MULTIVARIATE STATISTICS

Practical session





 Summarise multivariate data into a smaller number of variables that represent the main sources of variation in the data (ordination)

Site	Sp1	Sp2	Sp3	Sp4	Sp5
1	0	4	3	5	1
2	0	0	0	3	0
3	1	1	2	2	0
4	2	2	0	2	1
5	6	0	4	0	8
6	0	0	6	0	2



Site	Axis 1	Axis 2
1	-1.04	0.14
2	-1.12	-0.70
3	-0.65	0.13
4	-0.51	-1.48
5	2.87	-0.91
6	0.46	2.82





Non metric multidimensional scaling

- Common method for "unconstrained ordination"
- Uses dissimilarity between sites calculated using a dissimilarity index (can use a large range of indices)
- Makes no assumptions about how species are related to gradients of variation





Principal components analysis

- Very common method for unconstrained ordination
- Uses Euclidean distances
- Assumes a linear relationship between variables and ecological gradients – often unsuitable for species data





(Detrended) correspondence analysis

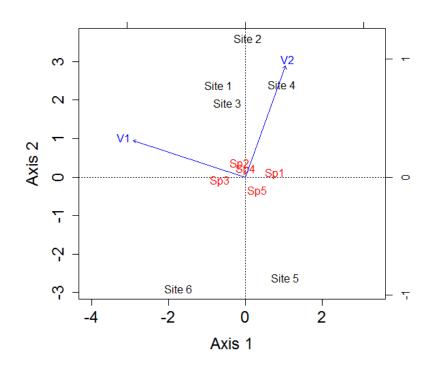
- Another common method of unconstrained ordination
- Dissimilarity is calculated based on Chi-square distances
- Assumes a unimodal relationship between species and ecological gradients
- Detrending procedure removes some issues with traditional correspondence analysis





 Test whether patterns in variation are explained by independent variables (constrained ordination)

Site	Sp1	Sp2	Sp3	Sp4	Sp5	V1	V2
1	0	4	3	5	1	4.5	1.2
2	0	0	0	3	0	2.4	1.1
3	1	1	2	2	0	5.3	2.1
4	2	2	0	2	1	2.4	1.4
5	6	0	4	0	8	2.5	1.3
6	0	0	6	0	2	5.5	0.8







Constrained correspondence analysis

- Considers the variation that can be explained by environmental variation (constraints)
- Can use an ANOVA-like permutation procedure to test whether constraints are significant





 Test for differences between groups of samples based on multiple variables (e.g. MANOVA)

Site	Sp1	Sp2	Sp3	Sp4	Sp5	Group
1	0	4	3	5	1	Α
2	0	0	0	3	0	Α
3	1	1	2	2	0	Α
4	2	2	0	2	1	Α
5	6	0	4	0	8	В
6	0	0	6	0	2	В

	Df	SS	MS	F	R2	Р
Group	1	0.65	0.65	4.61	0.53	0.06
Residuals	4	0.56	0.14		0.46	
Total	5	1.21				





Multivariate ANOVA (with dissimilarities)

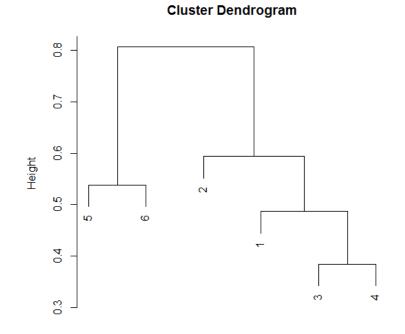
- Extension of ANOVA to use dissimilarities
- Can include either factor (e.g. group) predictors or continuous predictors
- Can use any dissimilarity index





 Find groups of samples that share similar properties based on multiple variables (e.g. cluster analysis)

Site	Sp1	Sp2	Sp3	Sp4	Sp5
1	0	4	3	5	1
2	0	0	0	3	0
3	1	1	2	2	0
4	2	2	0	2	1
5	6	0	4	0	8
6	0	0	6	0	2



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Cluster analysis

- Groups samples based on similarity
- Can use cut-offs to create clusters for further analysis





Practical

- Resources are in
- Using 'vegantutorial.pdf'
- Will require following R packages:
 - vegan
 - vegan3d
 - MASS



