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]))){
    sapply(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 = "_")
```

```r
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

```r
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"))
```
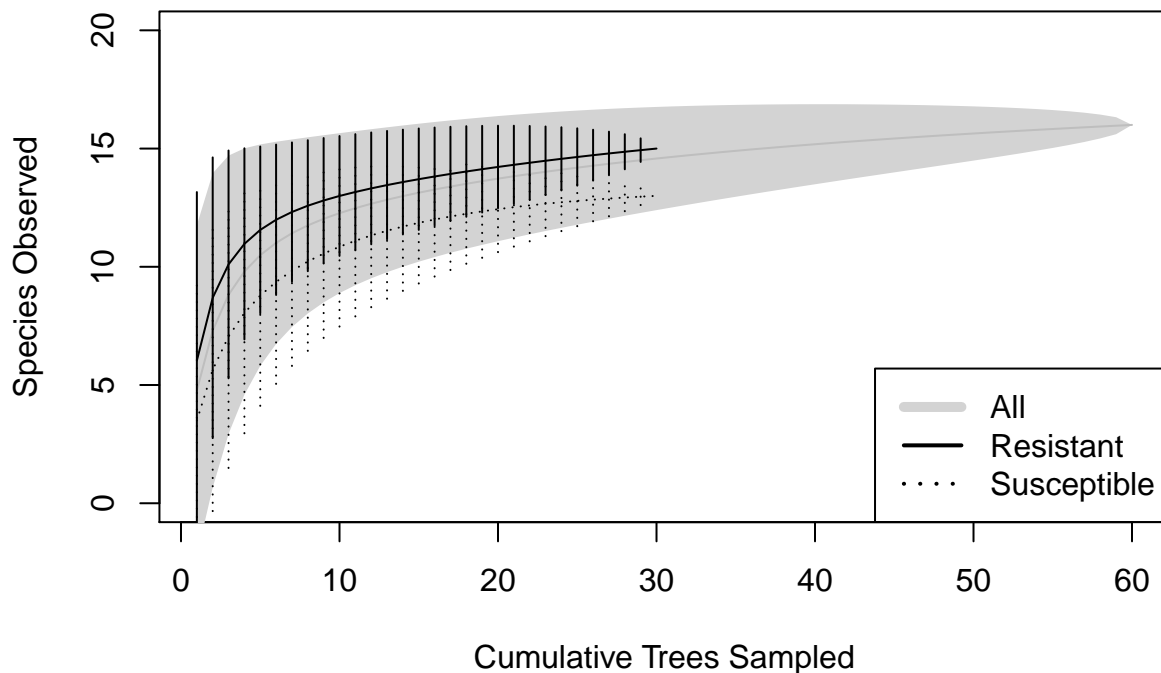


```r
pdf("./results/scrl_spp-accum.pdf", width = 5, height = 5)
plot(spa.all,
     ylim = c(0, 20),
```
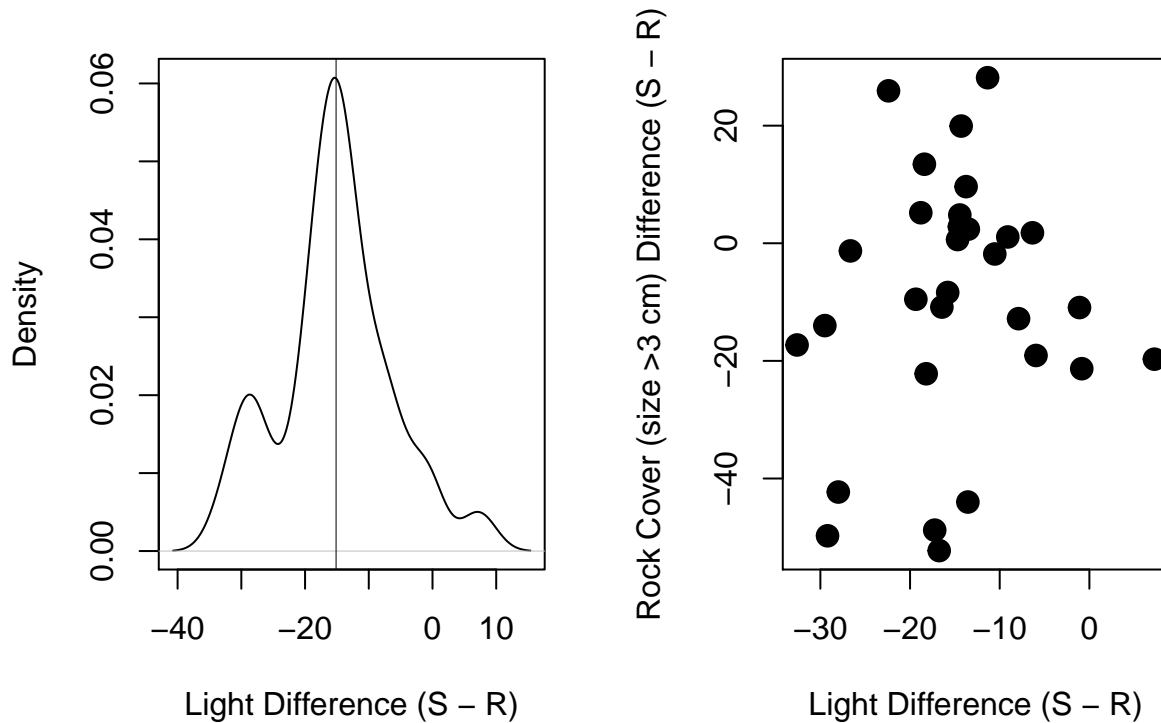
```
        xlab = "Cumulative Trees Sampled",
        ylab = "Species Observed",
        col = "grey", ci.col = 'lightgrey', ci.type = "poly", ci.lty = 0)
plot(spa.res, ci.col = "black", ci.type = "bar", lty = 1, add = TRUE, ci.lty = 1)
plot(spa.sus, ci.col = "black", ci.type = "bar", lty = 3, add = 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
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

	t	df	p-value	Mean Difference	Lower CI 95%	Upper CI 95%
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

	Df	SumOfSqs	R2	F	Pr(>F)
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 = l.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%
Acacon	-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
Cerpur.Bryarg	-1.2357	29	0.4027	-0.0173	-0.0460	0.0114

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

Calculate the average abundances of the indicators

```r
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.

```r
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

```r
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
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()
```
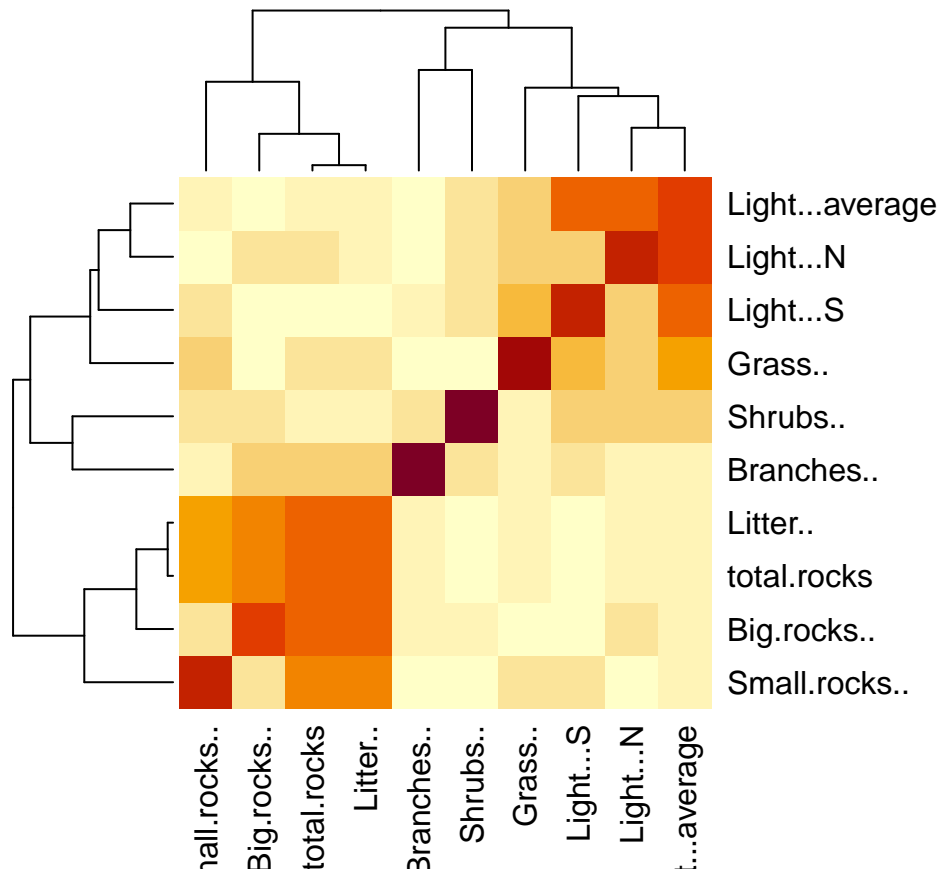
```
## X11cairo
##       2
```

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
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

```r
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

```r
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

```r
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

```r
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 differenes 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
```

```r
summary(lm(Light...average ~ Litter.., data = data.frame(env.dif)))
```
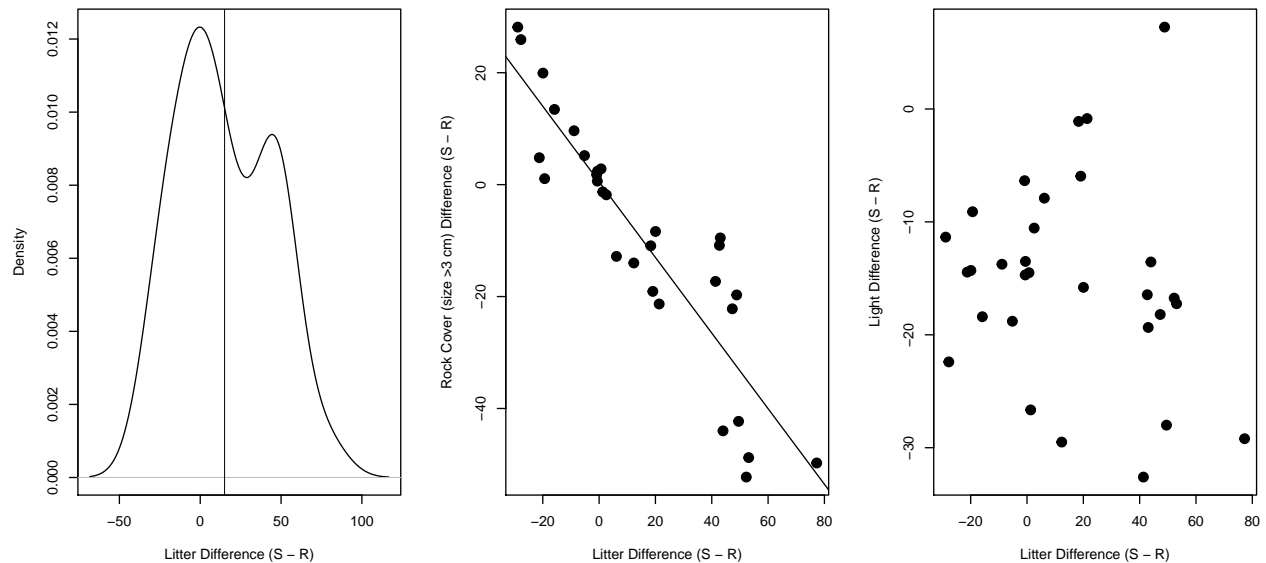
```
##
## Call:
## lm(formula = Light...average ~ Litter.., data = data.frame(env.dif))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -16.070  -4.241  -0.112   3.719  24.181
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -14.33153    1.85372  -7.731 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
```

```r
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
```

```r
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.rocks.."] ~ 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.rocks.."] ~ 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_litter_effects.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.rocks.."] ~ 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.rocks.."] ~ 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()
```

```
## pdf
##    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.rocks.."] ~ env.dif[, "Light...average"],
    xlab = "Light Difference (S - R)", ylab = "Rock Cover (size >3 cm) Difference (S - R)",
    pch = 19, cex = 1.5)
```
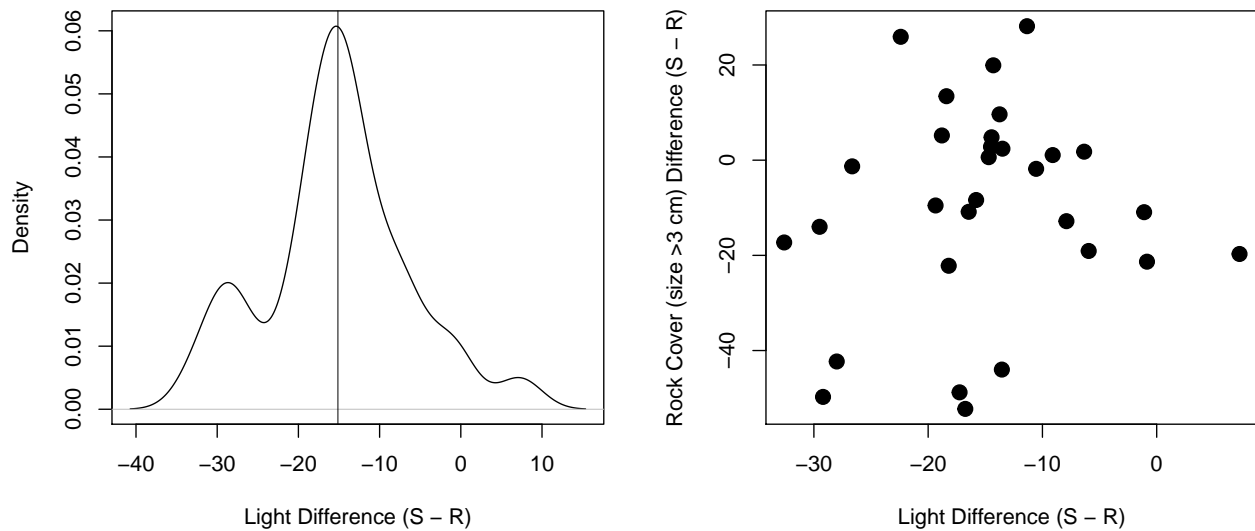
```r
nmds.out <- nmds(vegdist(com.ds), 2, 2)
ord <- nmds.min(nmds.out, dims = 2)
```

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

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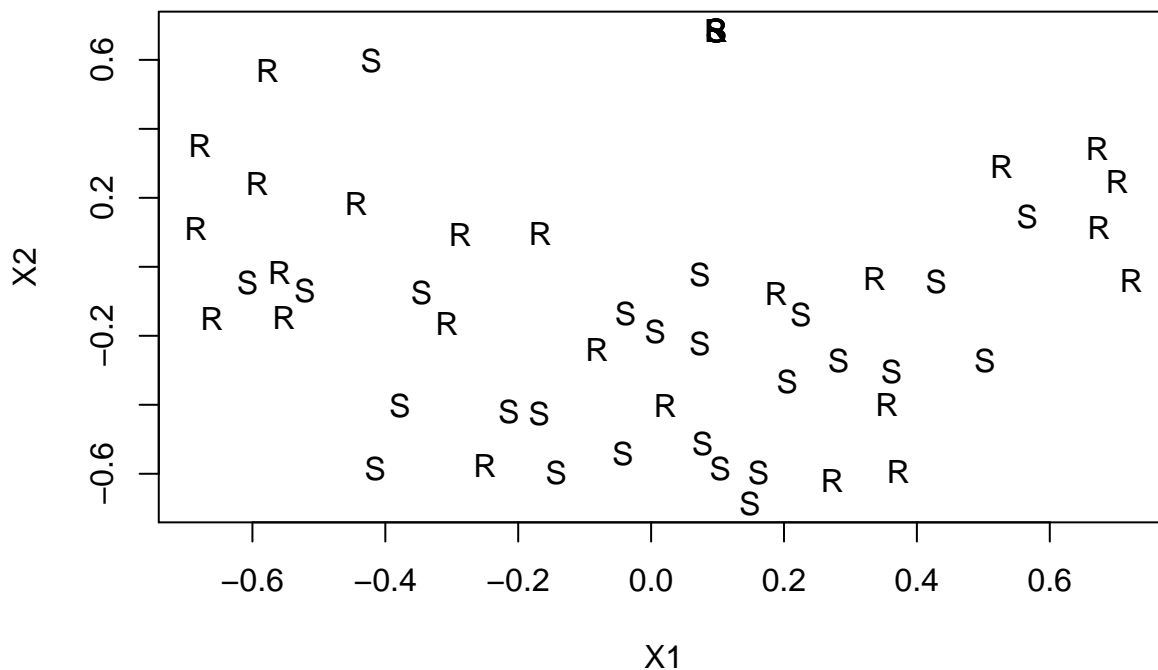

Litter not light was correlated with large rocks (dist cor, in text). Thus, higher amounts of litter under trees was not related to the penetration of light under the tree canopy.

```r
cor.test(tapply(l.dat[, "Big.rocks.."], 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...avera
## 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"]
## 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.."],
## 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 dissimiliarity and a PERMANOVA model that accounts for tree pairs is significantly affected by moth susceptibility (Tables 11-12)
- Using the light, littter 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 ovales.* 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-relatvized 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])
```

```r
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 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.

```r
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
```

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

```
##
##  Pearson's product-moment correlation
##
## data:  l.dat[, "Big.rocks.."] 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.rocks..,
                 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.rocks..,
                 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-relatvizied or relativized, respectivley.

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 ovales*.

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.ovales	-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.

```r
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
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
```

```r
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 asymptptote of accumulation; however, plant communitites under resistant trees were unlikely sampled to represent the full commmunity 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"))
```
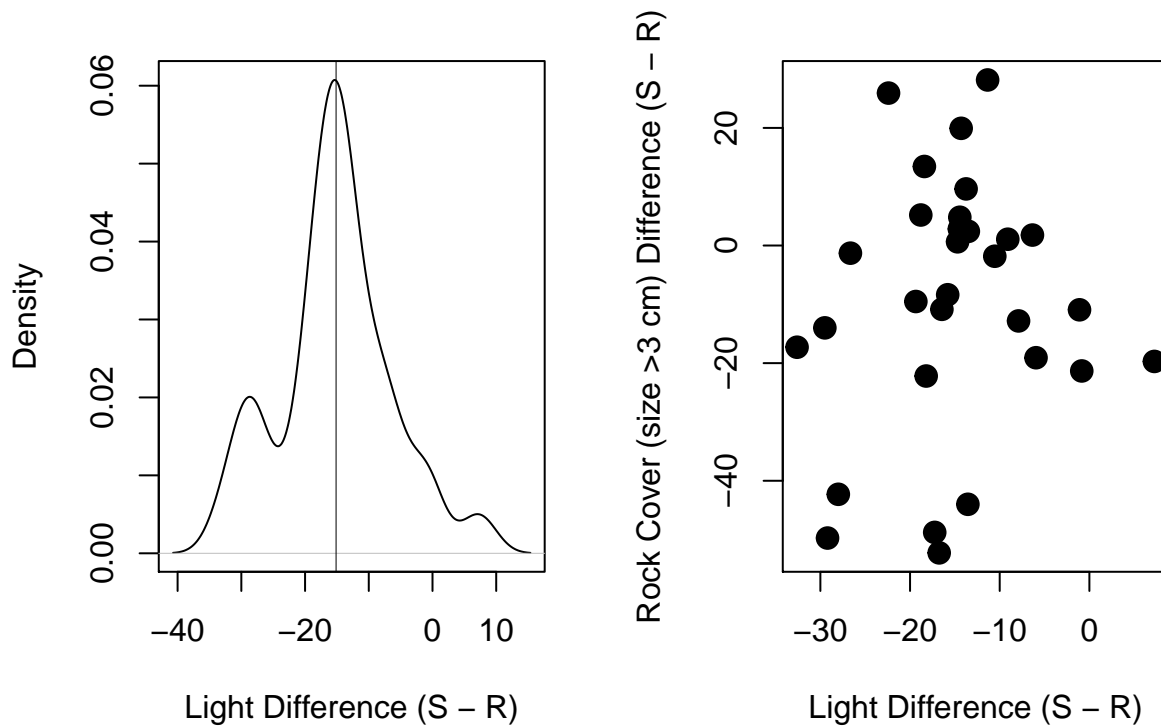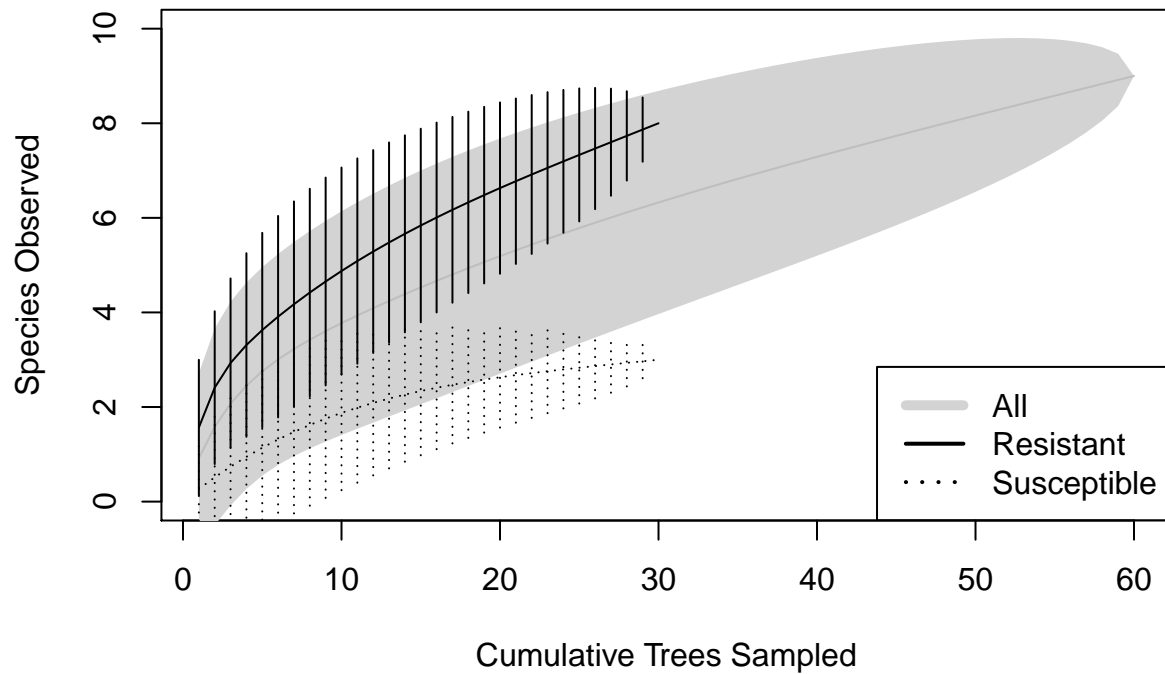
```
isp.names.v <- as.character(na.omit(rownames(isp.v[isp.v[, "p.value"] < 0.05, ])))
isp.com.v <- v.com[,colnames(v.com) %in% isp.names.v]
isp.dif.v <- apply(isp.com.v, 2, function(x,y) tapply(x, y, diff), y = l.dat[ ,"Tree.pairs"])
isp.dat.v <- melt(isp.dif.v)
colnames(isp.dat.v) <- c("Tree.pairs", "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)
```
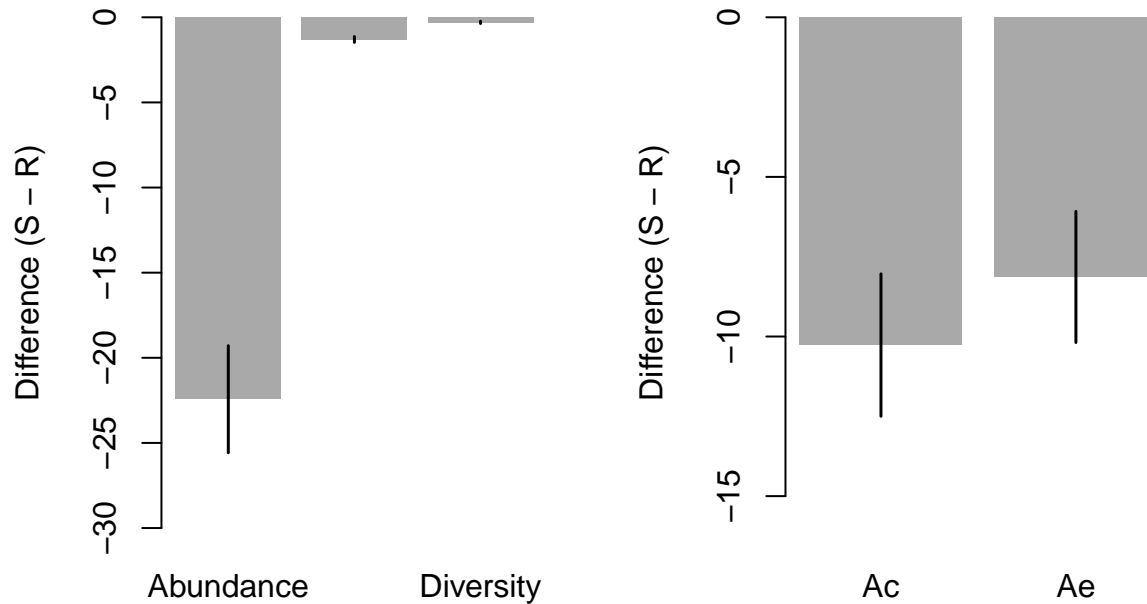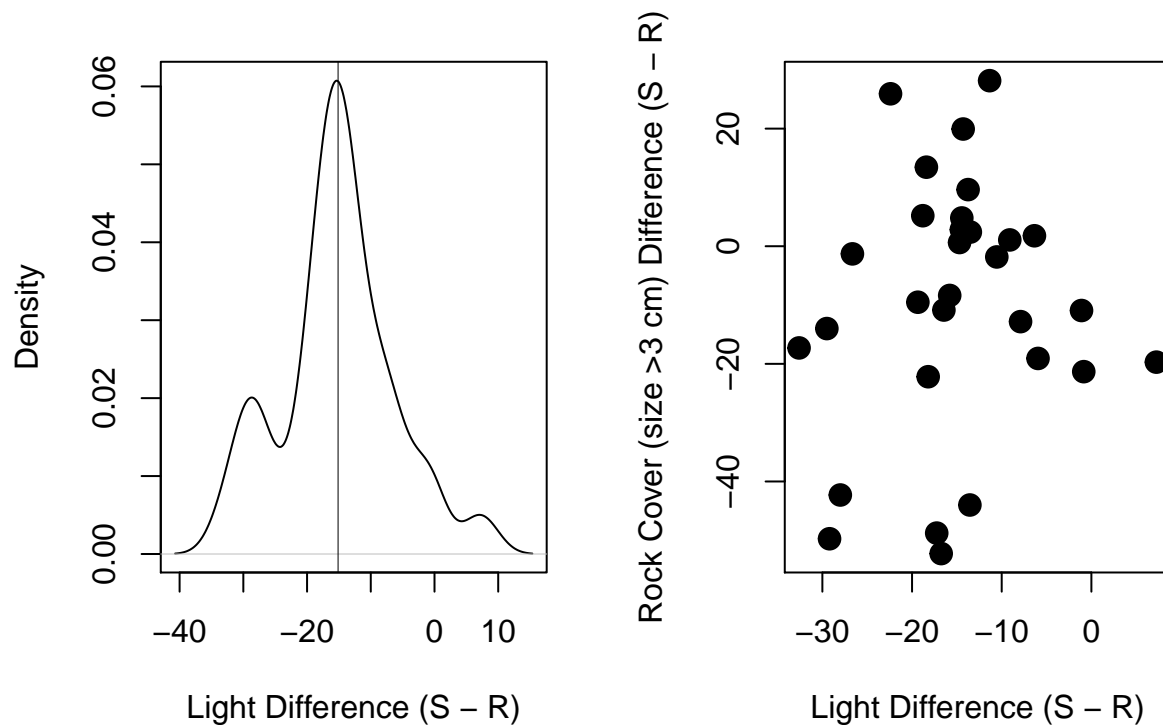
Similar to the ordination for the saxicole community, the NMDS ordination looks strange. This is possible due to the paired structure of the data as well. This should be handled with whatever ordination procedure is ultimately used.

```r
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
```

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