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 = "_")
```

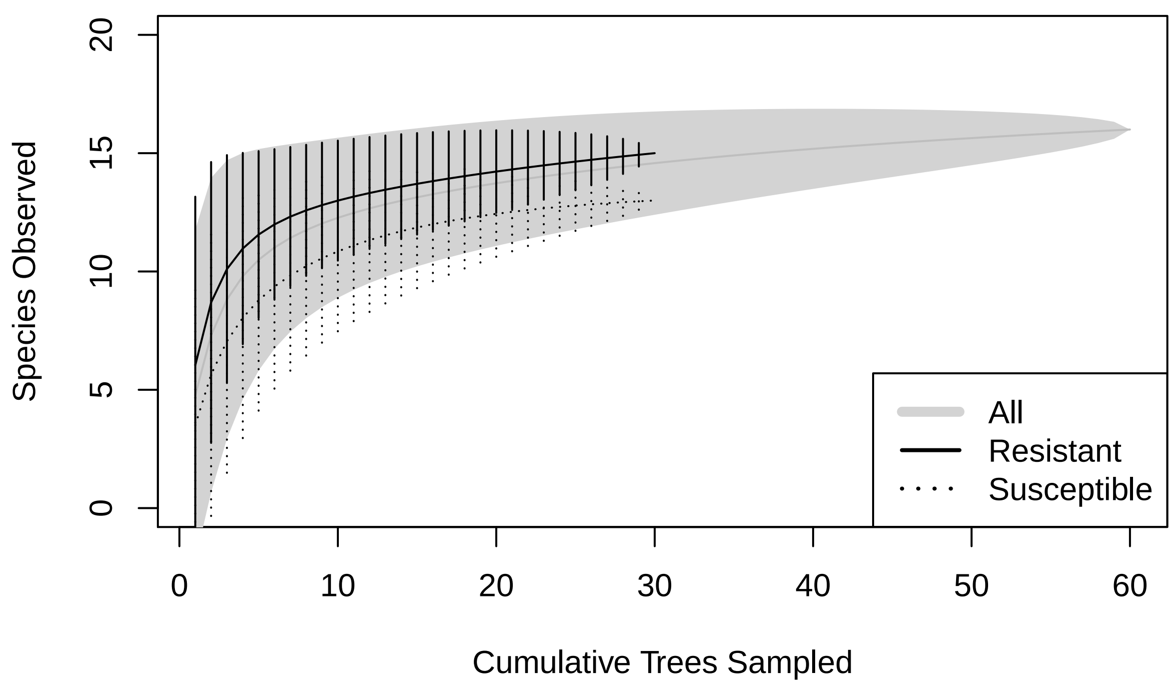
```r
rownames(com.moss) <- paste(l.dat[, "Moth"], l.dat[, "Tree.pairs"], sep = "_")
rownames(l.dat) <- paste(l.dat[, "Moth"], l.dat[, "Tree.pairs"], sep = "_")

## 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),
```

```r
     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()
```

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

Moth trees have different microenvironments

```r
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
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

```r
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)))
tt.arh <- apply(tt.arh[, 1:6], 2, as.numeric)
ard.mu <- rbind(tapply(abun, l.dat[, "Moth"], mean),
                tapply(rich, l.dat[, "Moth"], mean),
                tapply(shan, l.dat[, "Moth"], mean))
```

```
ard.se <- rbind(tapply(abun, l.dat[, "Moth"], se),
                tapply(rich, l.dat[, "Moth"], se),
                tapply(shan, l.dat[, "Moth"], se))
ard.tab <- cbind(ard.mu[, "0"], ard.se[, "0"],
                 ard.mu[, "1"], ard.se[, "1"])
colnames(ard.tab) <- c("Susceptible Mean", "Susceptible SE",
                       "Resistant Mean", "Resistant SE")
rownames(ard.tab) <- c("Abundance", "Richness", "Diversity (Shannon)")
```

```
kable(ard.tab, digits = 3)
```

	Susceptible Mean	Susceptible SE	Resistant Mean	Resistant SE
Abundance	1.210	0.351	2.754	0.567
Richness	3.500	0.542	6.033	0.662
Diversity (Shannon)	0.707	0.119	1.144	0.125

```
kable(tt.arh, digits = 3)
```

statistic.t	parameter.df	p.value	conf.int1	conf.int2	estimate.mean of x
-2.249	29	0.032	-2.948	-0.140	-1.544
-2.955	29	0.006	-4.287	-0.780	-2.533
-2.447	29	0.021	-0.802	-0.072	-0.437

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 = 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

```
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()
```

```
## pdf
##   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
dev.off()
```

```
## pdf
##   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()
```

```
## pdf
```

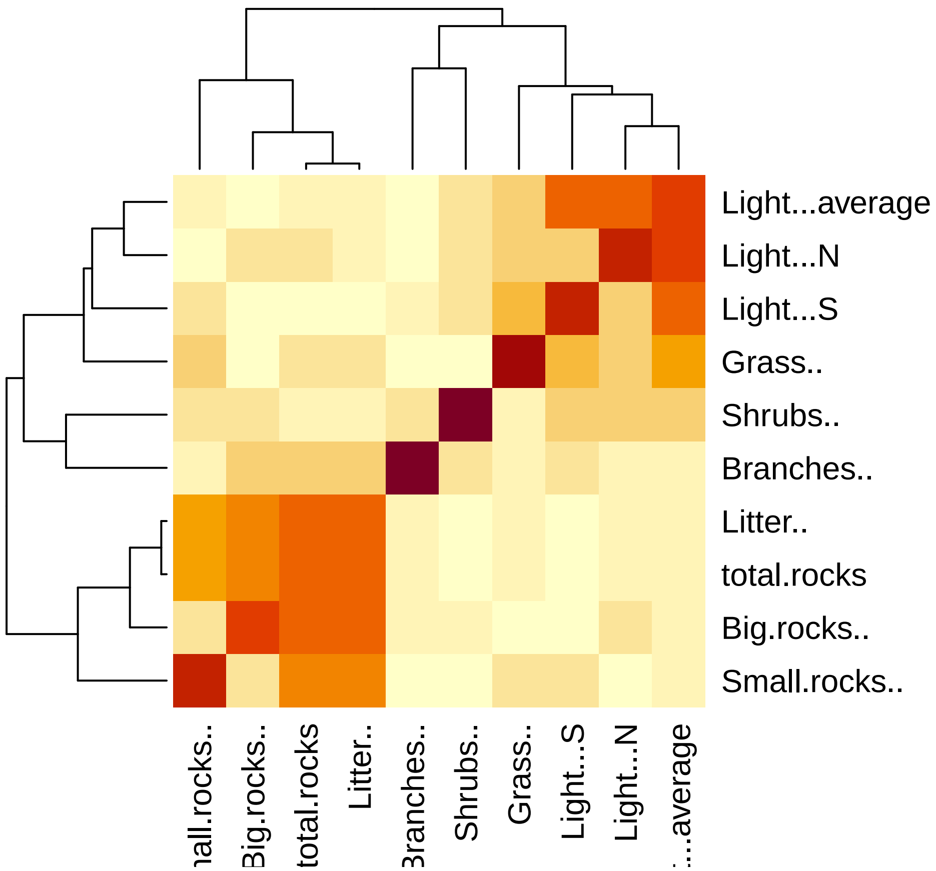
```
## 2
```

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

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

```r
                    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

```r
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.

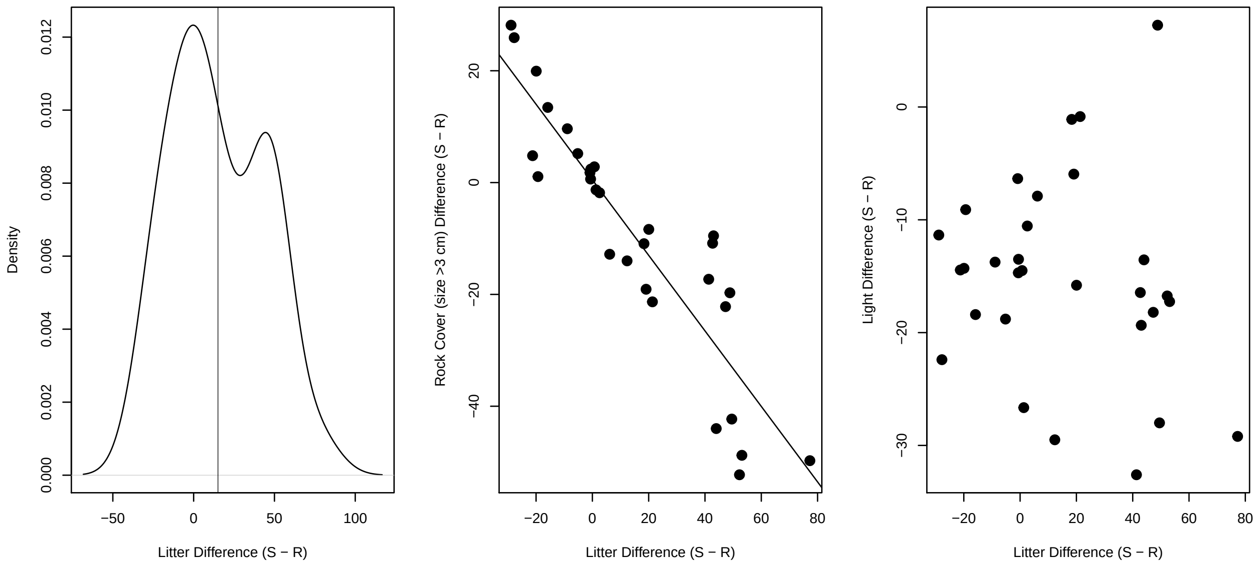
```
cor.test(env.dif[, "Big.rocks.."], env.dif[, "Litter.."])
```

```
##
##  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
```

```
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)
```



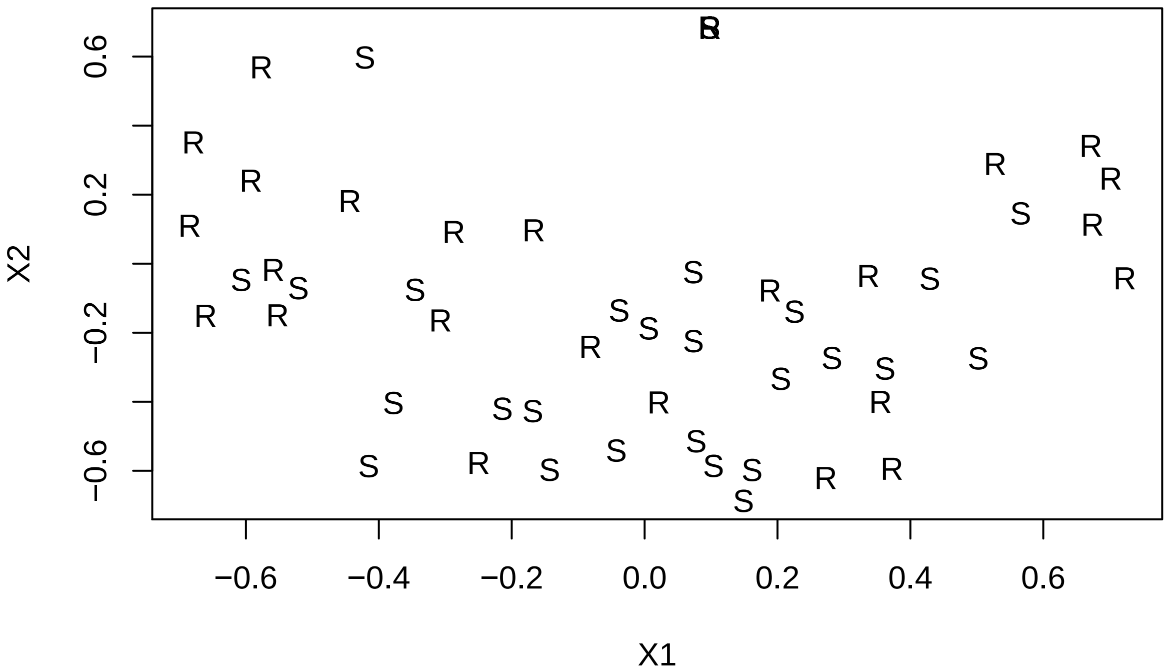

```r
pdf("./results/scrl_litter_effects.pdf", width = 10, height = 5)
par(mfrow = c(1,3))
plot(density(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)),
    main = "", xlab = "Litter Difference (S - R)")
abline(v = mean(tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)),
    lwd = 0.5)
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
```

```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.

```
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...averag
## 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
```

```r
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
```

```r
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])
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
```

```r
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
```

```r
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.abun <- v.dat[, "Vegetation.cover"]
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
```

```
v.ard.mu <- rbind(tapply(v.dat[, "Vegetation.cover"], l.dat[, "Moth"], mean),
                  tapply(rich, l.dat[, "Moth"], mean),
                  tapply(shan, l.dat[, "Moth"], mean))
v.ard.se <- rbind(tapply(v.dat[, "Vegetation.cover"], l.dat[, "Moth"], se),
                  tapply(rich, l.dat[, "Moth"], se),
                  tapply(shan, l.dat[, "Moth"], se))
v.ard.tab <- cbind(v.ard.mu[, "0"], v.ard.se[, "0"],
                     v.ard.mu[, "1"], v.ard.se[, "1"])
colnames(v.ard.tab) <- c("Susceptible Mean", "Susceptible SE",
                         "Resistant Mean", "Resistant SE")
rownames(v.ard.tab) <- c("Abundance", "Richness", "Diversity (Shannon)")
```

```
kable(v.ard.tab, digits = 3)
```

	Susceptible Mean	Susceptible SE	Resistant Mean	Resistant SE
Abundance	3.733	1.511	26.067	2.758
Richness	3.500	0.542	6.033	0.662
Diversity (Shannon)	0.707	0.119	1.144	0.125

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 14: 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 15: 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 16: 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 17: 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 18: 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 19: 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 20: 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
Rabbit.brush	-1.0000	29	0.3256	-0.6667	-2.0302	0.6968
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
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
Rosette.frisée	NaN	29	NaN	0.0000	NaN	NaN

	t	df	p-value	Mean Difference	Lower CI 95%	Upper CI 95%
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
Pinus.edulis.R	1.0000	29	0.3256	0.3333	-0.3484	1.0151

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
```

Structural Equation Modeling

```
library(piecewiseSEM)
library(distantia)

com.prepared <- cbind(id = l.dat[, "Moth"], tree  = l.dat[, "Tree.pairs"], com)
v.com.prepared <- cbind(id = l.dat[, "Moth"], tree  = l.dat[, "Tree.pairs"], v.com)

l.dist.euc <- distancePairedSamples(
    sequences = com.prepared,
    grouping.column = "id",
    time.column = "tree",
    exclude.columns = NULL,
    method = "euclidean",
    sum.distances = FALSE,
    parallel.execution = FALSE
)

l.dist.man <- distancePairedSamples(
    sequences = com.prepared,
    grouping.column = "id",
    time.column = "tree",
```

```r
    exclude.columns = NULL,
    method = "manhattan",
    sum.distances = FALSE,
    parallel.execution = FALSE
)

v.dist.euc <- distancePairedSamples(
    sequences = v.com.prepared,
    grouping.column = "id",
    time.column = "tree",
    exclude.columns = NULL,
    method = "euclidean",
    sum.distances = FALSE,
    parallel.execution = FALSE
)

v.dist.man <- distancePairedSamples(
    sequences = v.com.prepared,
    grouping.column = "id",
    time.column = "tree",
    exclude.columns = NULL,
    method = "manhattan",
    sum.distances = FALSE,
    parallel.execution = FALSE
)

cor(l.dist.man[[1]], l.dist.euc[[1]])
```

```
## [1] 0.9422796
```

```r
cor(v.dist.man[[1]], v.dist.euc[[1]])
```

```
## [1] 0.9612754
```

```r
d.litter <- tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)
d.rocks <- tapply((l.dat[, "Big.rocks.."] + l.dat[, "Small.rocks.."]),
                  l.dat[, "Tree.pairs"], diff)
d.light <- tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff)
d.com <- l.dist.man[[1]]
d.abun <- tapply(abun, l.dat[, "Tree.pairs"], diff)
d.rich <- tapply(rich, l.dat[, "Tree.pairs"], diff)
d.shan <- tapply(shan, l.dat[, "Tree.pairs"], diff)
d.isp <- apply(isp.com, 2, function(x, f) tapply(x, f, diff), f = l.dat[, "Tree.pairs"])
colnames(d.isp) <- paste("d", colnames(isp.com), sep = ".")

round(cor(cbind(d.litter, d.rocks, d.light, d.abun, d.rich, d.shan, d.com)), 3)
```

```
##          d.litter d.rocks d.light d.abun d.rich d.shan  d.com
## d.litter    1.000  -0.998  -0.171 -0.530 -0.695 -0.651  0.154
## d.rocks    -0.998   1.000   0.196  0.513  0.694  0.656 -0.140
## d.light    -0.171   0.196   1.000  0.108  0.268  0.290 -0.133
## d.abun     -0.530   0.513   0.108  1.000  0.649  0.353 -0.448
## d.rich     -0.695   0.694   0.268  0.649  1.000  0.888 -0.143
## d.shan     -0.651   0.656   0.290  0.353  0.888  1.000 -0.071
## d.com       0.154  -0.140  -0.133 -0.448 -0.143 -0.071  1.000
```

```
sem.dat <- data.frame(d.litter, d.rocks, d.light, d.abun, d.rich, d.shan, d.com, d.isp)
sem.path <- matrix(c(0, 1, 1, 0,
                     1, 0, 0, 1,
                     0, 0, 0, 1,
                     0, 0, 0, 0), 4, 4, byrow = TRUE)
rownames(sem.path) <- colnames(sem.path) <- c("d.litter", "d.light", "d.rocks", "d.com")

model.com  <- psem(lm(d.rocks ~ d.litter, sem.dat), lm(d.com ~ d.light + d.rocks, sem.dat))
model.com1  <- psem(lm(d.rocks ~ d.litter, sem.dat), lm(d.com ~ d.litter + d.light + d.rocks, sem.dat))
model.abun <- psem(lm(d.rocks ~ d.litter, sem.dat), lm(d.abun ~ d.light + d.rocks, sem.dat))
model.rich <- psem(lm(d.rocks ~ d.litter, sem.dat), lm(d.rich ~ d.light + d.rocks, sem.dat))
model.shan <- psem(lm(d.rocks ~ d.litter, sem.dat), lm(d.shan ~ d.light + d.rocks, sem.dat))
model.Acacon <- psem(lm(d.rocks ~ d.litter, sem.dat), lm(d.Acacon ~ d.light + d.rocks, sem.dat))
model.Acaame <- psem(lm(d.rocks ~ d.litter, sem.dat), lm(d.Acaame ~ d.light + d.rocks, sem.dat))
model.Canros <- psem(lm(d.rocks ~ d.litter, sem.dat), lm(d.Canros ~ d.light + d.rocks, sem.dat))
model.Canros1 <- psem(lm(d.rocks ~ d.litter, sem.dat),  lm(d.Canros ~ d.light + d.rocks, sem.dat))
```

```
d.litter <- tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff)
d.rocks <- tapply((l.dat[, "Big.rocks.."] + l.dat[, "Small.rocks.."]),
                  l.dat[, "Tree.pairs"], diff)
d.light <- tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff)

d.v.com <- v.dist.man[[1]]
d.v.abun <- tapply(v.abun, l.dat[, "Tree.pairs"], diff)
d.v.rich <- tapply(v.rich, l.dat[, "Tree.pairs"], diff)
d.v.shan <- tapply(v.shan, l.dat[, "Tree.pairs"], diff)
d.v.isp <- apply(v.isp.com, 2, function(x, f) tapply(x, f, diff), f = l.dat[, "Tree.pairs"])
colnames(d.v.isp) <- paste("d", colnames(v.isp.com), sep = ".")
v.sem.dat <- data.frame(d.litter, d.rocks, d.light, d.v.abun, d.v.rich, d.v.shan, d.v.com, d.v.isp)

model.v.com  <- psem(lm(d.rocks ~ d.litter, v.sem.dat), lm(d.v.com ~ d.light + d.rocks, v.sem.dat))
model.v.com1  <- psem(lm(d.rocks ~ d.litter, v.sem.dat), lm(d.v.com ~ d.litter + d.light + d.rocks, v.se
model.v.abun <- psem(lm(d.rocks ~ d.litter, v.sem.dat), lm(d.v.abun ~ d.light + d.rocks, v.sem.dat))
model.v.rich <- psem(lm(d.rocks ~ d.litter, v.sem.dat), lm(d.v.rich ~ d.light + d.rocks, v.sem.dat))
model.v.shan <- psem(lm(d.rocks ~ d.litter, v.sem.dat), lm(d.v.shan ~ d.light + d.rocks, v.sem.dat))
model.v.Apache.plume <- psem(lm(d.rocks ~ d.litter, v.sem.dat),
                             lm(d.Apache.plume ~ d.light + d.rocks, v.sem.dat))
model.v.Asteraceae.ovales <- psem(lm(d.rocks ~ d.litter, v.sem.dat),
                                  lm(d.Asteraceae.ovales ~ d.light + d.rocks, v.sem.dat))
```

Independent Test Method

Using indeendent tests for different effects along the hypothesized causal model that moth susceptibility affects tree traits (litter production), which affect the local environment (light, rocks), which in turn affect lichen, bryophyte and plant communities (abundance, richness, diversity, indicator species, composition).

moth-susceptibility -> tree traits -> local environment -> community

We can do this by parsing independent tests for each effect OR by using a structural equation model (SEM).

Testing for the effect of moth susceptibility:

```
t.test(d.litter)
```

```
##
```

```
## 	One Sample t-test
##
## data:  d.litter
## t = 2.8665, df = 29, p-value = 0.00765
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##   4.317792 25.822208
## sample estimates:
## mean of x
##     15.07
```

```r
t.test(d.light)
```

```
##
## 	One Sample t-test
##
## data:  d.light
## t = -9.2728, df = 29, p-value = 3.557e-10
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -18.47119 -11.79547
## sample estimates:
## mean of x
## -15.13333
```

```r
t.test(d.rocks)
```

```
##
## 	One Sample t-test
##
## data:  d.rocks
## t = -2.8178, df = 29, p-value = 0.008617
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -25.298305  -4.019028
## sample estimates:
## mean of x
## -14.65867
```

Effects of tree traits on local environment and environment correlations:

```r
cor.test(d.light, d.litter)
```

```
##
## 	Pearson's product-moment correlation
##
## data:  d.light and d.litter
## 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
```

```r
cor.test(d.rocks, d.light)
```

```
##
##  Pearson's product-moment correlation
##
## data:  d.rocks and d.light
## t = 1.0584, df = 28, p-value = 0.2989
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1766215  0.5196770
## sample estimates:
##       cor
## 0.1961275
```

```
summary(lm(d.rocks ~ d.litter))
```

```
##
## Call:
## lm(formula = d.rocks ~ d.litter)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.4466 -0.7468 -0.3273  0.2442  6.9590
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.22870    0.34616   0.661    0.514
## d.litter    -0.98788    0.01079 -91.529   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.674 on 28 degrees of freedom
## Multiple R-squared:  0.9967, Adjusted R-squared:  0.9965
## F-statistic:  8378 on 1 and 28 DF,  p-value: < 2.2e-16
```

Effects of local environment on lichen, and possible direct effects of tree traits:

```
summary(lm(d.abun ~ d.rocks))
```

```
##
## Call:
## lm(formula = d.abun ~ d.rocks)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7.8587 -1.3596  0.5429  1.6415  5.8098
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.55053    0.67673  -0.814  0.42279
## d.rocks      0.06777    0.02140   3.166  0.00371 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.284 on 28 degrees of freedom
## Multiple R-squared:  0.2637, Adjusted R-squared:  0.2374
## F-statistic: 10.03 on 1 and 28 DF,  p-value: 0.003706
```

```r
summary(lm(d.rich ~ d.rocks))
```

```
##
## Call:
## lm(formula = d.rich ~ d.rocks)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.7375 -2.3674 -0.1611  1.6950  7.5293
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.85626    0.70878  -1.208    0.237
## d.rocks      0.11441    0.02242   5.104 2.09e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.44 on 28 degrees of freedom
## Multiple R-squared:  0.4819, Adjusted R-squared:  0.4634
## F-statistic: 26.05 on 1 and 28 DF,  p-value: 2.089e-05
```

```r
summary(lm(d.shan ~ d.rocks))
```

```
##
## Call:
## lm(formula = d.shan ~ d.rocks)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.46785 -0.60402  0.04559  0.63369  1.38124
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.106623   0.154747  -0.689    0.496
## d.rocks      0.022537   0.004894   4.605 8.17e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.751 on 28 degrees of freedom
## Multiple R-squared:  0.4309, Adjusted R-squared:  0.4106
## F-statistic:  21.2 on 1 and 28 DF,  p-value: 8.167e-05
```

```r
summary(lm(d.Acacon ~ d.rocks, sem.dat))
```

```
##
## Call:
## lm(formula = d.Acacon ~ d.rocks, data = sem.dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.17556 -0.01439  0.01337  0.03252  0.09108
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.0238762  0.0126055  -1.894  0.06858 .
```

```
## d.rocks      0.0014183  0.0003987   3.557  0.00136 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06117 on 28 degrees of freedom
## Multiple R-squared:  0.3113, Adjusted R-squared:  0.2867
## F-statistic: 12.66 on 1 and 28 DF,  p-value: 0.001357
```

```
summary(lm(d.Acaame ~ d.rocks, sem.dat))
```

```
##
## Call:
## lm(formula = d.Acaame ~ d.rocks, data = sem.dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.64206 -0.09675  0.03298  0.07873  0.56715
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.068167   0.042641  -1.599    0.121
## d.rocks      0.006310   0.001349   4.679 6.67e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2069 on 28 degrees of freedom
## Multiple R-squared:  0.4388, Adjusted R-squared:  0.4188
## F-statistic: 21.89 on 1 and 28 DF,  p-value: 6.669e-05
```

```
summary(lm(d.Canros ~ d.rocks, sem.dat))
```

```
##
## Call:
## lm(formula = d.Canros ~ d.rocks, data = sem.dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.04560 -0.22148  0.06461  0.28602  0.81105
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.196087   0.096385  -2.034 0.051479 .
## d.rocks      0.012797   0.003048   4.198 0.000247 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4678 on 28 degrees of freedom
## Multiple R-squared:  0.3863, Adjusted R-squared:  0.3643
## F-statistic: 17.62 on 1 and 28 DF,  p-value: 0.0002467
```

```
summary(lm(d.abun ~ d.light))
```

```
##
## Call:
## lm(formula = d.abun ~ d.light)
##
```

```
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.3371 -2.7395  0.6687  1.5171  8.1163
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.85872    1.38331  -0.621    0.540
## d.light      0.04528    0.07905   0.573    0.571
##
## Residual standard error: 3.805 on 28 degrees of freedom
## Multiple R-squared:  0.01159,    Adjusted R-squared:  -0.02372
## F-statistic: 0.3282 on 1 and 28 DF,  p-value: 0.5713
```

```
summary(lm(d.rich ~ d.light))
```

```
##
## Call:
## lm(formula = d.rich ~ d.light)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -6.758 -3.199 -0.836  3.003 12.001
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.40551    1.67397  -0.242    0.810
## d.light      0.14061    0.09565   1.470    0.153
##
## Residual standard error: 4.605 on 28 degrees of freedom
## Multiple R-squared:  0.07164,    Adjusted R-squared:  0.03848
## F-statistic: 2.161 on 1 and 28 DF,  p-value: 0.1527
```

```
summary(lm(d.shan ~ d.light))
```

```
##
## Call:
## lm(formula = d.shan ~ d.light)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.5927 -0.7784  0.1074  0.5385  2.1225
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.04306    0.34638   0.124    0.902
## d.light      0.03172    0.01979   1.603    0.120
##
## Residual standard error: 0.9528 on 28 degrees of freedom
## Multiple R-squared:  0.08402,    Adjusted R-squared:  0.05131
## F-statistic: 2.568 on 1 and 28 DF,  p-value: 0.1202
```

```
summary(lm(d.Acacon ~ d.light, sem.dat))
```

```
##
## Call:
## lm(formula = d.Acacon ~ d.light, data = sem.dat)
```

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.21083 -0.02561  0.02198  0.04135  0.09381
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.007098   0.024294   0.292   0.7723
## d.light     0.003421   0.001388   2.464   0.0201 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06682 on 28 degrees of freedom
## Multiple R-squared:  0.1782, Adjusted R-squared:  0.1489
## F-statistic: 6.072 on 1 and 28 DF,  p-value: 0.02014
```

```
summary(lm(d.Acaame ~ d.light, sem.dat))
```

```
##
## Call:
## lm(formula = d.Acaame ~ d.light, data = sem.dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.85875 -0.06371  0.06088  0.15869  0.27225
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.03200    0.09117   0.351   0.7283
## d.light      0.01273    0.00521   2.444   0.0211 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2508 on 28 degrees of freedom
## Multiple R-squared:  0.1758, Adjusted R-squared:  0.1463
## F-statistic: 5.972 on 1 and 28 DF,  p-value: 0.0211
```

```
summary(lm(d.Canros ~ d.light, sem.dat))
```

```
##
## Call:
## lm(formula = d.Canros ~ d.light, data = sem.dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.9699 -0.3253  0.1547  0.3191  1.2307
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.03300    0.19704   0.168    0.868
## d.light      0.02753    0.01126   2.445    0.021 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.542 on 28 degrees of freedom
```

```
## Multiple R-squared:  0.176,  Adjusted R-squared:  0.1466
## F-statistic:  5.98 on 1 and 28 DF,  p-value: 0.02101
```

```r
summary(lm(d.abun ~ d.litter))
```

```
##
## Call:
## lm(formula = d.abun ~ d.litter)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -7.380 -1.218  0.494  1.607  5.733
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.50153    0.67144  -0.747  0.46132
## d.litter    -0.06917    0.02094  -3.304  0.00261 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.246 on 28 degrees of freedom
## Multiple R-squared:  0.2805, Adjusted R-squared:  0.2548
## F-statistic: 10.92 on 1 and 28 DF,  p-value: 0.002612
```

```r
summary(lm(d.rich ~ d.litter))
```

```
##
## Call:
## lm(formula = d.rich ~ d.litter)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.7618 -2.0890 -0.0954  1.7166  7.5545
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.82616    0.71101  -1.162    0.255
## d.litter    -0.11328    0.02217  -5.110 2.05e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.438 on 28 degrees of freedom
## Multiple R-squared:  0.4826, Adjusted R-squared:  0.4641
## F-statistic: 26.11 on 1 and 28 DF,  p-value: 2.053e-05
```

```r
summary(lm(d.shan ~ d.litter))
```

```
##
## Call:
## lm(formula = d.shan ~ d.litter)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.47085 -0.59769  0.03512  0.59650  1.39944
##
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.103513   0.156232  -0.663    0.513
## d.litter    -0.022128   0.004871  -4.543 9.68e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7554 on 28 degrees of freedom
## Multiple R-squared:  0.4243, Adjusted R-squared:  0.4037
## F-statistic: 20.64 on 1 and 28 DF,  p-value: 9.675e-05
```

```
summary(lm(d.Acacon ~ d.litter, sem.dat))
```

```
##
## Call:
## lm(formula = d.Acacon ~ d.litter, data = sem.dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.17743 -0.01528  0.01435  0.03220  0.09098
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.0240028  0.0127820  -1.878  0.07085 .
## d.litter    -0.0013712  0.0003985  -3.441  0.00184 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0618 on 28 degrees of freedom
## Multiple R-squared:  0.2971, Adjusted R-squared:  0.272
## F-statistic: 11.84 on 1 and 28 DF,  p-value: 0.001839
```

```
summary(lm(d.Acaame ~ d.litter, sem.dat))
```

```
##
## Call:
## lm(formula = d.Acaame ~ d.litter, data = sem.dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.64969 -0.10426  0.03407  0.08146  0.56925
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.067611   0.043169  -1.566    0.129
## d.litter    -0.006175   0.001346  -4.588 8.56e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2087 on 28 degrees of freedom
## Multiple R-squared:  0.4291, Adjusted R-squared:  0.4087
## F-statistic: 21.05 on 1 and 28 DF,  p-value: 8.558e-05
```

```
summary(lm(d.Canros ~ d.litter, sem.dat))
```

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

```
## lm(formula = d.Canros ~ d.litter, data = sem.dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.06651 -0.21741  0.05103  0.27634  0.81235
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.193646   0.097001  -1.996 0.055705 .
## d.litter    -0.012609   0.003024  -4.169 0.000267 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.469 on 28 degrees of freedom
## Multiple R-squared:  0.383,  Adjusted R-squared:  0.361
## F-statistic: 17.38 on 1 and 28 DF,  p-value: 0.0002666
```

SEM testing for this pathway, note that here community distance is the sum of squared differences for each tree pair (susceptible - resistant) for all species:

```
summary(model.abun, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.abun
##
## Call:
##   d.rocks ~ d.litter
##   d.abun ~ d.light + d.rocks
##
##     AIC      BIC
##  28.447   38.255
##
## ---
## Tests of directed separation:
##
##            Independ.Claim Test.Type DF Crit.Value P.Value
##   d.abun ~ d.litter + ...      coef 26    -2.1260  0.0432 *
##   d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 14.447 with P-value = 0.006 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##     d.abun   d.light   0.0030    0.0709 27     0.0428  0.9662       0.0072
##     d.abun   d.rocks   0.0676    0.0222 27     3.0408  0.0052       0.5121  **
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
```

```
##
##   Response method R.squared
##    d.rocks   none      1.00
##     d.abun   none      0.26
```

```r
summary(model.rich, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.rich
##
## Call:
##   d.rocks ~ d.litter
##   d.rich ~ d.light + d.rocks
##
##     AIC      BIC
##  23.564   33.372
##
## ---
## Tests of directed separation:
##
##            Independ.Claim Test.Type DF Crit.Value P.Value
##   d.rich ~ d.litter + ...      coef 26    -0.6906  0.4960
##   d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 9.564 with P-value = 0.048 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##     d.rich   d.light   0.0718    0.0729 27     0.9854  0.3332       0.1368
##     d.rich   d.rocks   0.1100    0.0229 27     4.8086  0.0001       0.6674 ***
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##   Response method R.squared
##    d.rocks   none       1.0
##     d.rich   none       0.5
```

```r
summary(model.shan, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.shan
##
## Call:
##   d.rocks ~ d.litter
##   d.shan ~ d.light + d.rocks
##
##     AIC      BIC
```

```
##  22.182   31.99
##
## ---
## Tests of directed separation:
##
##            Independ.Claim Test.Type DF Crit.Value P.Value
##   d.shan ~ d.litter + ...      coef 26    -0.0130  0.9897
##   d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 8.182 with P-value = 0.085 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##     d.shan   d.light   0.0183    0.0158 27     1.1596  0.2563       0.1676
##     d.shan   d.rocks   0.0214    0.0050 27     4.3156  0.0002       0.6236 ***
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##   Response method R.squared
##    d.rocks   none      1.00
##     d.shan   none      0.46
```

```
summary(model.com, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.com
##
## Call:
##   d.rocks ~ d.litter
##   d.com ~ d.light + d.rocks
##
##     AIC      BIC
##  27.066   36.874
##
## ---
## Tests of directed separation:
##
##            Independ.Claim Test.Type DF Crit.Value P.Value
##    d.com ~ d.litter + ...      coef 26     1.7840  0.0861
##   d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 13.066 with P-value = 0.011 and on 4 degrees of freedom
##
## ---
## Coefficients:
```

```
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##      d.com   d.light  -0.0350    0.0617 27    -0.5673  0.5752      -0.1096
##      d.com   d.rocks  -0.0119    0.0193 27    -0.6129  0.5450      -0.1184
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##   Response method R.squared
##    d.rocks   none      1.00
##      d.com   none      0.03
```

```
summary(model.Acacon, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.Acacon
##
## Call:
##   d.rocks ~ d.litter
##   d.Acacon ~ d.light + d.rocks
##
##     AIC      BIC
##  23.133   32.941
##
## ---
## Tests of directed separation:
##
##              Independ.Claim Test.Type DF Crit.Value P.Value
##   d.Acacon ~ d.litter + ...      coef 26     0.5085  0.6154
##     d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 9.133 with P-value = 0.058 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##   d.Acacon   d.light   0.0026    0.0012 27     2.1628  0.0396       0.3252   *
##   d.Acacon   d.rocks   0.0013    0.0004 27     3.2863  0.0028       0.4941  **
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##   Response method R.squared
##    d.rocks   none      1.00
##   d.Acacon   none      0.41
```

```r
summary(model.Acaame, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.Acaame
##
## Call:
##   d.rocks ~ d.litter
##   d.Acaame ~ d.light + d.rocks
##
##     AIC      BIC
##  22.423   32.231
##
## ---
## Tests of directed separation:
##
##              Independ.Claim Test.Type DF Crit.Value P.Value
##   d.Acaame ~ d.litter + ...      coef 26    -0.1558  0.8774
##     d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 8.423 with P-value = 0.077 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##   d.Acaame   d.light   0.0091    0.0041 27     2.2267  0.0345       0.3009   *
##   d.Acaame   d.rocks   0.0057    0.0013 27     4.4650  0.0001       0.6034 ***
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##   Response method R.squared
##    d.rocks   none      1.00
##   d.Acaame   none      0.53
```

```r
summary(model.Canros, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.Canros
##
## Call:
##   d.rocks ~ d.litter
##   d.Canros ~ d.light + d.rocks
##
##     AIC      BIC
##  23.898   33.706
##
## ---
## Tests of directed separation:
```

```
##
##              Independ.Claim Test.Type DF Crit.Value P.Value
##   d.Canros ~ d.litter + ...      coef 26    -0.8201  0.4196
##     d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 9.898 with P-value = 0.042 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##   d.Canros   d.light   0.0203    0.0093 27     2.1836  0.0379       0.3095   *
##   d.Canros   d.rocks   0.0115    0.0029 27     3.9562  0.0005       0.5608 ***
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##   Response method R.squared
##    d.rocks   none      1.00
##   d.Canros   none      0.48
```

```r
summary(lm(d.v.abun ~ d.rocks))
```

```
##
## Call:
## lm(formula = d.v.abun ~ d.rocks)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -46.548  -9.167  -0.371  11.836  29.860
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -23.61098    3.52322  -6.702 2.83e-07 ***
## d.rocks      -0.08716    0.11143  -0.782    0.441
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.1 on 28 degrees of freedom
## Multiple R-squared:  0.02138,    Adjusted R-squared:  -0.01357
## F-statistic: 0.6118 on 1 and 28 DF,  p-value: 0.4407
```

```r
summary(lm(d.v.rich ~ d.rocks))
```

```
##
## Call:
## lm(formula = d.v.rich ~ d.rocks)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -1.6195 -0.7375  0.2342  0.3760  2.3148
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.259773   0.199030  -6.330 7.57e-07 ***
## d.rocks      0.002744   0.006295   0.436    0.666
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9659 on 28 degrees of freedom
## Multiple R-squared:  0.006742,   Adjusted R-squared:  -0.02873
## F-statistic: 0.1901 on 1 and 28 DF,  p-value: 0.6662
```

```r
summary(lm(d.v.shan ~ d.rocks))
```

```
##
## Call:
## lm(formula = d.v.shan ~ d.rocks)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.63077 -0.28155  0.02544  0.29568  0.97384
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.335709   0.078745  -4.263 0.000207 ***
## d.rocks     -0.002745   0.002491  -1.102 0.279691
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3821 on 28 degrees of freedom
## Multiple R-squared:  0.04159,    Adjusted R-squared:  0.007366
## F-statistic: 1.215 on 1 and 28 DF,  p-value: 0.2797
```

```r
summary(lm(d.Apache.plume ~ d.rocks, v.sem.dat))
```

```
##
## Call:
## lm(formula = d.Apache.plume ~ d.rocks, data = v.sem.dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -28.028  -4.455   4.278   6.677  14.799
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -12.13756    2.44690  -4.960 3.09e-05 ***
## d.rocks      -0.12763    0.07739  -1.649     0.11
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.87 on 28 degrees of freedom
## Multiple R-squared:  0.08854,    Adjusted R-squared:  0.05598
## F-statistic:  2.72 on 1 and 28 DF,  p-value: 0.1103
```

```r
summary(lm(d.Asteraceae.ovales ~ d.rocks, v.sem.dat))
```

```
##
## Call:
## lm(formula = d.Asteraceae.ovales ~ d.rocks, data = v.sem.dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -31.976  -7.315   5.782   7.526  19.463
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -7.44665    2.34354  -3.178   0.0036 **
## d.rocks      0.04684    0.07412   0.632   0.5325
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.37 on 28 degrees of freedom
## Multiple R-squared:  0.01406,    Adjusted R-squared:  -0.02115
## F-statistic: 0.3994 on 1 and 28 DF,  p-value: 0.5325
```

```r
summary(lm(d.v.abun ~ d.litter))
```

```
##
## Call:
## lm(formula = d.v.abun ~ d.litter)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -46.743  -8.907   0.019  11.943  30.269
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -23.44568    3.54674  -6.610  3.6e-07 ***
## d.litter      0.07381    0.11059   0.667     0.51
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.15 on 28 degrees of freedom
## Multiple R-squared:  0.01566,    Adjusted R-squared:  -0.01949
## F-statistic: 0.4455 on 1 and 28 DF,  p-value: 0.5099
```

```r
summary(lm(d.v.rich ~ d.litter))
```

```
##
## Call:
## lm(formula = d.v.rich ~ d.litter)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.6111 -0.7427  0.2214  0.3838  2.3153
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.253709   0.199585  -6.282 8.61e-07 ***
```

```
## d.litter    -0.003072   0.006223  -0.494    0.625
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.965 on 28 degrees of freedom
## Multiple R-squared:  0.008626,   Adjusted R-squared:  -0.02678
## F-statistic: 0.2436 on 1 and 28 DF,  p-value: 0.6254
```

```r
summary(lm(d.v.shan ~ d.litter))
```

```
##
## Call:
## lm(formula = d.v.shan ~ d.litter)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.62023 -0.28853  0.04059  0.29668  0.97632
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.332721   0.079334  -4.194 0.000249 ***
## d.litter     0.002472   0.002474   0.999 0.326145
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3836 on 28 degrees of freedom
## Multiple R-squared:  0.03444,    Adjusted R-squared:  -3.912e-05
## F-statistic: 0.9989 on 1 and 28 DF,  p-value: 0.3261
```

```r
summary(lm(d.Apache.plume ~ d.litter, v.sem.dat))
```

```
##
## Call:
## lm(formula = d.Apache.plume ~ d.litter, data = v.sem.dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -28.098  -4.465   4.364   6.975  14.577
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -12.05623    2.46985  -4.881 3.84e-05 ***
## d.litter      0.11875    0.07701   1.542    0.134
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.94 on 28 degrees of freedom
## Multiple R-squared:  0.07828,    Adjusted R-squared:  0.04536
## F-statistic: 2.378 on 1 and 28 DF,  p-value: 0.1343
```

```r
summary(lm(d.Asteraceae.ovales ~ d.litter, v.sem.dat))
```

```
##
## Call:
## lm(formula = d.Asteraceae.ovales ~ d.litter, data = v.sem.dat)
##
```

```
## Residuals:
##     Min      1Q  Median      3Q     Max
## -32.006  -7.296   5.653   7.482  19.553
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -7.36833    2.34896  -3.137  0.00399 **
## d.litter    -0.05076    0.07324  -0.693  0.49395
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.36 on 28 degrees of freedom
## Multiple R-squared:  0.01687,    Adjusted R-squared:  -0.01824
## F-statistic: 0.4804 on 1 and 28 DF,  p-value: 0.494
```

```r
summary(lm(d.v.abun ~ d.light))
```

```
##
## Call:
## lm(formula = d.v.abun ~ d.light)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -47.204  -7.755   1.085  11.993  31.908
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -23.8611     6.2747  -3.803 0.000711 ***
## d.light      -0.1010     0.3585  -0.282 0.780349
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.26 on 28 degrees of freedom
## Multiple R-squared:  0.002823,   Adjusted R-squared:  -0.03279
## F-statistic: 0.07928 on 1 and 28 DF,  p-value: 0.7803
```

```r
summary(lm(d.v.rich ~ d.light))
```

```
##
## Call:
## lm(formula = d.v.rich ~ d.light)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.7203 -0.7086  0.2372  0.4718  2.3085
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.10636    0.34979  -3.163  0.00374 **
## d.light      0.01280    0.01999   0.640  0.52727
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9622 on 28 degrees of freedom
## Multiple R-squared:  0.01443,    Adjusted R-squared:  -0.02077
```

```
## F-statistic: 0.4098 on 1 and 28 DF,  p-value: 0.5273
```

```r
summary(lm(d.v.shan ~ d.light))
```

```
##
## Call:
## lm(formula = d.v.shan ~ d.light)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5917 -0.3570  0.1214  0.2817  0.9857
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.362101   0.141162  -2.565    0.016 *
## d.light     -0.004403   0.008066  -0.546    0.589
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3883 on 28 degrees of freedom
## Multiple R-squared:  0.01053,    Adjusted R-squared:  -0.02481
## F-statistic: 0.298 on 1 and 28 DF,  p-value: 0.5895
```

```r
summary(lm(d.Apache.plume ~ d.light, v.sem.dat))
```

```
##
## Call:
## lm(formula = d.Apache.plume ~ d.light, data = v.sem.dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -33.062  -4.319   4.807   9.297  16.737
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -14.6411     4.4197  -3.313  0.00256 **
## d.light      -0.2891     0.2525  -1.145  0.26208
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.16 on 28 degrees of freedom
## Multiple R-squared:  0.0447, Adjusted R-squared:  0.01058
## F-statistic:  1.31 on 1 and 28 DF,  p-value: 0.2621
```

```r
summary(lm(d.Asteraceae.ovales ~ d.light, v.sem.dat))
```

```
##
## Call:
## lm(formula = d.Asteraceae.ovales ~ d.light, data = v.sem.dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -31.874  -6.867   6.133   8.134  18.131
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept) -8.1407349  4.1640687  -1.955   0.0606 .
## d.light     -0.0004891  0.2379432  -0.002   0.9984
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.45 on 28 degrees of freedom
## Multiple R-squared:  1.509e-07,  Adjusted R-squared:  -0.03571
## F-statistic: 4.225e-06 on 1 and 28 DF,  p-value: 0.9984
```

```r
summary(model.v.com, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.v.com
##
## Call:
##   d.rocks ~ d.litter
##   d.v.com ~ d.light + d.rocks
##
##     AIC      BIC
##  28.300   38.108
##
## ---
## Tests of directed separation:
##
##             Independ.Claim Test.Type DF Crit.Value P.Value
##   d.v.com ~ d.litter + ...      coef 26     2.0909  0.0465 *
##    d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 14.3 with P-value = 0.006 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##    d.v.com   d.light   0.0177    0.3475 27     0.0508  0.9598       0.0099
##    d.v.com   d.rocks   0.0595    0.1090 27     0.5453  0.5900       0.1064
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##   Response method R.squared
##    d.rocks   none      1.00
##    d.v.com   none      0.01
```

```r
summary(model.v.abun, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.v.abun
##
## Call:
```

```
##   d.rocks ~ d.litter
##   d.v.abun ~ d.light + d.rocks
## 
##     AIC      BIC
##  28.663   38.471
## 
## ---
## Tests of directed separation:
## 
##              Independ.Claim Test.Type DF Crit.Value P.Value  
##   d.v.abun ~ d.litter + ...      coef 26    -2.1770  0.0387 *
##     d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
## 
## Global goodness-of-fit:
## 
##   Fisher's C = 14.663 with P-value = 0.005 and on 4 degrees of freedom
## 
## ---
## Coefficients:
## 
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate    
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##   d.v.abun   d.light  -0.0483    0.3688 27    -0.1310  0.8967      -0.0254    
##   d.v.abun   d.rocks  -0.0842    0.1157 27    -0.7277  0.4731      -0.1412    
## 
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
## 
## ---
## Individual R-squared:
## 
##   Response method R.squared
##    d.rocks   none      1.00
##   d.v.abun   none      0.02
```

```r
summary(model.v.rich, .progressBar = FALSE)
```

```
## 
## Structural Equation Model of model.v.rich 
## 
## Call:
##   d.rocks ~ d.litter
##   d.v.rich ~ d.light + d.rocks
## 
##     AIC      BIC
##  25.623   35.431
## 
## ---
## Tests of directed separation:
## 
##              Independ.Claim Test.Type DF Crit.Value P.Value  
##   d.v.rich ~ d.litter + ...      coef 26    -1.3873  0.1771  
##     d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
## 
## Global goodness-of-fit:
## 
```

```
##   Fisher's C = 11.623 with P-value = 0.02 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##   d.v.rich   d.light   0.0115    0.0207 27     0.5561  0.5827       0.1082
##   d.v.rich   d.rocks   0.0020    0.0065 27     0.3131  0.7566       0.0609
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##   Response method R.squared
##    d.rocks   none      1.00
##   d.v.rich   none      0.02
```

```r
summary(model.v.shan, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.v.shan
##
## Call:
##   d.rocks ~ d.litter
##   d.v.shan ~ d.light + d.rocks
##
##     AIC      BIC
##  26.895   36.703
##
## ---
## Tests of directed separation:
##
##              Independ.Claim Test.Type DF Crit.Value P.Value
##   d.v.shan ~ d.litter + ...      coef 26    -1.7395  0.0938
##     d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 12.895 with P-value = 0.012 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##   Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##    d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983 ***
##   d.v.shan   d.light  -0.0028    0.0082 27    -0.3397  0.7367      -0.0651
##   d.v.shan   d.rocks  -0.0026    0.0026 27    -0.9971  0.3276      -0.1912
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
```

```
##   Response method R.squared
##    d.rocks   none      1.00
##   d.v.shan   none      0.05
```

```r
summary(model.v.Apache.plume, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.v.Apache.plume
##
## Call:
##   d.rocks ~ d.litter
##   d.Apache.plume ~ d.light + d.rocks
##
##     AIC      BIC
##  25.830   35.638
##
## ---
## Tests of directed separation:
##
##                    Independ.Claim Test.Type DF Crit.Value P.Value
##   d.Apache.plume ~ d.litter + ...      coef 26    -1.4474  0.1597
##           d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 11.83 with P-value = 0.019 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##         Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
##          d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000      -0.9983
##   d.Apache.plume   d.light  -0.2176    0.2527 27    -0.8611  0.3968      -0.1592
##   d.Apache.plume   d.rocks  -0.1142    0.0793 27    -1.4408  0.1611      -0.2663
##
##   ***
##
##
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##         Response method R.squared
##          d.rocks   none      1.00
##   d.Apache.plume   none      0.11
```

```r
summary(model.v.Asteraceae.ovales, .progressBar = FALSE)
```

```
##
## Structural Equation Model of model.v.Asteraceae.ovales
##
## Call:
##   d.rocks ~ d.litter
```

```
##   d.Asteraceae.ovales ~ d.light + d.rocks
##
##     AIC      BIC
##  24.690   34.498
##
## ---
## Tests of directed separation:
##
##                          Independ.Claim Test.Type DF Crit.Value P.Value
##   d.Asteraceae.ovales ~ d.litter + ...      coef 26    -1.0976  0.2824
##                d.rocks ~ d.light + ...      coef 27     2.5465  0.0169 *
##
## Global goodness-of-fit:
##
##   Fisher's C = 10.69 with P-value = 0.03 and on 4 degrees of freedom
##
## ---
## Coefficients:
##
##              Response Predictor Estimate Std.Error DF Crit.Value P.Value
##               d.rocks  d.litter  -0.9879    0.0108 28   -91.5294  0.0000
##   d.Asteraceae.ovales   d.light  -0.0310    0.2453 27    -0.1262  0.9005
##   d.Asteraceae.ovales   d.rocks   0.0488    0.0770 27     0.6335  0.5317
##   Std.Estimate
##        -0.9983 ***
##        -0.0246
##         0.1234
##
##   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## ---
## Individual R-squared:
##
##              Response method R.squared
##               d.rocks   none      1.00
##   d.Asteraceae.ovales   none      0.01
```