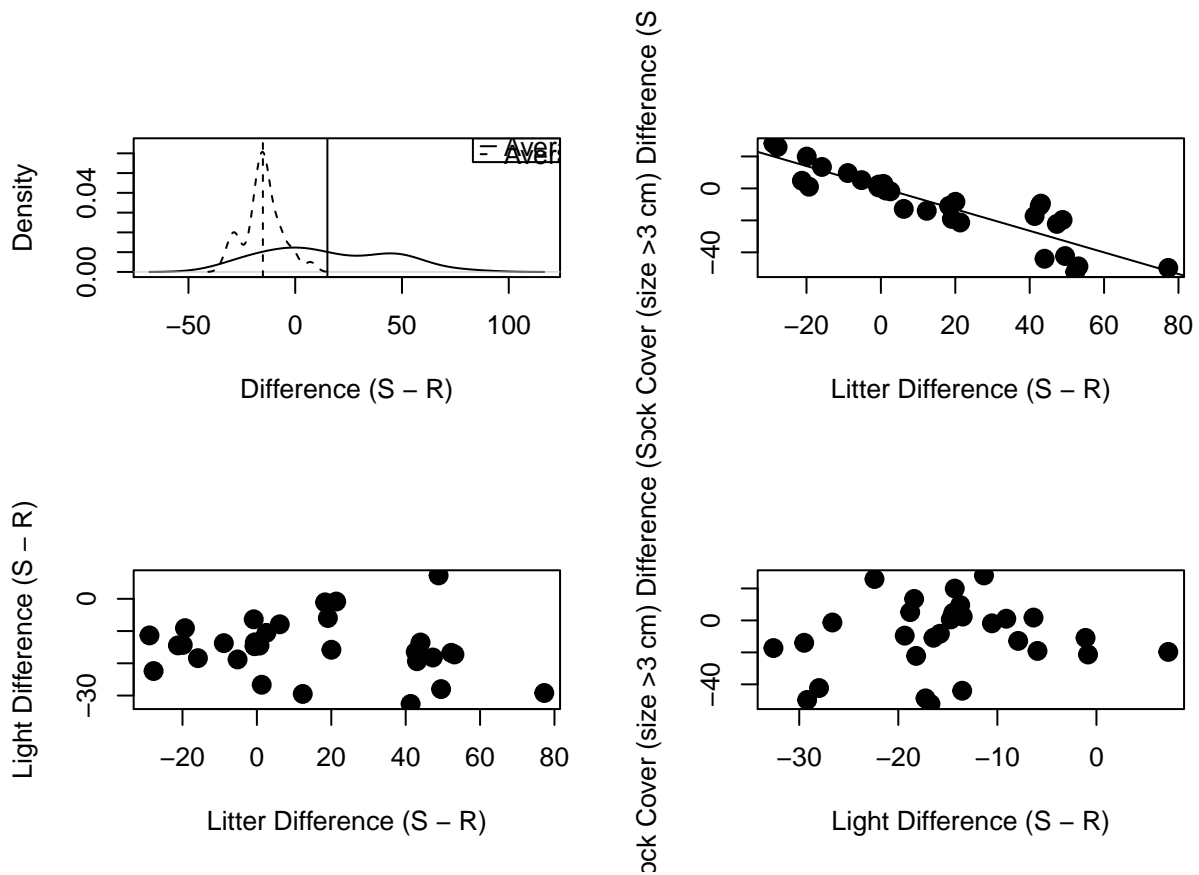
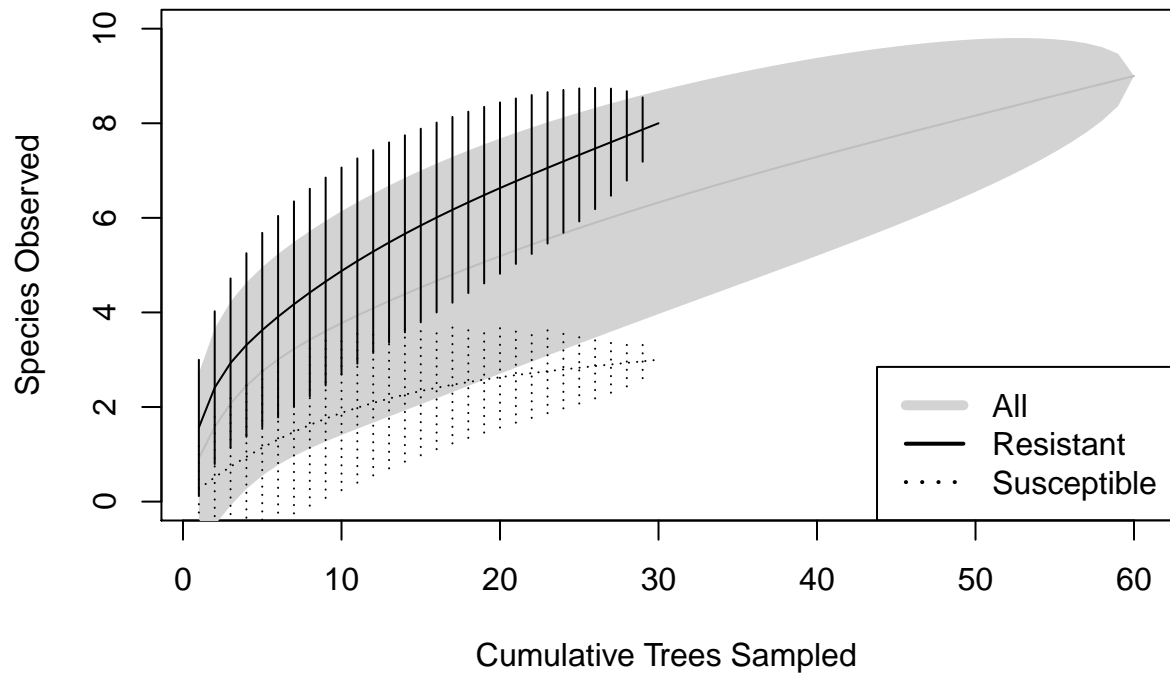
##      mantelr      pval1      pval2      pval3      llim.2.5%      ulim.97.5%
##  0.02328021  0.21200000  0.78900000  0.44300000 -0.01176642  0.05838093
```

Plant analysis figures

Plant communities under susceptible trees were adequately sampled, reaching a clear asymptote of accumulation; however, plant communities under resistant trees were unlikely sampled to represent the full community and were clearly much richer than susceptible tree communities.

```
spa.all.v <- specaccum(v.com, method = "exact")
spa.res.v <- specaccum(v.com[l.dat[, "Moth"] == 1, ], method = "exact")
spa.sus.v <- specaccum(v.com[l.dat[, "Moth"] == 0, ], method = "exact")

plot(spa.all.v,
     ylim = c(0, 10),
     xlab = "Cumulative Trees Sampled",
     ylab = "Species Observed",
     col = "grey", ci.col = 'lightgrey', ci.type = "poly", ci.lty = 0)
plot(spa.res.v, ci.col = "black", ci.type = "bar", lty = 1, add = TRUE, ci.lty = 1)
plot(spa.sus.v, ci.col = "black", ci.type = "bar", lty = 3, add = TRUE, ci.lty = 3)
legend("bottomright",
     legend = c("All", "Resistant", "Susceptible"),
     lty = c(1, 1, 3), lwd = c(5, 2, 2), col = c("lightgrey", "black", "black"))
```

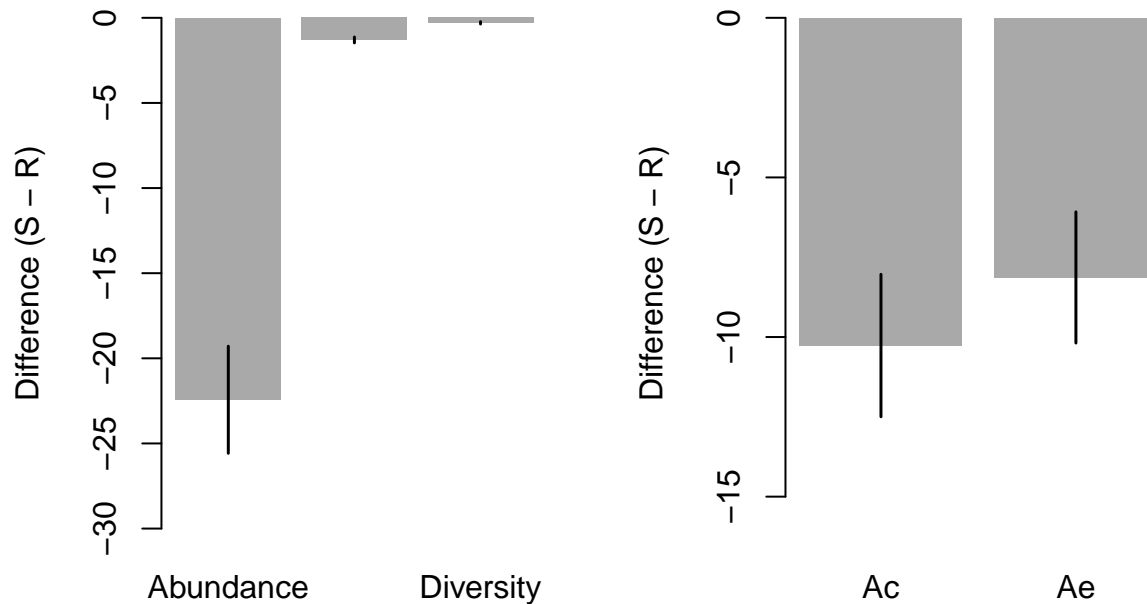
```
isp.names.v <- as.character(na.omit(rownames(isp.v[isp.v[, "p.value"] < 0.05, ])))
isp.com.v <- v.com[,colnames(v.com) %in% isp.names.v]
isp.dif.v <- apply(isp.com.v, 2, function(x,y) tapply(x, y, diff), y = l.dat[, "Tree.pairs"])
isp.dat.v <- melt(isp.dif.v)
colnames(isp.dat.v) <- c("Tree.pairs", "Species", "diff")
```

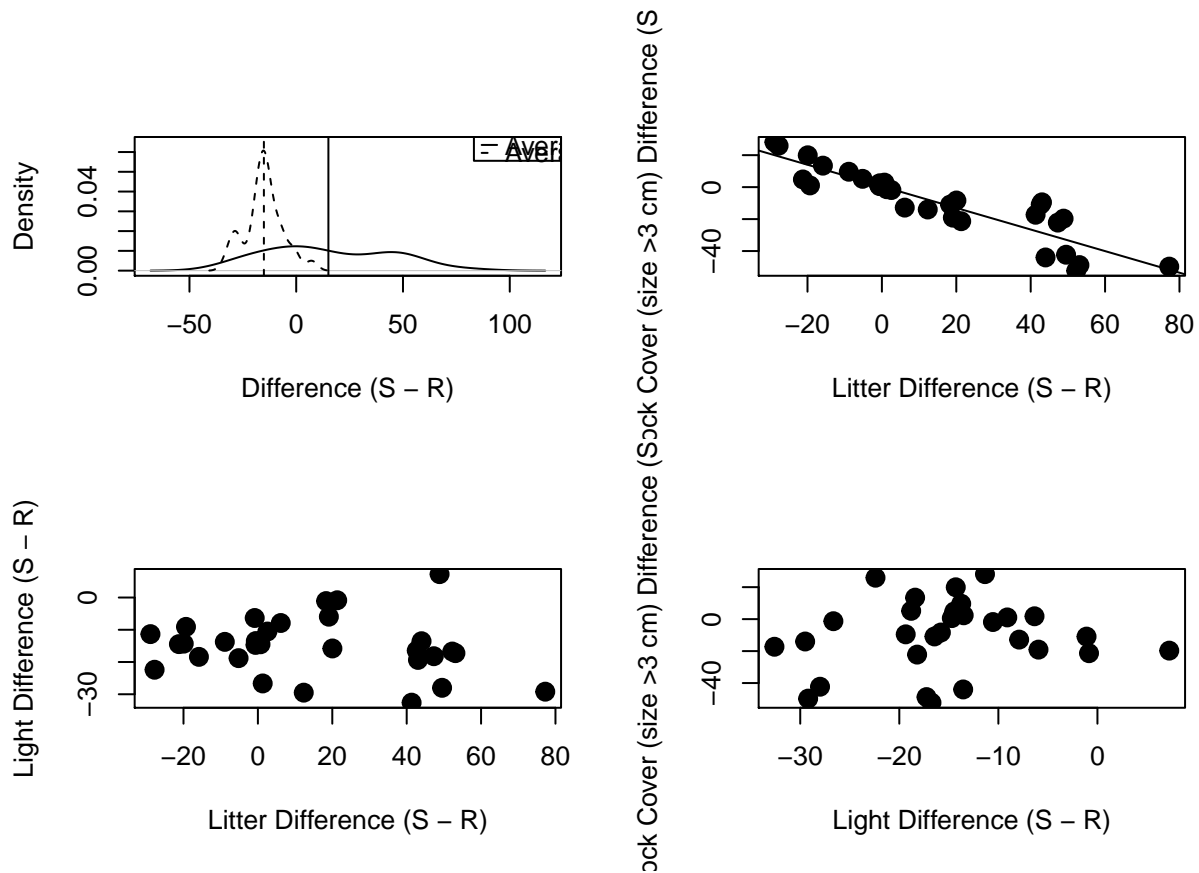
```

isp.mu.v <- tapply(isp.dat.v[, "diff"], isp.dat.v[, "Species"], mean)
isp.se.v <- tapply(isp.dat.v[, "diff"], isp.dat.v[, "Species"], se)
ard.dif.v <- cbind(tapply(abun.v, l.dat[, "Tree.pairs"], diff),
                  tapply(rich.v, l.dat[, "Tree.pairs"], diff),
                  tapply(shan.v, l.dat[, "Tree.pairs"], diff))
colnames(ard.dif.v) <- c("Abundance", "Richness", "Diversity")
ard.dat.v <- melt(ard.dif.v)
colnames(ard.dat.v) <- c("Tree.pairs", "Stat", "diff")
ard.mu.v <- tapply(ard.dat.v[, "diff"], ard.dat.v[, "Stat"], mean)
ard.se.v <- tapply(ard.dat.v[, "diff"], ard.dat.v[, "Stat"], se)

par(mfrow = c(1,2))
bp.out.v <- barplot(ard.mu.v, col = "darkgrey", ylim = c(-30, 0),
                   ylab = "Difference (S - R)", border = "NA")
segments(bp.out.v[, 1], ard.mu.v + ard.se.v,
         bp.out.v[, 1], ard.mu.v - ard.se.v,
         lwd = 1.5)
bp.out.v <- barplot(isp.mu.v, col = "darkgrey", ylim = c(-16.00, 0),
                   ylab = "Difference (S - R)", border = "NA",
                   axisnames = TRUE,
                   names.arg = sapply(names(isp.mu.v),
                                       function(x)
                                           paste(c(substr(x, 1, 1),
                                                  substr(x, 4, 4)), collapse = "")))
segments(bp.out.v[, 1], isp.mu.v + isp.se.v,
         bp.out.v[, 1], isp.mu.v - isp.se.v,
         lwd = 1.5)

```





Similar to the ordination for the saxicole community, the NMDS ordination looks strange. This is possible due to the paired structure of the data as well. This should be handled with whatever ordination procedure is ultimately used.

```
nmds.out.v <- nmds(vegdist(v.com.ds), 2, 2)
ord.v <- nmds.min(nmds.out.v, dims = 2)

## Minimum stress for given dimensionality: 0.1191663
## r^2 for minimum stress configuration: 0.9264456

ord.pch.v <- c("R", "S")[(l.dat[, "Moth"] + 1)]
plot(X2 ~ X1, data = ord.v, pch = ord.pch.v)
```

