

# Genetics of Lichen Networks

M.K. Lau

January 16, 2012

## Contents

<b>1</b>	<b>Summary</b>	<b>1</b>
<b>2</b>	<b>Data</b>	<b>2</b>
<b>3</b>	<b>Modeling</b>	<b>2</b>
<b>4</b>	<b>Analyses</b>	<b>3</b>
<b>5</b>	<b>Results</b>	<b>4</b>
<b>6</b>	<b>Discussion</b>	<b>7</b>
<b>7</b>	<b>References</b>	<b>7</b>

## 1 Summary

- Intraspecific variation is an important contributor to ecological diversity
- It is still not clear whether or not this is direct by influencing species abundances directly or if this is also through indirect effects
- The complex structure and dynamics of communities is a potential source of unpredicted variation
- Here, we present the results of a study of lichen species associated with cottonwood trees in a common garden and show that:

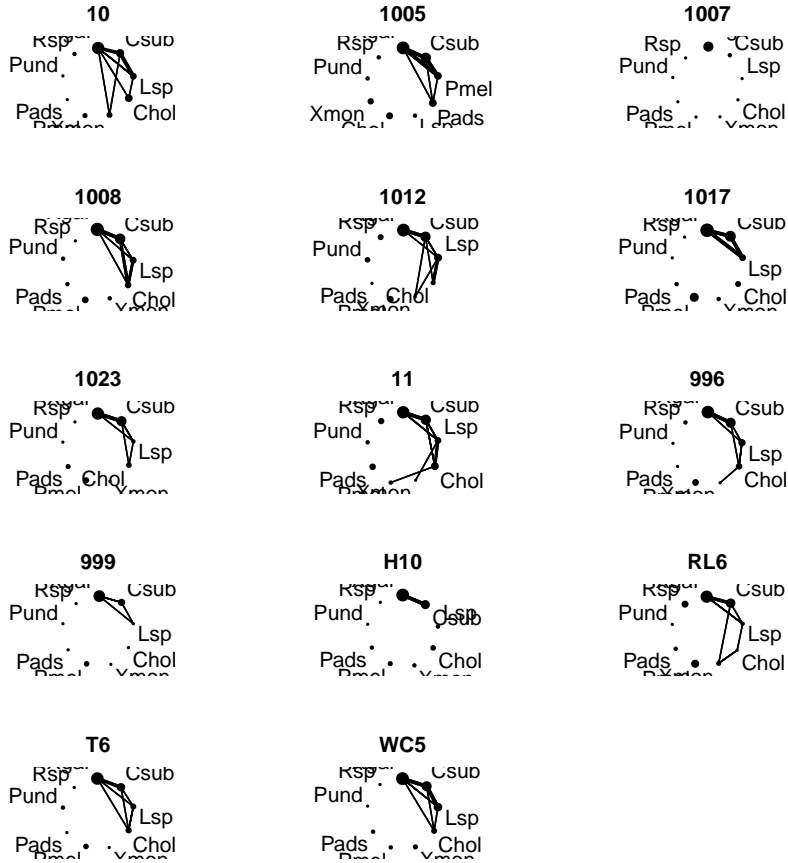
1. There is structure of co-occurrence patterns even in a small community of species (9 total)
2. The structure of covariance networks varied significantly among genotypes

## 2 Data

- Data were collected in April 2011 in the North Garden of the Ogden Nature Center UT
- Presence-absences of lichen species in every other 1  $cm^2$  of a 10  $cm^2$  grid on the north side of each tree at 45 cm from the ground
- Trees were of known genotype as determined by neutral RFLP markers

## 3 Modeling

```
>
>                                     #plots of the networks
> ##Graph plots
>
> genomu.nets45 <- tapply(Inet,net.geno,edge.mean)
> par(mfrow=c(5,3),mai=c(0.3,0.3,0.3,0.3))
> for (i in 1:length(genomu.nets45)){
+   v.cex <- v.col<- apply(lco.com[LCO$Geno == names(genomu.nets45)[i],],2,sum)
+   v.col[v.col > 0] <- 'black'
+   v.col[v.col == 0] <- 'white'
+   v.cex <- log(v.cex+1)
+   v.cex <- v.cex + 1
+   e.lwd <- (abs(genomu.nets45[[i]])*100)^9
+   e.lwd[e.lwd > 25 & e.lwd < 50] <- 15
+   e.lwd[e.lwd > 50] <- 25
+   gplot(abs(genomu.nets45[[i]]),edge.col=pnEdges(genomu.nets45[[i]]),mode='circle'
+         gmode='graph',vertex.sides=50,vertex.col=v.col,displaylabels=TRUE,vertex.b
+         'black',vertex.cex=v.cex,label.cex=1.25,edge.lwd=e.lwd)
+   title(main=names(genomu.nets45)[i],cex=3)
+ }
>
```



## 4 Analyses

```

> #get the factors for analyses
> net.info <- unique(tree.info)
> info.info <- rep(paste('tree','geno','quad','year',sep='_'),length(net.info))
> tree.factor <- unlist(strsplit(net.info,split='_')) #tree-level information for ea
> info.factor <- unlist(strsplit(info.info,split='_')) #sep information for tree inf
> net.quad <- tree.factor[info.factor == 'quad'] #quadrat information for each netwo
> net.quad <- factor(net.quad)
> net.tree <- tree.factor[info.factor == 'tree'] #tree number information for each n
> net.geno <- tree.factor[info.factor == 'geno'] #genotype information for each netw
> net.geno <- factor(net.geno)
> net.year <- tree.factor[info.factor == 'year'] #year of sampling for each network

```

```

>                                     #Calculate species richness
> net.rich <- numeric()
> for (i in (1:length(unique(tree.info)))){
+   x <- lco.com[tree.info == unique(tree.info)[i],]
+   net.rich[i] <- sum(apply(x,2,function(x) if (any(x) > 0){1}else{0}))
+ }
>

```

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
net.geno	13	11.70	0.90	1.68	0.16	0.0088
net.rough	1	0.70	0.70	1.31	0.01	0.2449
net.lat	1	1.66	1.66	3.09	0.02	0.0239
net.geno:net.rough	13	5.92	0.46	0.85	0.08	0.7355
net.geno:net.lat	11	7.24	0.66	1.23	0.10	0.1763
net.rough:net.lat	1	0.44	0.44	0.82	0.01	0.4951
net.geno:net.rough:net.lat	3	2.94	0.98	1.83	0.04	0.0523
Residuals	78	41.76	0.54		0.58	
Total	121	72.35			1.00	

## 5 Results

```

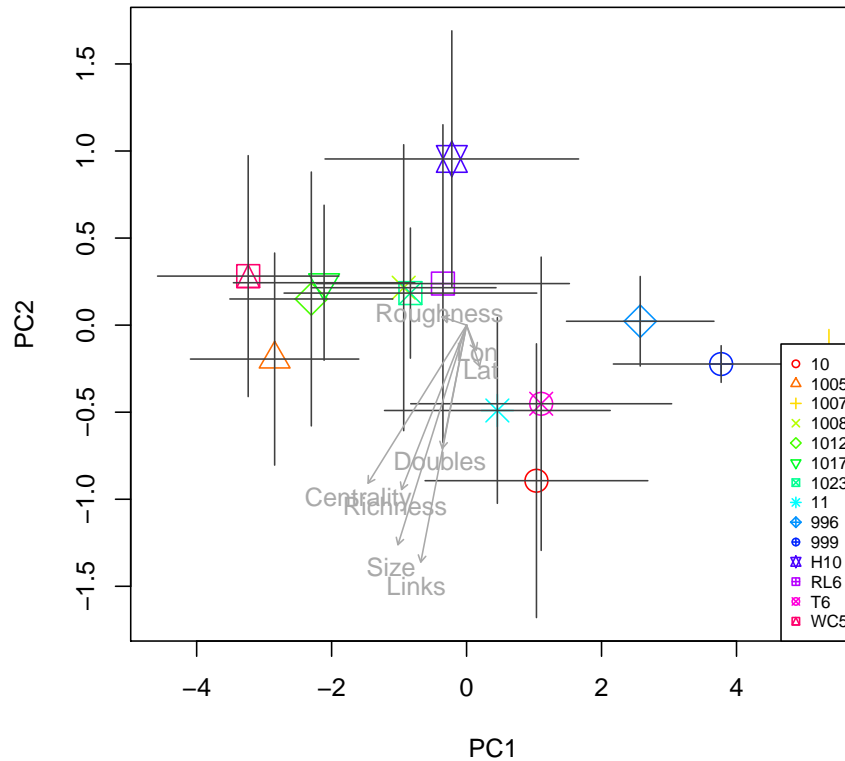
> ##Ordination of networks and vectors of statistics
>                                     #principal components
> pc.45 <- princomp(Inet.dist)
>                                     #caculate the network statistics
> net.S <- lapply(Inet,function(x) length(apply(x,2,bin.sum)[apply(x,2,bin.sum) !=
> net.L <- lapply(Inet,function(x) length(x[x != 0])))
> net.C <- unlist(lapply(Inet,function(x) centralization(x,degree,mode='undirected')
> net.n2 <- lapply(lco.com.all,function(x) length(apply(x,2,bin.sum)[apply(x,2,bin.
> env.45 <- cbind(net.rough,net.rich,net.S,net.L,net.C,net.n2,net.lat,net.lon)
> ord.45 <- pc.45$scores[,1:2]
> colnames(env.45) <- c('Roughness','Richness','Size','Links','Centrality','Doubles','Lat
> vfit45 <- envfit(ord.45,env.45)
>                                     #calculated the means and standard errors
> ord.mu45 <- cbind(tapply(ord.45[,1],net.geno,mean),tapply(ord.45[,2],net.geno,mea

```

```

> ord.se45 <- cbind(tapply(ord.45[,1],net.geno,function(x) sd(x)/sqrt(length(x))),t
> ord.sd45 <- cbind(tapply(ord.45[,1],net.geno,sd),tapply(ord.45[,2],net.geno,sd))
> ord.ciu45 <- ord.mu45 + ord.se45
> ord.cil45 <- ord.mu45 - ord.se45
>
>                                     #plot the ordination
> plot(ord.mu45,col=rainbow(max(as.numeric(factor(rownames(ord.mu45)))))[as.numeric
>                                     #plot the se bars
> for (i in 1:nrow(ord.mu45)){
+   lines(c(ord.mu45[i,1],ord.mu45[i,1]),c(ord.cil45[i,2],ord.ciu45[i,2]),col=grey(
+   lines(c(ord.cil45[i,1],ord.ciu45[i,1]),c(ord.mu45[i,2],ord.mu45[i,2]),col=grey(
+ }
>
>                                     #plot vectors and legend
> plot(vfit45,col='darkgrey',lwd=5)
> legend('bottomright',legend=rownames(ord.mu45),pch=as.numeric(factor(rownames(ord.
>
>

```



```

>                                                                 #Barplot of pc1
> pc1 <- ord.45[,1]
> pc1.m <- tapply(pc1,net.geno,mean)
> pc1.se <- tapply(pc1,net.geno,se)
> barplot2(pc1.m,las=2,plot.ci=TRUE,ci.u=pc1.m+pc1.se,ci.l=pc1.m-pc1.se)
> legend('topright',legend=round(pc.45$sdev[1]^2/(sum(pc.45$sdev^2)),2),bty='n')
>

> ##                                                                 #SEM
> ## summary(aov(pc1~net.geno*net.lat*net.rough))
> ## summary(aov(net.rough~net.geno*net.lat))
> ##                                                                 #specify model
> ##                                                                 #Build genotype composite
> ## geno.comp <- my.latent(net.geno)

```

```
> ## sem.data <- cbind(geno.comp,net.rough,net.lat,pc1)
> ## sem.data <- cbind(geno.comp,net.rough,pc1)
> ## sigma <- cov(sem.data)
> ## sigma
> ## sem.mod <- specifyModel(file='gln_sem.R')
> ## sem1 <- sem(sem.mod,S=sigma,N=nrow(sem.data))
>
```

## 6 Discussion

## 7 References