PRIMER-e
Empowering Research

PRIMER 7 Online Workshop

Outline of Topics

*Each **lecture topic** below is followed by a **computer practical** session where participants explore the topic using literature/published datasets.*

1	Measures of resemblance (similarity/dissimilarity/distance) in multivariate structure for assemblage and environmental data, including shade plots to assess the effects of pre-treatment options (standardisation, transformation, normalisation), and guidelines for coefficient choices for different data types.
2	Hierarchical agglomerative clustering of samples (**CLUSTER**) and brief mention of other clustering methods. Includes discussion of a global test for the presence of any multivariate structure in *a priori* unstructured biotic or abiotic samples, using similarity profiles (**SIMPROF** tests).
3	Ordination (for environmental data) by principal components analysis (**PCA**).
4	Ordination (of assemblage data) by non-metric multi-dimensional scaling (**nMDS**) and MDS diagnostics (e.g. stress, minimum spanning tree, cluster overlay) for adequacy of low-d representation. Also how this relates, through the Shepard diagram, to metric MDS (**mMDS**).
5	Global hypothesis tests of no agreement between two resemblance matrices (**RELATE**), comparing assemblage (or environmental) structure with linear or cyclic models in space and time.
6	Dispersion weighting to down-weight highly clumped/schooled species having erratic abundances over replicates at the same time/place. Lab session also includes a method for 'fixing' collapsed **nMDS** plots.
7	Multivariate testing for differences among *a priori* specified groups of samples using non-parametric analysis of similarities (one-way **ANOSIM**, global and pairwise tests). Ordination plots to examine multivariate means. Introduction to bootstrap computation of approximate region estimates for means in **mMDS** plots.
8	**ANOSIM** tests for factors with ordered levels and for multi-way designs (up to 3 factors).
9	Linking potential environmental drivers to an observed assemblage pattern, via the matching of multivariate structures (the **BEST** procedure). Test of no evidence for a biota-environment link, allowing for selection effects in finding an optimum match (global **BEST** test).
10	Linkage trees as a further technique for 'explaining' assemblage patterns by environmental variables (**LINKTREE**), and its relation to unconstrained divisive clustering (**UNCTREE**).
11	Species' contributions to sample patterns: **BIOENV** as a step-wise form of **BEST** to identify minimal-sized species subsets required to reconstruct the full assemblage pattern, and species' contributions to similarities (**SIMPER**), a pairwise approach for statistically established groups.
12	Direct analysis of species (or other variables) through species resemblances: a technique for identifying coherent groups of species (or other variables) in their response across samples.
13	Diversity measures (**DIVERSE**); multivariate treatment of multiple indices; dominance plots; taxonomic (or phylogenetic) diversity and distinctness, sampling properties and testing structures (**TAXDTEST**).
14	Second-stage analysis (**2STAGE**) to compare taxonomic levels and transformations, etc.; also for a possible testing framework in some repeated measures designs.
15	Any methods that have not arisen in earlier discussion (e.g., further resemblance options: modifying Bray-Curtis for denuded samples; resemblance calculations when some data are missing; dissimilarity measures based on taxonomic distinctness, etc.). Wrap-up of the week with an overview of the **PRIMER** tools.
16	Own-data analysis sessions, in consultation with the presenter.

PRIMER 7 Online workshop

Provisional Time-Table

The timetable below is a rough guide only. Lectures and labs may flow over or under allotted time-slots, depending on the depth of coverage of specific topics, the number and length of participant-led questions and ensuing discussions, etc. The flow between lectures and labs will be seamless. All times below are given in USA Eastern Standard Time (UTC -5 hrs).

	Monday	**Tuesday**	**Wednesday**	**Thursday**	**Friday**
Session 1 09:00 – 11:00	(1) Resemblance measures; pre-treatment options	(4) Ordination with nMDS; mMDS	(7) ANOSIM; Bootstrap averages	(11) Species' contributions; BIOENV; SIMPER	(15) Wrap-up; overview of PRIMER v7
Coffee Break 11:00 – 11:30					
Session 2 11:30 – 13:00	(2) CLUSTER; SIMPROF	(4) Ordination with nMDS; mMDS (cont'd)	(8) Ordered and multi-way ANOSIM	(12) Coherent species; SIMPROF	(16) 'Own-data' session
Lunch 13:00 – 14:00					
Session 3 14:00 – 16:00	(2) CLUSTER; SIMPROF (cont'd)	(5) RELATE; seriation or cyclical models	(9) BEST; global test	(13) DIVERSE; dominance plots; TAXDTEST	(16) 'Own-data' session (cont'd)
Coffee Break 16:00 – 16:30					
Session 4 16:30 – 18:00	(3) Ordination with PCA	(6) Dispersion weighting; "fix" nMDS	(10) LINKTREE; UNCTREE	(14) Second-stage analyses; 2STAGE	(16) 'Own-data' session (cont'd)

Throughout, participants will be given real data sets to analyse, but they are also encouraged to bring their own data. These should be in numeric, rectangular arrays, with variables (e.g. species) as rows, samples as columns (**or** *vice-versa*), in an Excel spreadsheet or text file. Non-numeric information (factors) on each sample are placed below (or to the side of) this table, separated by a blank row (or blank column). There is also a 3-column format (sample label, variable label, non-zero entry) suitable for entry from large record-type databases. Participants will have the opportunity (during the 'own-data' sessions scheduled for Friday) to connect with other participants and to discuss their own data, projects, sampling designs and analyses in direct consultation with the presenter.