BIO 682
Quantitative Biology
Spring 2010

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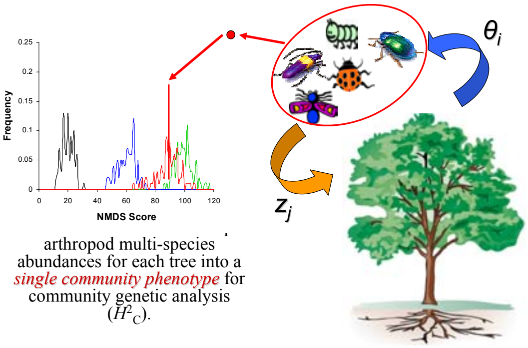
http://www4.nau.edu/shustercourses/BIO682/index.htm

Lecture 14

NMDS

1. User selects the # of dimensions (N) and the distance measure (Bray Curtis)
2. A distance matrix is calculated
3. An initial configuration of samples in N dimensions is selected. This configuration can be random
4. A measure of 'stress' (mismatch between the rank order of distances in the data, and the rank order of distances in the ordination) is calculated
5. The samples are moved slightly in a direction that decreases the stress
6. 4 and 5 are repeated until 'stress' appears to reach a minimum. The final configuration of points may be rotated if desired.

Arthropod Communities on Trees



arthropod multi-species abundances for each tree into a *single community phenotype* for community genetic analysis (H^2_C).

The Bray-Curtis Dissimilarity Coefficient

$$BC_{ij} = \sum \frac{|n_{ik} - n_{jk}|}{(n_{ik} + n_{jk})}$$

Where i and j refer to the cell values in each k-th dissimilarity matrix and BCij is the dissimilarity score for that matrix.

The Bray-Curtis Dissimilarity Coefficient

	Value1	**Value2**	**Value3**	**Value4**
Object A	0	3	4	5
Object B	7	6	3	-1

$$d_{BA} = \frac{|0-7| + |3-6| + |4-3| + |5+1|}{(0+7)+(3+6)+(4+3)+(5-1)}$$

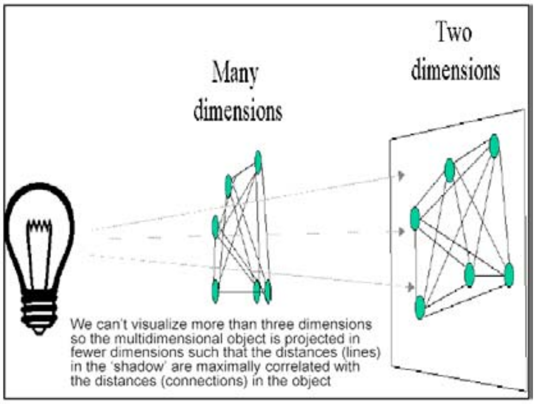
$$= \frac{7+3+1+6}{7+9+7+4} = \frac{17}{27} = 0.630$$

Stress

$$S = \left\{ \left[\sum_{i<j} [d_{ij} - \hat{d}_{ij}]^2 \right] \Big/ \left[\sum_{i<j} d_{ij}{}^2 \right] \right\}^{1/2}.$$

Where d_{ij} is the distance in ordination space between samples i and j, and

for each sample pair, i and j; the regression between the distance measure and distance produces a value, *d*^ij



We can't visualize more than three dimensions so the multidimensional object is projected in fewer dimensions such that the distances (lines) in the 'shadow' are maximally correlated with the distances (connections) in the object

Questions:

Is it possible to detect differences in in the communities of arthropods that assemble on different genotypes of the same host tree?

Questions:

Is it possible to detect the community level consequences of selection on foundation tree species?

When community level selection occurs, how can the significance of its effects be measured?

The Central Prediction of Community Genetics

(Whitham et al. 2003, 2006)

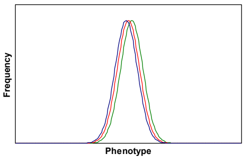
Genetically based interactions between foundation species and their associated organisms generate particular community phenotypes.

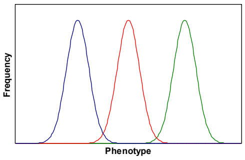
Partitioning Variance Components

ANOVA Asks:

Does the variance exist mainly ***within groups*** (are group means similar?)

Does it exist mainly ***among groups*** (are group means different?)





Broad Sense Community Heritability, H^2_C

Measures the phenotypic covariance of arthropod communities on related cottonwood trees.

(Shuster et al. 2006; Whitham et al. 2006).

When groups are clones,

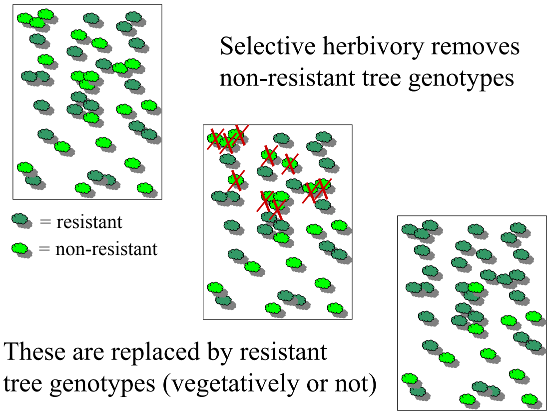
$H^2_C = [\sigma^2_{\text{among host genotype}} / \sigma^2_{\text{total}}]$

The contribution of all genetic factors influencing community phenotypic variation.

Questions:

Is it possible to detect the community level consequences of selection on foundation species?

When community level selection occurs, how can the significance of its effects be measured?



Selective herbivory removes non-resistant tree genotypes

These are replaced by resistant tree genotypes (vegetatively or not)

Which Phenotypes?

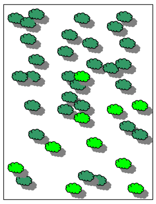
Trees (genotypic and phenotypic variation)

Arthropods (Genotypic and phenotypic variation)

Communities

(phenotypic variation)

What to Measure?



$X_{1j.} = \Sigma\, p_{1jk} x_{1jk}$

$V_{x1j.} = \Sigma\, p_{1jk}(X_{1j} - x_{1jk})^2$

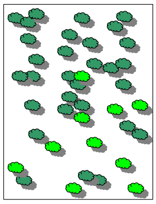
x_{ijk} = the NMDS score of the k-th community in the j-th stand of trees in the i-th treatment.

p_{ijk} = the frequency of the k-th community in the j-th stand of trees in the i-th treatment.

$X_{ij.}$ = the average community phenotype in the j-th stand of trees in the i-th treatment.

$V_{Xij.}$ = the variance in community phenotype in the j-th stand of trees in the i-th treatment.

Two Treatments, n Replicates

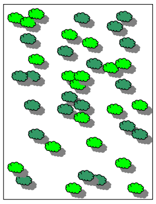


With beavers

$X_{1j.} = \Sigma\, p_{1jk} x_{1jk}$

$V_{x1j.} = \Sigma\, p_{1jk}(X_{1j} - x_{1jk})^2$

x_{11} V_{x11}	x_{21} V_{x21}
x_{12} V_{x12}	x_{22} V_{x22}
x_{13} V_{x13}	x_{23} V_{x23}
⋮	⋮
x_{1n} V_{x1n}	x_{2n} V_{x2n}



Without beavers

$X_{2j.} = \Sigma\, p_{2jk} x_{2jk}$

$V_{x2j.} = \Sigma\, p_{2jk}(X_{2j} - x_{2jk})$

The Total Variance

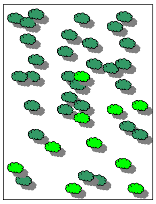
$$V_{total} = V_{within} + V_{among}$$

= The *average of the variances* within the classes (groups)

\+

The *variance of the averages* among the classes (groups)

With beavers



x_{11} V_{x11}

x_{12} V_{x12}

x_{13} V_{x13}

⋮

x_{1n} V_{x1n}

The Variance Within Stands

$$V_{1within} = \Sigma V_{1j.}/n_{stand} = \Sigma p_{1j.}V_{1j.}$$

The Variance Among Stands

$$V_{1among} = \Sigma(X_{1..} - X_{1j.})^2/n_{stand} = \Sigma\, p_{1j}(X_{1..} - X_{1j.})^2$$

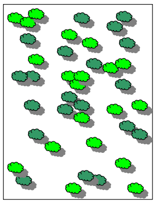
The Total Variance

$$V_{1total} = V_{1within} + V_{1among}$$

The Treatment Average

$$\mathbf{X}_{1..} = \Sigma\, p_{1jk}\, x_{1jk}$$

Without beavers



x_{21} V_{x21}

x_{22} V_{x22}

x_{23} V_{x23}

⋮

x_{2n} V_{x2n}

The Variance Within Stands

$$V_{2within} = \Sigma V_{2j.}/n_{stand} = \Sigma p_{2j.}V_{2j.}$$

The Variance Among Stands

$$V_{1among} = \Sigma(X_{2..} - X_{2j.})^2/n_{stand} = \Sigma\, p_{2j}(X_{2..} - X_{2j.})^2$$

The Total Variance

$$V_{2total} = V_{2within} + V_{2among}$$

The Treatment Average

$$\mathbf{X}_{2..} = \Sigma\, p_{2jk}\, x_{2jk}$$

The Grand Average

$$\mathbf{X}... = \Sigma\, p_{ijk}\, x_{ijk}$$

The Total Variance

$$V_{total} = V_{within} + V_{among}$$

= The *average of the variances*
within the classes (groups)
+
The *variance of the averages*
among the classes (groups)

The Total Variance

$$V_{total} = V_{within} + V_{among}$$

$$= \{[V_{1total}+V_{2total}]/2\} + \{\Sigma (X_{...}-X_{i..})^2]/2\}$$

Wade 1976

“Just as individual selection requires that there be differences between individuals, group selection requires that there be differences between populations.

…this between-populations variance is the *sine qua non* of group selection.”

Has Community-Level Selection Occurred?

$$V_{1among} / V_{total}$$

= The fraction of the total variance in community phenotype that arises due to beaver herbivory

Questions:

Is it possible to detect the community level consequences of selection on foundation species?

When community level selection occurs, how can the significance of its effects be measured?

F-tests

Snedecor and Cochran, 1983

The formula for *F* (for R.A. Fisher) is

$$F = \frac{s_1^2}{s_2^2}$$

The variance are usually arranged so that F>1. i.e., $s_1^2 > s_2^2$.

$F = \frac{s_1^2}{s_2^2}$

Degrees of Freedom

Sokal and Rohlf 1981

The upper variance (among groups) is based on the variance of some number of averages.

Usually, $v_1 = a(k - 1)$,

Where k = the number of individuals per group

Or, v_1 may = $(n - 1)$.

The lower variance (within groups) is based on the mean of some number of variances.

Usually, $v_2 = a - 1$

Where a = the number of variances.

In Most Cases

You test for significant differences in the variances (4 steps).

1) Invoke a null hypothesis that the two variances are from the same population. (i.e., they are not statistically different)

2) Calculate the F value (the ratio of the two variances)

3) Look up the table value of F for the degrees of freedom used to calculate both variances and for a given confidence level.

4) If the calculated F is greater than the table value, then the null hypothesis is not correct.

Conclusions:

It IS possible to detect the community level consequences of selection on foundation species.

When community level selection occurs, the significance of its effects can be measured using variance ratio tests.

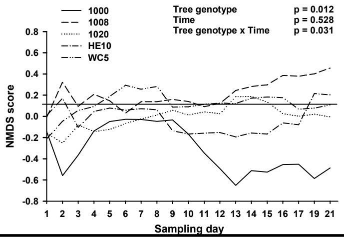
Chaitophorus on Narrowleaf

(Wooley et al. almost in review)

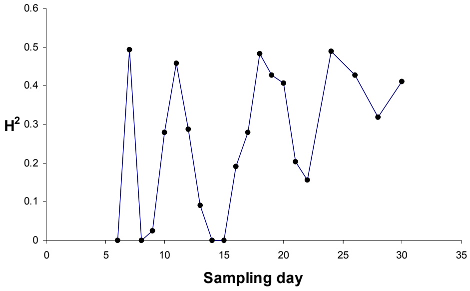
Four aphid clones on 5 *P. angustifolia* genotypes

Clone abundances monitored over 32 days

Figure 2



Heritability of aphid genotypic community structure over time



The Opportunity for Selection

(Crow 1958, 1962; Wade 1979)

$$I = V_W/\bar{W}^2 = V_w$$

Compares the fitness of favored individuals *relative* to the population before selection.

The **variance in relative fitness**, V_w, provides an empirical estimate for selection's strength.

The Opportunity for Selection on Community Phenotype

					Within trees								
TreeGeno	TreeLoc	AphidGeno	day	Number	Waphgen	Vaphgen	Vwithin	Vamong	Vtotal	Wgrand	Iwithin	Iamong	Itotal
1000	N7-6	NU	6	1	0.50	0.25	0.25	0.13	0.38	1.00	0.25	0.13	0.38
1000	S5-6	NU	6	1									
1000	S6-14	NU	6	0									
1000	SSG1-1	NU	6	0									
1000	N7-6	RB4	6	3	1.50	0.75							
1000	S5-6	RB4	6	1									
1000	S6-14	RB4	6	1									
1000	SSG1-1	RB4	6	1									
1000	N7-6	S9	6	1	1.00	0.00							
1000	S5-6	S9	6	1									
1000	S6-14	S9	6	1									
1000	SSG1-1	S9	6	1									
1000	N7-6	T	6	1	1.00	0.00							
1000	S5-6	T	6	1									
1000	S6-14	T	6	1									
1000	SSG1-1	T	6	1									
1008	N3-22	NU	6	3	1.00	1.50	0.42	0.01	0.43	0.94	0.48	0.01	0.49
1008	N4-14	NU	6	0									
1008	S3-7	NU	6	1									
1008	S5-23	NU	6	0									
1008	N3-22	RB4	6	1	0.75	0.19							
1008	N4-14	RB4	6	1									
1008	S3-7	RB4	6	0									
1008	S5-23	RB4	6	1									
1008	N3-22	S9	6	1	1.00	0.00							
1008	N4-14	S9	6	1									
1008	S3-7	S9	6	1									
1008	S5-23	S9	6	1									
1008	N3-22	T	6	1	1.00	0.00							
1008	N4-14	T	6	1									
1008	S3-7	T	6	1									
1008	S5-23	T	6	1									

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