

Hey Rikke,

Thanks for sending me these data! It's cool just to take a look.

I did some analyses similar to Cam, but I included some more of the variables. Regardless of any data adjustments that I did (e.g., removing species with total abundances less than 5%, removing samples with no species observations) the results were all pretty much the same. Everything that was significant had a very low r^2 (i.e., less than 0.1). Some interesting results:

1) Total abundance of lichens/byros differed significantly between the susceptible and resistant trees (also see attached barplot):

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
factor(Moth)	1	5.806	5.8064	8.0188	0.005838 **
Residuals	81	58.652	0.7241		

***Response was square-root transformed to normalize residuals

2) Although the community composition effects of susceptibility are marginal, I did an indicator species analysis for the species that had a total abundance of at least 5% and found that the following species are all found consistently more often than due to chance under resistant trees (indicated by the cluster number 2):

	cluster	indicator_value	probability
Canros	2	0.6294	0.001
Rhichr	2	0.5225	0.005
Phydub	2	0.4387	0.005
Acastr	2	0.4363	0.004
Acatha	2	0.3725	0.037

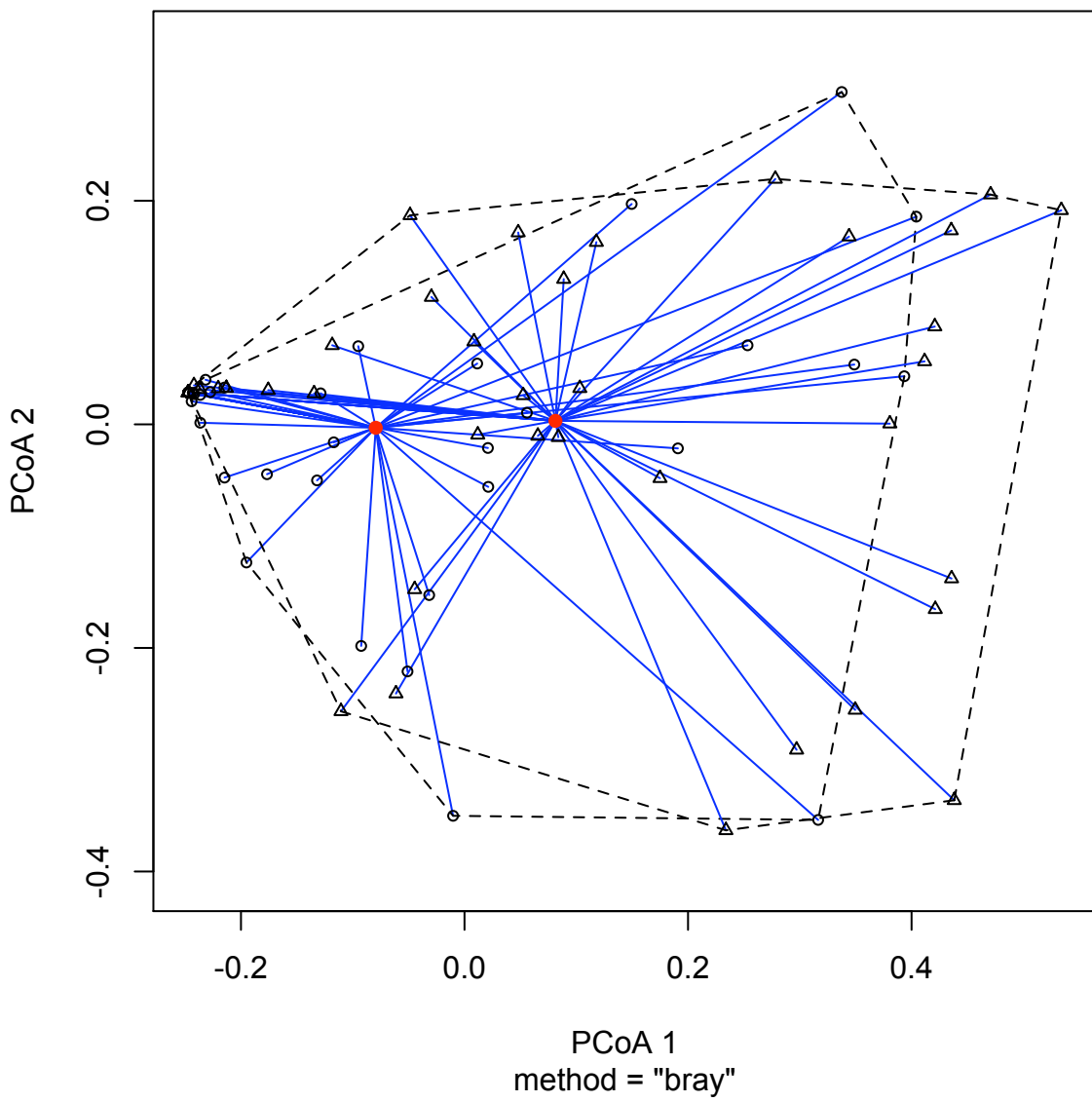
Also, if you look at the cluster diagram I've attached where I've clustered species based on there plot preferences, the same indicators tend to fall out together. Could this be co-habitation or evidence for facilitation of species?

3) Multivariate version of a Levene's Test that it looks for differences in the variance of the multivariate observations. The results suggest that the Moth Resistant Trees had more variable communities than the Susceptible Trees (see first figure).

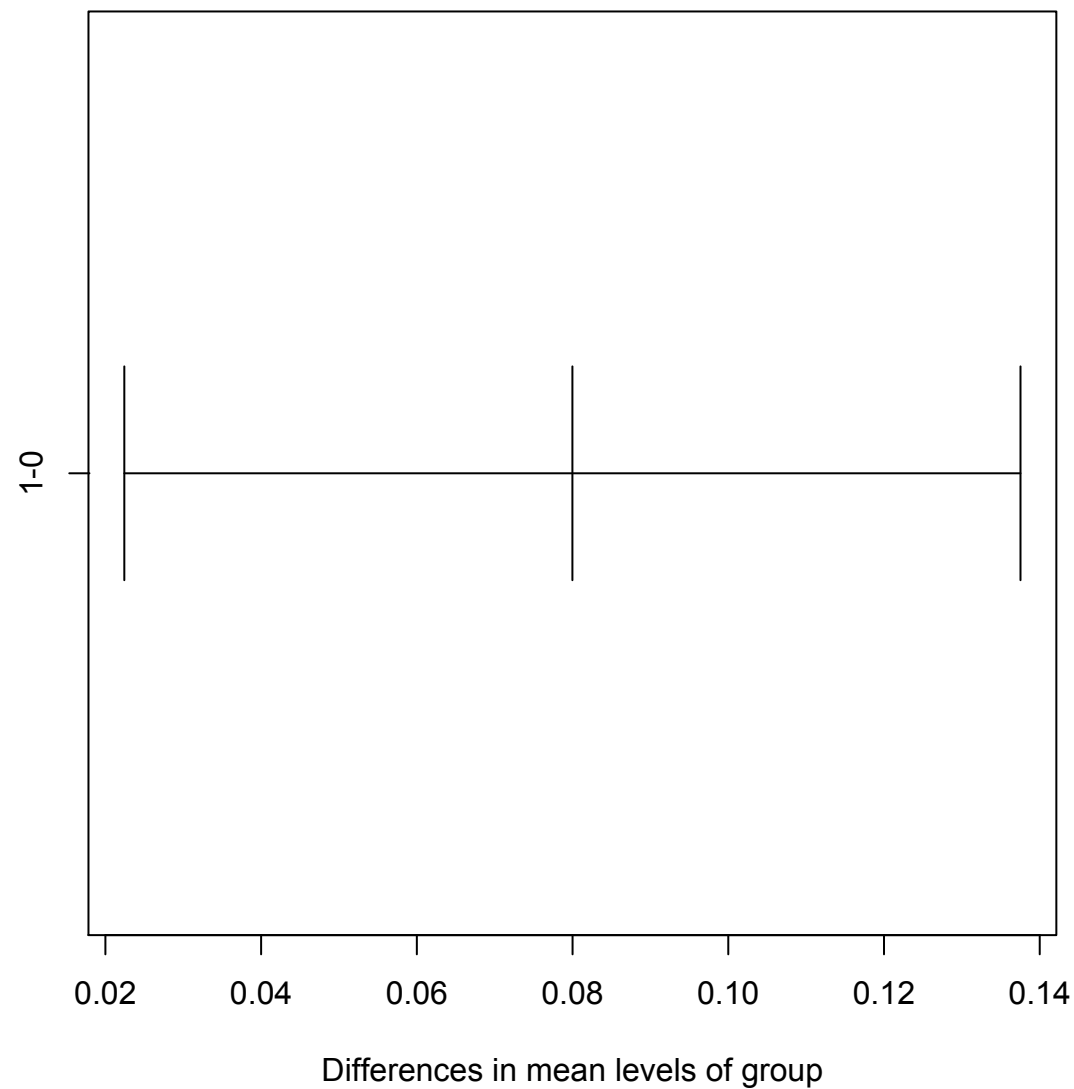
Anywho! Looks like there might be a story in this, but what do you think?

M

Dispersion



95% family-wise confidence level



Cluster Dendrogram

