

Sunset Crater Rock Lichen Analyses

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1 Notes on data analyses

My overall approach here is to analyze what I'm referring to as univariate (i.e., abundance, richness and diversity) and multivariate community statistics.

* I removed dead trees from the analysis. They did not correlate well with moth susceptibility and unnecessarily complicated analyses.

I first proceed through the analyses of the univariate and multivariate statistics using moth susceptibility (variable name = `Moth`) as a single predictor. This allows us to first see if there is some potential effect of moth susceptibility. Here, I did use the pairing scheme (variable name = `Tree.pairs`) in the analyses to factor out environmental noise.

I then conducted a series of analyses looking at the relationship between moth susceptibility and various factors that had good correlations with the community composition based on vector analysis of the NMS ordination.

Next, I used multiple regressions and PerMANOVA to look at the effects of these factors on the univariate and multivariate community response variables.

Last, I used SEM (Structural Equation Modeling) to begin to tease apart a mechanistic story of how moth susceptibility affects the rock lichen/moss community. Since tree pairing did not have a statistically significant effect on community composition or show any relationship with any of the other predictor variables, I did not include it in any of the SEMs. This will only make the results conservative, because we are not using it to account for environmental variation.

```
> summary(com)
```

Acacon		Acasup		Acaobp		Sterile.sp	
Min.	:0.00000	Min.	:0.00	Min.	:0.0000	Min.	:0.000
1st Qu.:	:0.00000	1st Qu.:	:0.00	1st Qu.:	:0.0000	1st Qu.:	:0.000
Median	:0.00000	Median	:0.05	Median	:0.0000	Median	:0.000
Mean	:0.02833	Mean	:0.14	Mean	:0.1493	Mean	:0.001
3rd Qu.:	:0.02500	3rd Qu.:	:0.17	3rd Qu.:	:0.0200	3rd Qu.:	:0.000
Max.	:0.26000	Max.	:1.04	Max.	:8.0000	Max.	:0.060

Brown.cr		Lobalp		Canros		Calare	
Min.	:0	Min.	:0.000000	Min.	:0.0000	Min.	:0.00000
1st Qu.:	:0	1st Qu.:	:0.000000	1st Qu.:	:0.0000	1st Qu.:	:0.00000
Median	:0	Median	:0.000000	Median	:0.1400	Median	:0.00000
Mean	:0	Mean	:0.002333	Mean	:0.3202	Mean	:0.01967
3rd Qu.:	:0	3rd Qu.:	:0.000000	3rd Qu.:	:0.4225	3rd Qu.:	:0.00000
Max.	:0	Max.	:0.040000	Max.	:1.7000	Max.	:0.56000

Phydub		Rhichr		Xanlin		Xanpli	
Min.	:0.00000	Min.	:0.0000	Min.	:0.0000	Min.	:0.0000
1st Qu.:	:0.00000	1st Qu.:	:0.0000	1st Qu.:	:0.0000	1st Qu.:	:0.0000
Median	:0.00000	Median	:0.0400	Median	:0.0300	Median	:0.0000
Mean	:0.09633	Mean	:0.2915	Mean	:0.6223	Mean	:0.2115
3rd Qu.:	:0.09500	3rd Qu.:	:0.3650	3rd Qu.:	:0.7025	3rd Qu.:	:0.2450
Max.	:1.19000	Max.	:2.8500	Max.	:5.9300	Max.	:1.6300

Xanele		GrBr.cr		Gray.cr	
Min.	:0.00000	Min.	:0.0000000	Min.	:0.0000
1st Qu.:	:0.00000	1st Qu.:	:0.0000000	1st Qu.:	:0.0000
Median	:0.00000	Median	:0.0000000	Median	:0.0000
Mean	:0.03867	Mean	:0.0006667	Mean	:0.0025
3rd Qu.:	:0.00000	3rd Qu.:	:0.0000000	3rd Qu.:	:0.0000
Max.	:0.81000	Max.	:0.0400000	Max.	:0.0700

Synrur		Cerpur.Bryarg	
Min.	:0.00000	Min.	:0.000000
1st Qu.:	:0.00000	1st Qu.:	:0.000000
Median	:0.00000	Median	:0.000000
Mean	:0.04933	Mean	:0.008667
3rd Qu.:	:0.00000	3rd Qu.:	:0.000000
Max.	:1.70000	Max.	:0.410000

```
> summary(env)
```

Tree.pairs		Moth		Litter..		Big.rocks..	
Min.	: 1.0	Min.	:0.0	Min.	: 19.04	Min.	: 0.000
1st Qu.:	: 8.0	1st Qu.:	:0.0	1st Qu.:	: 73.89	1st Qu.:	: 2.322
Median	:15.5	Median	:0.5	Median	: 86.39	Median	:11.575
Mean	:15.5	Mean	:0.5	Mean	: 79.81	Mean	:14.901
3rd Qu.:	:23.0	3rd Qu.:	:1.0	3rd Qu.:	: 95.82	3rd Qu.:	:19.995
Max.	:30.0	Max.	:1.0	Max.	:100.00	Max.	:59.670

Small.rocks..		Shrubs..		Grass..		Branches..	
Min.	: 0.000	Min.	:0.0000	Min.	:0.00000	Min.	:0.000
1st Qu.:	: 0.000	1st Qu.:	:0.0000	1st Qu.:	:0.00000	1st Qu.:	:0.000
Median	: 0.000	Median	:0.0000	Median	:0.00000	Median	:0.000
Mean	: 4.798	Mean	:0.4057	Mean	:0.02467	Mean	:0.071
3rd Qu.:	: 3.072	3rd Qu.:	:0.0000	3rd Qu.:	:0.00000	3rd Qu.:	:0.000
Max.	:35.370	Max.	:7.5900	Max.	:1.48000	Max.	:4.260

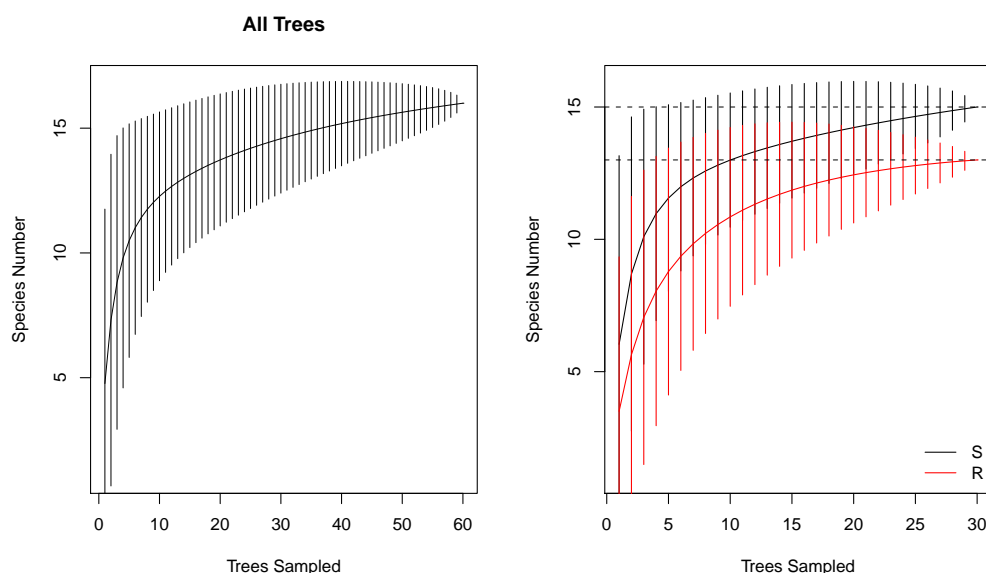
Light...N		Light...S		Light...average	
Min.	: 1.80	Min.	: 1.80	Min.	: 2.400
1st Qu.:	: 8.00	1st Qu.:	: 9.70	1st Qu.:	: 9.213
Median	:15.00	Median	:16.00	Median	:16.050
Mean	:17.68	Mean	:17.81	Mean	:17.743
3rd Qu.:	:26.10	3rd Qu.:	:26.15	3rd Qu.:	:25.525
Max.	:45.10	Max.	:44.60	Max.	:41.300

```
> library(vegan)
> library(gplots)
> attach(env)
```

2 Species Accumulation Curves

Although the sampling curves are not fully asymptotic, they are beginning to level off, which to me suggests that sampling is at an acceptable level.

```
> par(mfrow = c(1, 2))
> plot(specaccum(com), lwd = 0.5, xlab = "Trees Sampled",
+      ylab = "Species Number", main = "All Trees")
> plot(specaccum(com[tree == 1, ]), add = FALSE, xlab = "Trees Sampled",
+      ylab = "Species Number")
> abline(h = 15, lwd = 0.3, lty = 2)
> plot(specaccum(com[tree == 0, ]), add = TRUE, col = "red")
> abline(h = 13, lwd = 0.3, lty = 2)
> legend("bottomright", c("S", "R"), lty = 1, col = c("black",
+      "red"), bty = "n")
```



3 Univariate Community Analyses

All of the univariate summary statistics (abundance, species richness and Shannon's diversity index) were significantly increased by moth resistance.

3.1 Abundance

```
> a = apply(com, 1, sum)
> wilcox.test(a, y = Tree.pairs, alternative = "less",
+   paired = TRUE)
```

Wilcoxon signed rank test with continuity correction

data: a and Tree.pairs

V = 47, p-value = 8.501e-11

alternative hypothesis: true location shift is less than 0

3.2 Species Richness

```
> r = com
> r[r != 0] <- 1
> r = apply(r, 1, sum)
> wilcox.test(r, y = Tree.pairs, alternative = "less",
+   paired = TRUE)
```

Wilcoxon signed rank test with continuity correction

```
data:  r and Tree.pairs
V = 107.5, p-value = 8.975e-09
alternative hypothesis: true location shift is less than 0
```

3.3 Shannon's Diversity Index

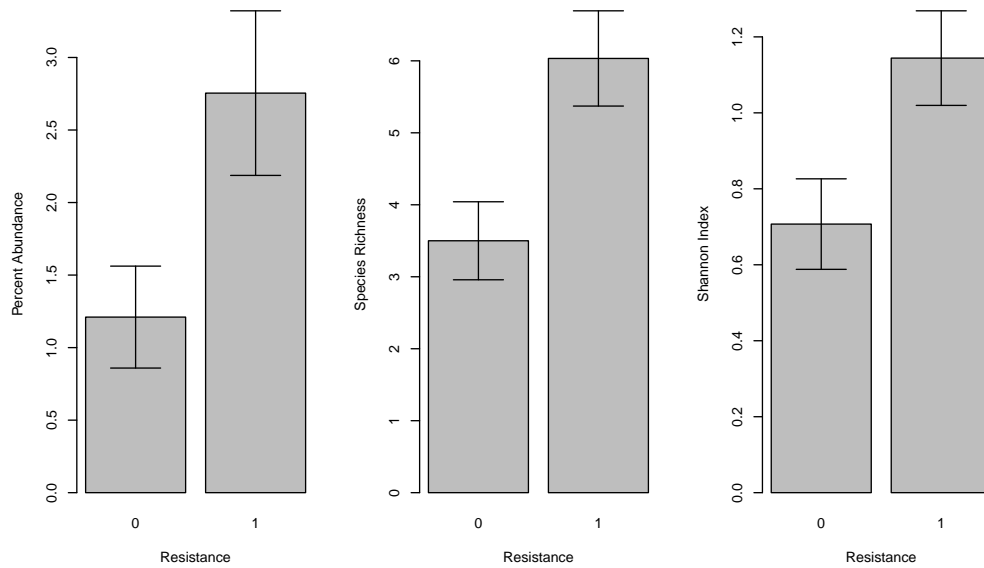
```
> h = diversity(com)
> wilcox.test(h, y = Tree.pairs, alternative = "less",
+   paired = TRUE)
```

Wilcoxon signed rank test with continuity correction

```
data:  h and Tree.pairs
V = 5, p-value = 1.075e-11
alternative hypothesis: true location shift is less than 0
```

3.4 Barplot of Abundance, Richness and Diversity Response to Moth Resistance

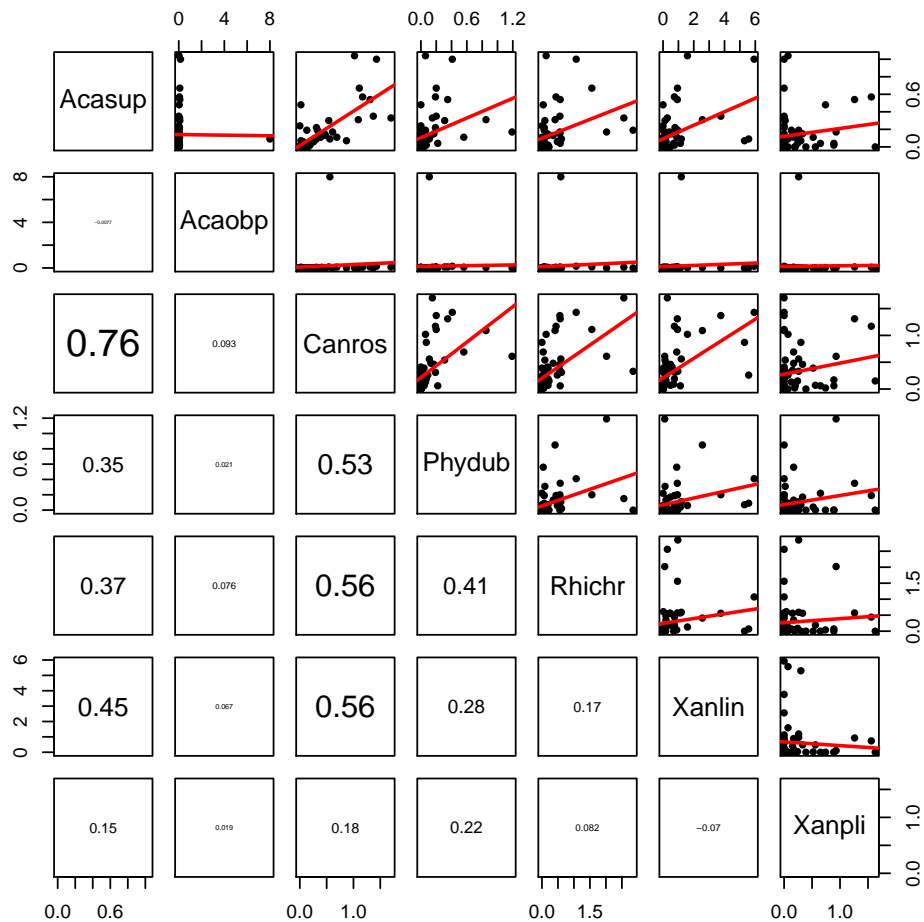
```
> se = function(x) {
+   sd(x)/sqrt(length(x))
+ }
> par(mfrow = c(1, 3))
> barplot2(tapply(a, tree, mean), xlab = "Resistance",
+   ylab = "Percent Abundance", plot.ci = TRUE, ci.u = tapply(a,
+   tree, mean) + tapply(a, tree, se), ci.l = tapply(a,
+   tree, mean) - tapply(a, tree, se))
> barplot2(tapply(r, tree, mean), xlab = "Resistance",
+   ylab = "Species Richness", plot.ci = TRUE, ci.u = tapply(r,
+   tree, mean) + tapply(r, tree, se), ci.l = tapply(r,
+   tree, mean) - tapply(r, tree, se))
> barplot2(tapply(h, tree, mean), xlab = "Resistance",
+   ylab = "Shannon Index", plot.ci = TRUE, ci.u = tapply(h,
+   tree, mean) + tapply(h, tree, se), ci.l = tapply(h,
+   tree, mean) - tapply(h, tree, se))
```



4 Multivariate Community Analyses

4.1 Pairwise Plot of Species with at Least 5% Total Abundance

```
> source("/Users/artemis/Documents/R_Docs/Scripts/Functions/pairs.R")
> pairs(com[apply(com, 2, sum) >= 5], lower.panel = panel.cor,
+       upper.panel = panel.lmr)
```



4.2 PerMANOVA

```
> d = vegdist(cbind(com, rep(0.01, nrow(com))))
> adonis(d ~ Moth + Tree.pairs/Moth, permutations = 99999)
```

Call:

```
adonis(formula = d ~ Moth + Tree.pairs/Moth, permutations = 99999)
```

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
Moth	1.00000	0.88978	0.88978	2.81680	0.0441	0.01682 *
Tree.pairs	1.00000	0.65644	0.65644	2.07814	0.0326	0.05763 .
Moth:Tree.pairs	1.00000	0.92389	0.92389	2.92479	0.0458	0.01391 *
Residuals	56.00000	17.68936	0.31588		0.8775	
Total	59.00000	20.15947			1.0000	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

4.3 Indicator Species Analysis

```
> library(labdsf)
> indsp = indval(com, (tree + 1))
> summary(indsp)
```

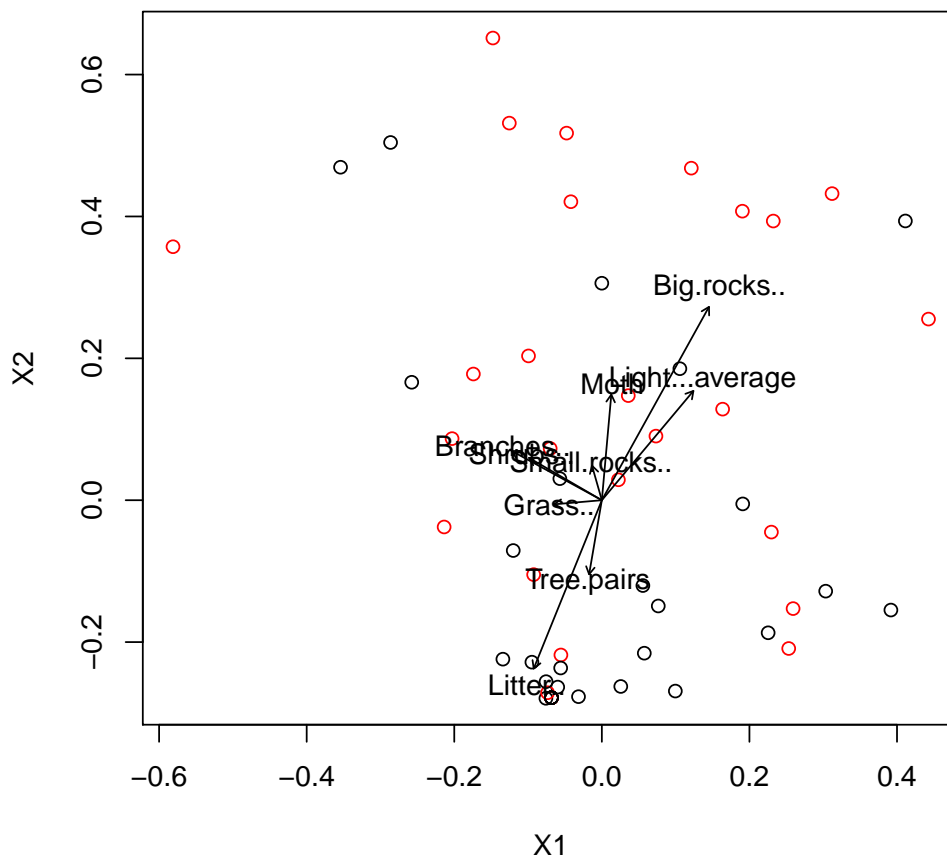
	cluster	indicator_value	probability
Canros	2	0.6397	0.002
Acasup	2	0.6295	0.002
Acacon	2	0.4769	0.001
Acaobp	2	0.4241	0.010

Phydub	2	0.4125	0.025
Calare	2	0.2966	0.034
Sum of probabilities		=	6.669
Sum of Indicator Values		=	4.64
Sum of Significant Indicator Values		=	2.88
Number of Significant Indicators		=	6
Significant Indicator Distribution			
2			
6			

```
> detach(package:labdsv)
```

4.4 Ordination with Vectors

```
> nms.x = read.csv("moth_nms.csv")
> plot(nms.x, col = (env$Moth + 1))
> fit = envfit(nms.x, env[, c(-9, -10)], permutations = 99999)
> plot(fit, col = "black")
```



4.4.1 Analysis of NMS Ordination Vector

```
> fit
```

***VECTORS

	X1	X2	r2	Pr(>r)
Tree.pairs	-0.163158	-0.986600	0.0605	0.16812
Moth	0.085751	0.996317	0.1206	0.02574 *
Litter..	-0.362543	-0.931967	0.3502	3e-05 ***
Big.rocks..	0.470257	0.882530	0.5148	1e-05 ***
Small.rocks..	-0.264370	0.964421	0.0138	0.67347
Shrubs..	-0.855552	0.517717	0.0719	0.11165
Grass..	-0.996016	-0.089179	0.0229	0.33554
Branches..	-0.869419	0.494076	0.1061	0.04987 *
Light...average	0.627335	0.778749	0.2112	0.00121 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
P values based on 99999 permutations.

5 Mechanistic Explorations of the Effects of Moth Resistance

5.1 Relationship between Moth Resistance and Factors

```
> pairs(cbind(Moth, Litter.., Big.rocks.., Small.rocks..,
+   Light...average), lower.panel = panel.cor, upper.panel = panel.lmr)
> cor.test(Litter.., Moth)
```

Pearson's product-moment correlation

```
data: Litter.. and Moth
t = -3.0871, df = 58, p-value = 0.003098
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5747658 -0.1345822
sample estimates:
      cor
-0.3756689
```

```
> cor.test(Big.rocks.., Moth)
```

Pearson's product-moment correlation

```
data: Big.rocks.. and Moth
t = 2.6217, df = 58, p-value = 0.01115
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.07802678 0.53519178
sample estimates:
      cor
0.3255023
```

```
> cor.test(Small.rocks.., Moth)
```

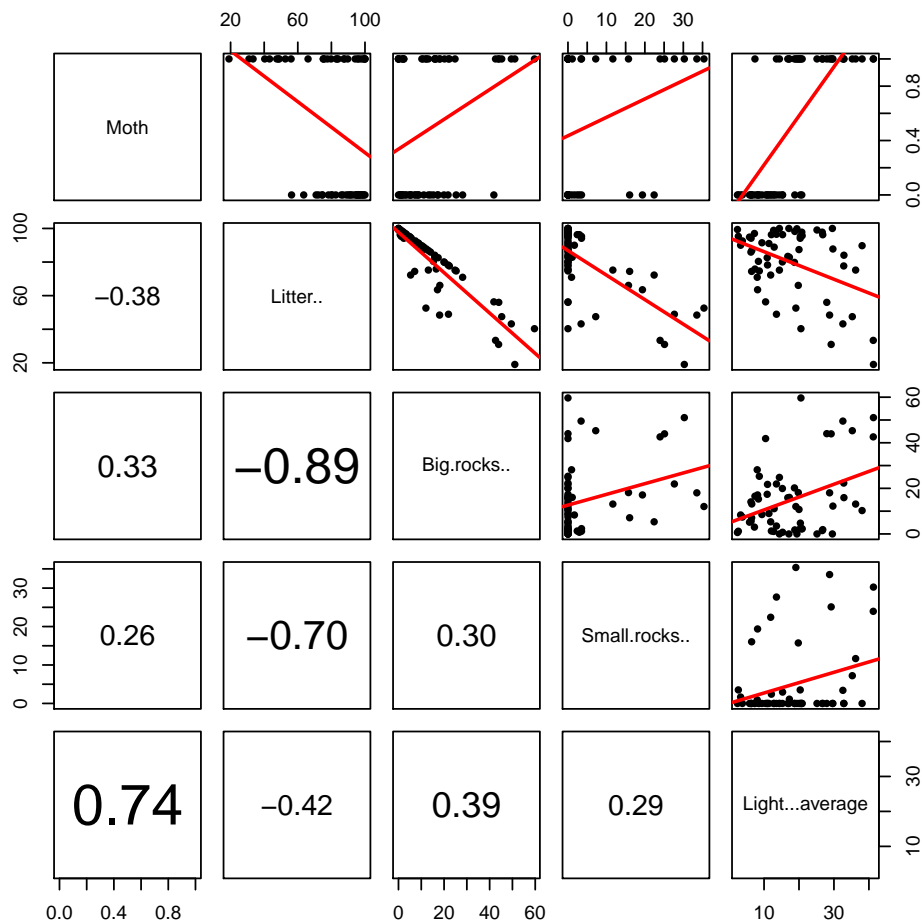
Pearson's product-moment correlation

```
data: Small.rocks.. and Moth
t = 2.0478, df = 58, p-value = 0.04511
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.006150592 0.481824590
sample estimates:
      cor
0.2596697
```

```
> cor.test(Light...average, Moth)
```


Pearson's product-moment correlation

```
data: Light...average and Moth
t = 8.3514, df = 58, p-value = 1.582e-11
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.5969840 0.8359747
sample estimates:
      cor
0.7388996
```



5.2 Moth Resistance Factors Affecting Abundance, Richness and Diversity

5.2.1 Abundance

```
> par(mfrow = c(1, 3))
> hist(residuals(lm(a ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth)), main = "untransformed")
> log.a = log(a + 1e-07)
> hist(residuals(lm(log.a ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth)), main = "log transformed")
> sqrt.a = sqrt(a)
> hist(residuals(lm(sqrt.a ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth)), main = "sqrt transformed")
> summary(lm(a ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth))
```

Call:

```
lm(formula = a ~ Litter.. + Big.rocks.. + Small.rocks.. + Light...average +
```

Moth)

Residuals:

Min	1Q	Median	3Q	Max
-3.1072	-0.8651	-0.3544	0.2685	7.2474

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	85.24680	21.82436	3.906	0.000263	***
Litter..	-0.85572	0.22000	-3.890	0.000277	***
Big.rocks..	-0.77126	0.22359	-3.449	0.001097	**
Small.rocks..	-0.87067	0.21868	-3.981	0.000206	***
Light...average	0.04653	0.04168	1.116	0.269228	
Moth	-0.25567	0.83501	-0.306	0.760638	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.039 on 54 degrees of freedom

Multiple R-squared: 0.4695, Adjusted R-squared: 0.4204

F-statistic: 9.558 on 5 and 54 DF, p-value: 1.422e-06

```
> summary(lm(sqrt.a ~ Litter.. + Big.rocks.. + Small.rocks.. +  
+ Light...average + Moth))
```

Call:

```
lm(formula = sqrt.a ~ Litter.. + Big.rocks.. + Small.rocks.. +  
Light...average + Moth)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.08070	-0.38246	-0.07297	0.27107	1.74901

Coefficients:

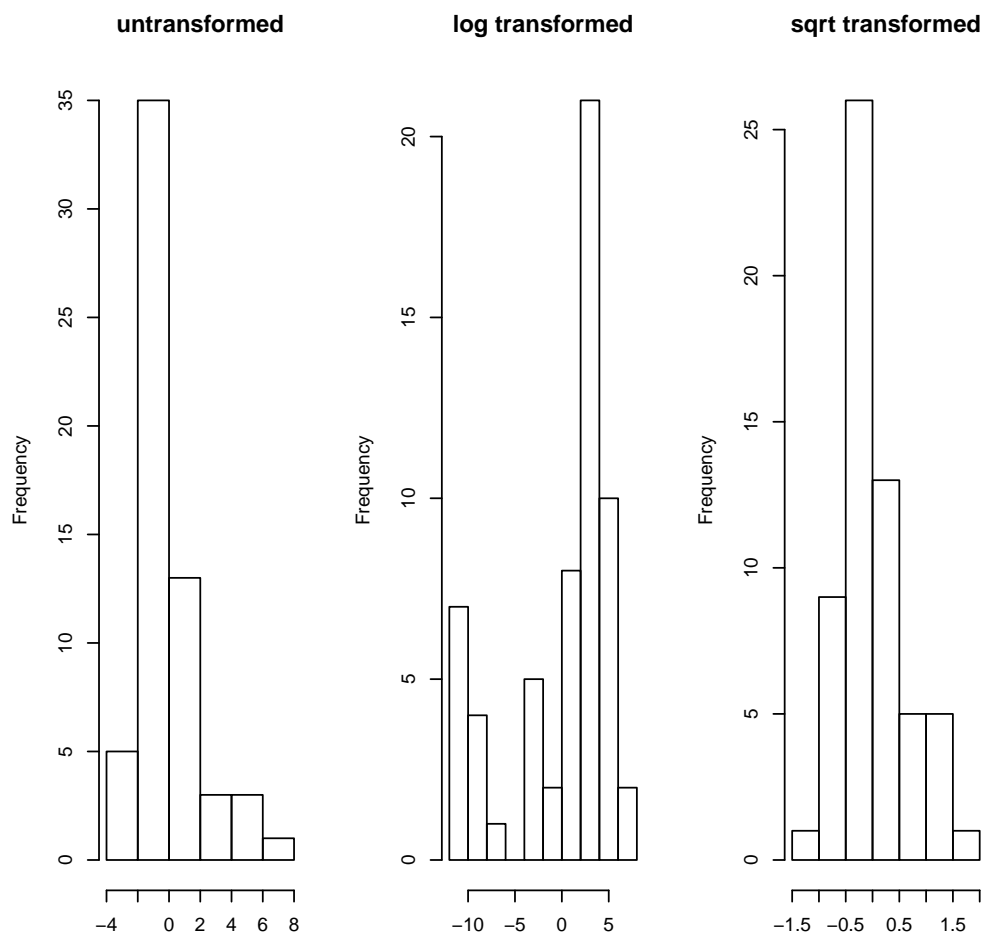
	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	25.77513	6.98099	3.692	0.000519	***
Litter..	-0.25605	0.07037	-3.639	0.000614	***
Big.rocks..	-0.22174	0.07152	-3.100	0.003069	**
Small.rocks..	-0.26658	0.06995	-3.811	0.000357	***
Light...average	0.02302	0.01333	1.727	0.089900	.
Moth	-0.18254	0.26710	-0.683	0.497265	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6522 on 54 degrees of freedom

Multiple R-squared: 0.5372, Adjusted R-squared: 0.4944

F-statistic: 12.54 on 5 and 54 DF, p-value: 4.292e-08



Litter.. + Big.rocks.. + Small.rocks.. + Lig ~ Litter.. + Big.rocks.. + Small.rocks.. + l ~ Litter.. + Big.rocks.. + Small.rocks.. + l

5.2.2 Richness

```
> par(mfrow = c(1, 3))
> hist(residuals(lm(r ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth)), main = "untransformed")
> hist(residuals(lm(sqrt(r) ~ Litter.. + Big.rocks.. +
+   Small.rocks.. + Light...average + Moth)), main = "sqrt transformed")
> hist(residuals(lm(r^2 ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth)), main = "square transformed")
> summary(lm(r ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth))
```

Call:

```
lm(formula = r ~ Litter.. + Big.rocks.. + Small.rocks.. + Light...average +
    Moth)
```

Residuals:

Min	1Q	Median	3Q	Max
-4.4856	-1.8706	-0.3768	1.7516	5.6450

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	57.22541	26.76674	2.138	0.0371 *
Litter..	-0.56141	0.26982	-2.081	0.0422 *
Big.rocks..	-0.42130	0.27422	-1.536	0.1303
Small.rocks..	-0.61029	0.26820	-2.275	0.0269 *
Light...average	0.09404	0.05112	1.840	0.0713 .
Moth	-0.23426	1.02410	-0.229	0.8199

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.501 on 54 degrees of freedom
Multiple R-squared:  0.5392,    Adjusted R-squared:  0.4965 
F-statistic: 12.64 on 5 and 54 DF,  p-value: 3.856e-08

> summary(lm(r^2 ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth))

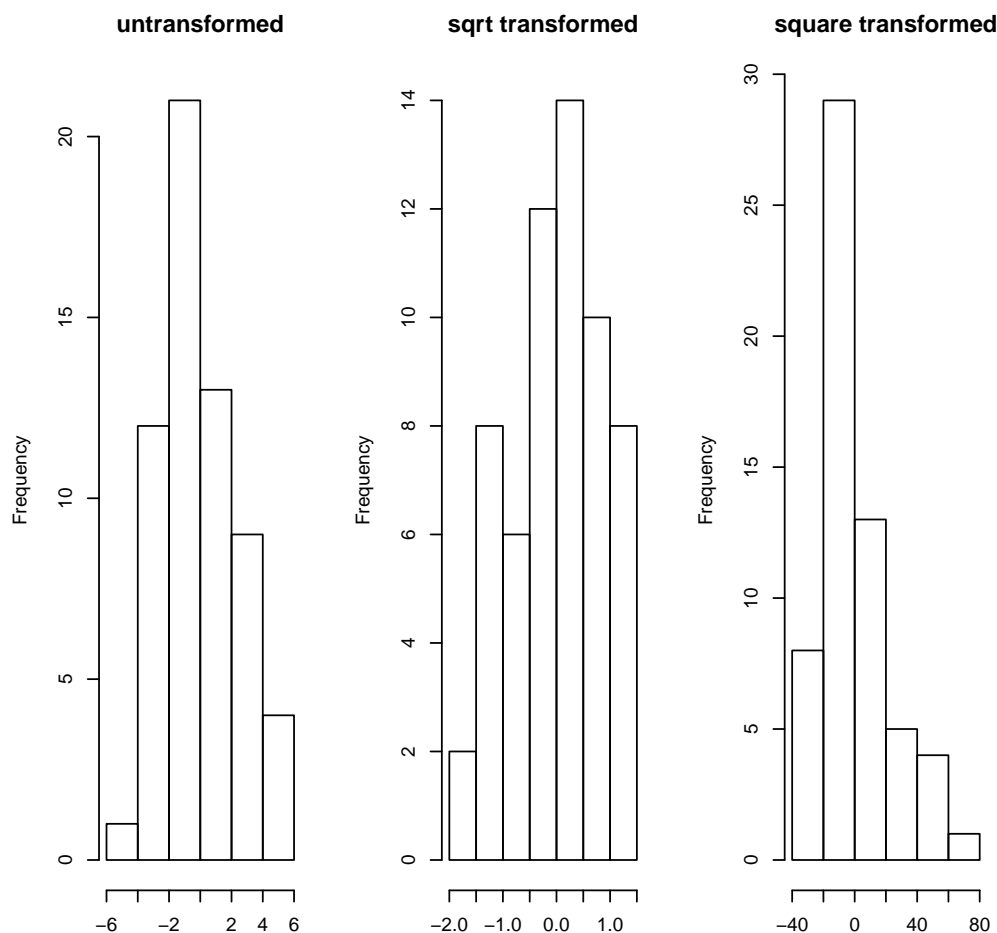
Call:
lm(formula = r^2 ~ Litter.. + Big.rocks.. + Small.rocks.. + Light...average +
    Moth)

Residuals:
    Min       1Q   Median       3Q      Max 
-33.42 -16.67  -5.87   11.72   78.40 

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)    579.1453   263.4597   2.198  0.0322 *
Litter..        -5.8314    2.6558  -2.196  0.0324 *
Big.rocks..     -4.4782    2.6991  -1.659  0.1029
Small.rocks..   -6.2763    2.6399  -2.378  0.0210 *
Light...average  1.0309    0.5031   2.049  0.0453 *
Moth            -0.5560   10.0801  -0.055  0.9562
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 24.61 on 54 degrees of freedom
Multiple R-squared:  0.5571,    Adjusted R-squared:  0.5161 
F-statistic: 13.58 on 5 and 54 DF,  p-value: 1.384e-08

```



Litter.. + Big.rocks.. + Small.rocks.. + Lig) ~ Litter.. + Big.rocks.. + Small.rocks.. + Litter.. + Big.rocks.. + Small.rocks.. + Li

5.2.3 Diversity

```
> par(mfrow = c(2, 2))
> hist(residuals(lm(h ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth)), main = "untransformed")
> hist(residuals(lm(h^2 ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth)), main = "square transformed")
> hist(residuals(lm(sqrt(h) ~ Litter.. + Big.rocks.. +
+   Small.rocks.. + Light...average + Moth)), main = "sqrt transformed")
> hist(residuals(lm(log(h + 1e-07) ~ Litter.. + Big.rocks.. +
+   Small.rocks.. + Light...average + Moth)), main = "log transformed")
> summary(lm(h ~ Litter.. + Big.rocks.. + Small.rocks.. +
+   Light...average + Moth))
```

Call:

```
lm(formula = h ~ Litter.. + Big.rocks.. + Small.rocks.. + Light...average +
    Moth)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.94610	-0.48766	-0.06364	0.58525	0.99877

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2.176658	5.855802	0.372	0.712
Litter..	-0.018851	0.059029	-0.319	0.751
Big.rocks..	0.007832	0.059992	0.131	0.897
Small.rocks..	-0.025606	0.058675	-0.436	0.664

Light...average	0.015461	0.011183	1.383	0.173
Moth	-0.029532	0.224045	-0.132	0.896

Residual standard error: 0.5471 on 54 degrees of freedom
Multiple R-squared: 0.437, Adjusted R-squared: 0.3849
F-statistic: 8.384 on 5 and 54 DF, p-value: 6.401e-06

```
> summary(lm(h^2 ~ Litter.. + Big.rocks.. + Small.rocks.. +
+ Light...average + Moth))
```

Call:

```
lm(formula = h^2 ~ Litter.. + Big.rocks.. + Small.rocks.. + Light...average +
Moth)
```

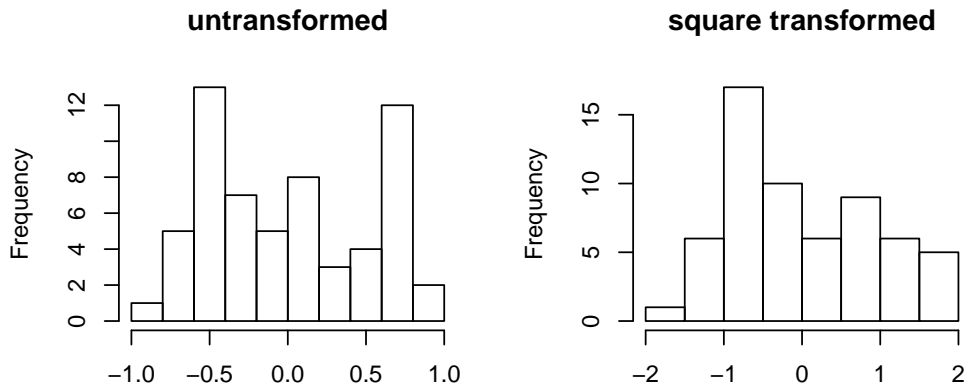
Residuals:

Min	1Q	Median	3Q	Max
-1.5414	-0.6235	-0.2444	0.7020	1.7744

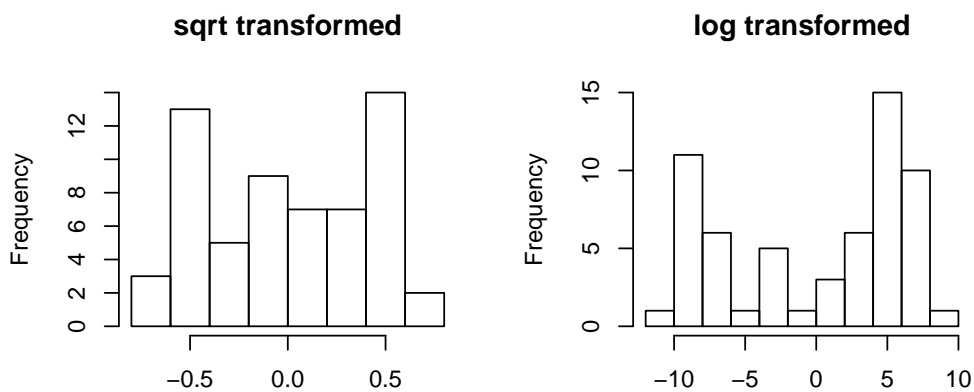
Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.1782364	9.8765336	0.018	0.986
Litter..	-0.0003917	0.0995594	-0.004	0.997
Big.rocks..	0.0473428	0.1011843	0.468	0.642
Small.rocks..	-0.0106344	0.0989632	-0.107	0.915
Light...average	0.0310721	0.0188615	1.647	0.105
Moth	-0.0350014	0.3778796	-0.093	0.927

Residual standard error: 0.9227 on 54 degrees of freedom
Multiple R-squared: 0.4827, Adjusted R-squared: 0.4348
F-statistic: 10.08 on 5 and 54 DF, p-value: 7.49e-07



$h \sim \text{Litter..} + \text{Big.rocks..} + \text{Small.rocks..} + \text{Light...}h^2 \sim \text{Litter..} + \text{Big.rocks..} + \text{Small.rocks..} + \text{Light..}$



$\sqrt{h} \sim \text{Litter..} + \text{Big.rocks..} + \text{Small.rocks..} + \text{Light} + 1e-07) \sim \text{Litter..} + \text{Big.rocks..} + \text{Small.rocks..} +$

5.3 Factors Resistance Factors Affecting the Community

```
> adonis(d ~ Litter.. + Big.rocks.. + Small.rocks.. + Light...average +
+       Moth, permutations = 9999)
```

Call:

```
adonis(formula = d ~ Litter.. + Big.rocks.. + Small.rocks.. +       Light...average + Moth, permutations
```

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
Litter..	1.00000	2.02064	2.02064	6.85110	0.1002	0.0002
Big.rocks..	1.00000	1.02549	1.02549	3.47698	0.0509	0.0045
Small.rocks..	1.00000	0.44991	0.44991	1.52546	0.0223	0.1373
Light...average	1.00000	0.42702	0.42702	1.44784	0.0212	0.1772
Moth	1.00000	0.30983	0.30983	1.05049	0.0154	0.3618
Residuals	54.00000	15.92658	0.29494		0.7900	
Total	59.00000	20.15947			1.0000	

```
Litter..      ***
Big.rocks..   **
Small.rocks..
Light...average
Moth
Residuals
Total
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

5.4 Structural Equation Modeling

5.5 Notes on the SEMs

SEM allows us to account for and isolate the covariances in multiple correlated variables.

This is not the same as conducting an experiment, but it gives us more accurate information than multiple regressions because we can assess both the direct and *indirect*, sometimes termed informally as interactive, effects of variables.

Numbers above paths in the path diagrams are standardized path coefficient, which can be thought of as the amount of change one variable due to another variable in standard deviations.

The numbers next to the top right corner of variables that are endogenous (i.e., there are arrows pointing into them) are squared multiple correlations, which can be treated as multiple r^2 (i.e., the total variance explained in that variable by all the variables pointing into it).

Things to look for and remember:

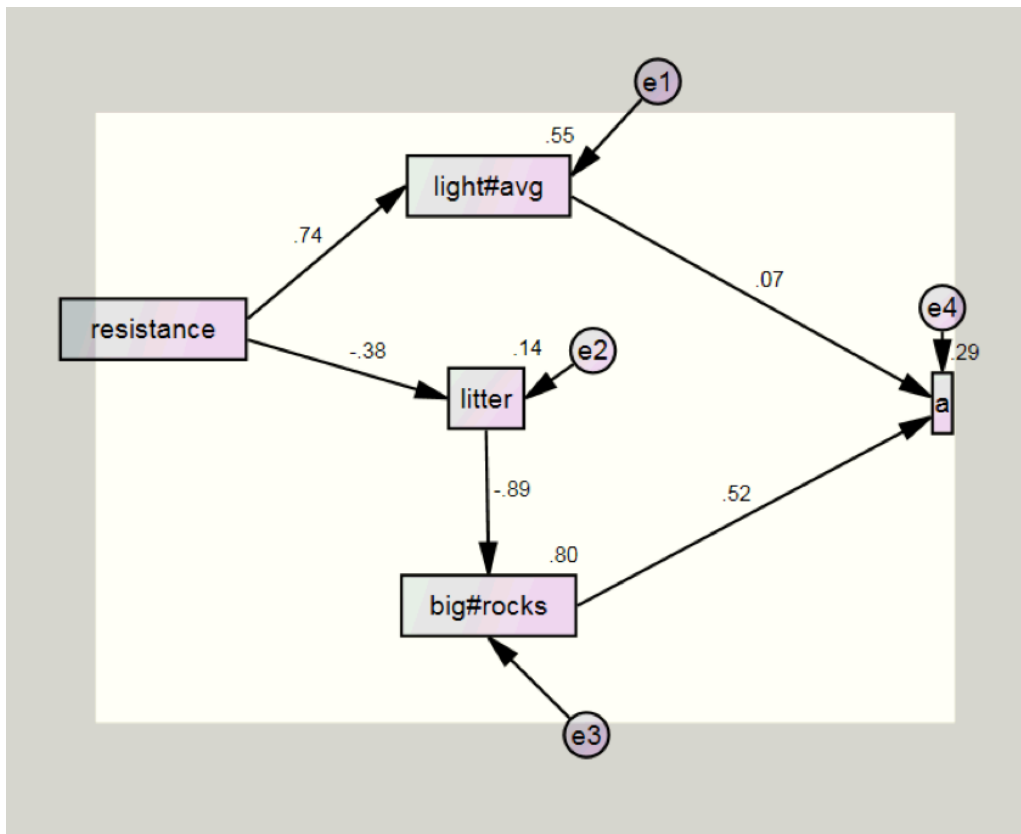
1. SEM works by testing *a priori* models against the data.
2. In the notes for the models, a small χ^2 and a large p-value indicate good model fit, because it shows that the model predicted covariances are statistically similar to the raw covariances.
3. There are two main pathways in each model, one is a path through Average Light (variable name = **Light...average**) and the other is a more complex path through percent litter (variable name = **Litter..**) and percent rocks > 3cm (variable name = **Big.rocks..**).
4. In addition to whole model fit, we also need to look at the significance of each path, which can be done by looking at the regression weights output (NOTE: the asterisks indicate that a variable is significant below 0.001).

I built the *a priori* models based on what we have discussed about the system and the multiple regressions.

I have also presented the model modification output, which would indicate variables in the model that need to be changed; however, we had not variables recommended for change, another suggestion of the validity of our models.

Here I use **resistance**, such that **resistance** increases from 0 = susceptible to 1 = resistant. This makes more intuitive sense than **Moth**, but is numerically equivalent.

5.5.1 Abundance



Notes for Model (Default model)

Computation of degrees of freedom (Default model)

Number of distinct sample moments:	15
Number of distinct parameters to be estimated:	10
Degrees of freedom (15 - 10):	5

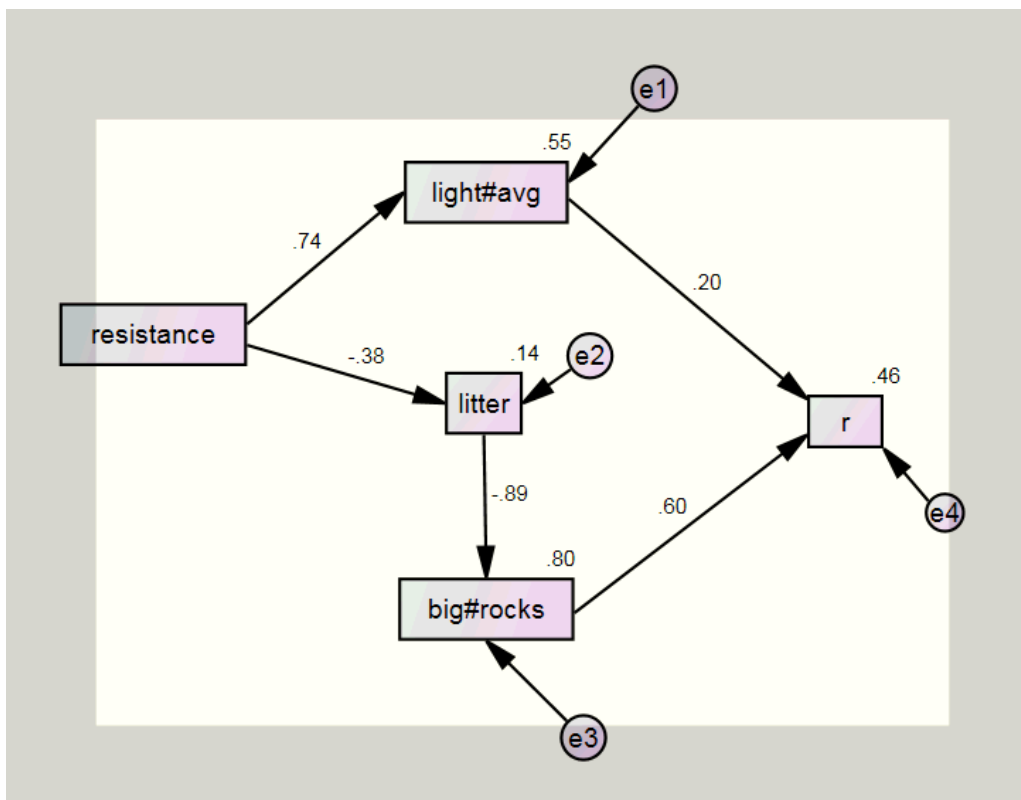
Result (Default model)

Minimum was achieved
Chi-square = 4.459
Degrees of freedom = 5
Probability level = .485

Regression Weights: (Group number 1 - Default model)

			Estimate	S.E.	C.R.	P	Label
litter	<---	resistance	-15.070	4.840	-3.114	.002	
light#avg	<---	resistance	15.133	1.797	8.423	***	
big#rocks	<---	litter	-.661	.044	-15.130	***	
a	<---	big#rocks	.092	.020	4.606	***	
a	<---	light#avg	.019	.029	.639	.523	

5.5.2 Richness



Notes for Model (Default model)

Computation of degrees of freedom (Default model)

Number of distinct sample moments: 15
Number of distinct parameters to be estimated: 10
Degrees of freedom (15 - 10): 5

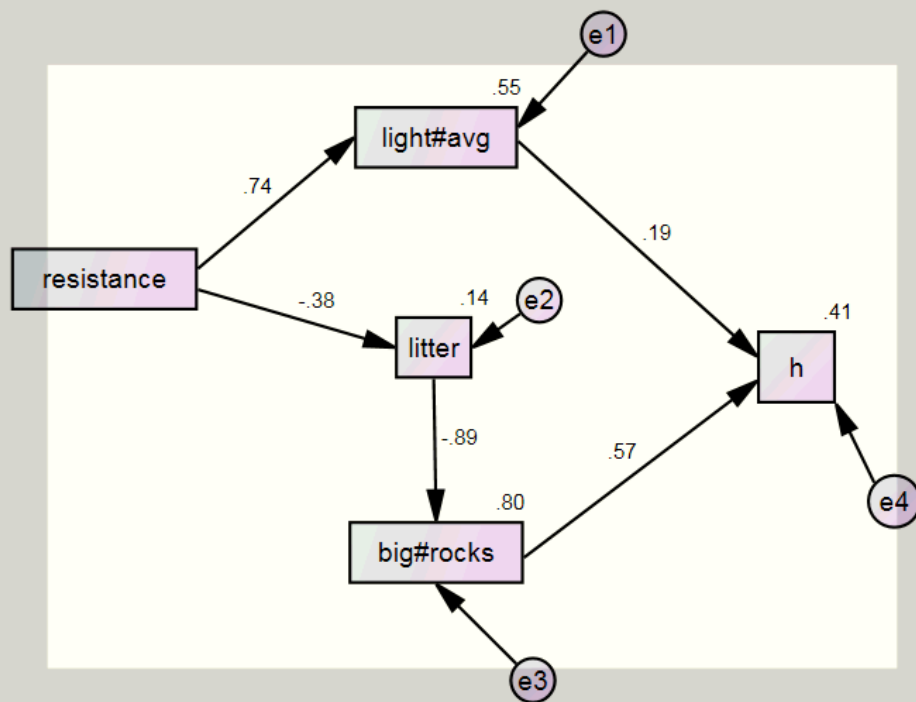
Result (Default model)

Minimum was achieved
Chi-square = 5.226
Degrees of freedom = 5
Probability level = .389

Regression Weights: (Group number 1 - Default model)

			Estimate	S.E.	C.R.	P	Label
litter	<---	resistance	-15.070	4.840	-3.114	.002	
light#avg	<---	resistance	15.133	1.797	8.423	***	
big#rocks	<---	litter	-.661	.044	-15.130	***	
r	<---	light#avg	.066	.033	1.997	.046	
r	<---	big#rocks	.140	.023	6.123	***	

5.5.3 Diversity



Notes for Model (Default model)

Computation of degrees of freedom (Default model)

Number of distinct sample moments:	15
Number of distinct parameters to be estimated:	10
Degrees of freedom (15 - 10):	5

Result (Default model)

Minimum was achieved
Chi-square = 4.182
Degrees of freedom = 5
Probability level = .524

Regression Weights: (Group number 1 - Default model)

			Estimate	S.E.	C.R.	P	Label
litter	<---	resistance	-15.070	4.840	-3.114	.002	
light#avg	<---	resistance	15.133	1.797	8.423	***	
big#rocks	<---	litter	-.661	.044	-15.130	***	
h	<---	light#avg	.013	.007	1.864	.062	
h	<---	big#rocks	.026	.005	5.476	***	

5.5.4 Community Composition

NOTE: I need to confer with other folks (Matt Bowker, Daniel Laughlin and Jamie Lamit) on the best way to approach our SEM based analysis of community composition.

6 Conclusion

1. Based on univariate and multivariate statistical analyses of the effect of moth susceptibility, we can conclude that moth susceptibility has a statistically significant effect on rock lichen epiphyte abundance, richness, diversity and community composition with multiple species changing in response (see the indicator species analyses).
2. The analyses of the predictor variables and moth susceptibility suggested that there were several key factors related to moth susceptibility: percent rocks > 3cm, percent litter cover and average incident light.
3. SEM models indicate that there the effect of moth resistance on rock lichen/moss abundance, species richness and diversity is primarily due to an indirect effect where resistance has a negative effect on the abundance of litter, which also has a negative effect on the abundance of percent large rocks. Thus, because there is a positive relationship between percent large rocks and abundance, species richness and diversity, the net, indirect, effect of resistance on rock lichen/moss communities is positive.

Thus, we can conclude that evolutionary shifts in *Pinus edulis* moth susceptibility could have significant community level consequences for sub-canopy rock lichen/moss communities.