PRIMER-e
empowering research

ADVANCED WORKSHOP on
PRIMER v7 and PERMANOVA+
Multivariate Analysis in Ecology (& other Sciences)

OUTLINE of TOPICS – ADVANCED PRIMER/PERMANOVA WORKSHOP

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

1	***Introduction and mini-review*** – typical exploratory multivariate analysis pathway in PRIMER (Data > Transform > Resemblance > Cluster > MDS); the wizards.
2	***Get the data in and check it out*** – Data types, transformations (including shade plots, histograms, etc.), standardisations, normalisation, overview of dissimilarity measures and their properties, handling of missing data, dispersion weighting, zero-adjusted Bray-Curtis.
3	***Cluster analysis and recent extensions*** – flexible beta, similarity profiles (SIMPROF) for assessing "significant" splits (Type I) and derived factors.
4	***Cluster analysis, continued*** – unconstrained divisive method (UNCTREE), non-hierarchical method (kRCLUSTER), constrained clustering (LINKTREE).
5	***MDS and beyond, part 1*** – Shepard plots; new diagnostics and plotting options for non-metric MDS (minimum spanning trees; display of iteration progress and time-series animations; 2d & 3d cluster overlays).
6	***MDS and beyond, part 2*** – Metric MDS, threshold metric MDS; combined MDS, including a new feature to "Fix collapse"; bootstrap averages for visualising variation in averaged data.
7	***Species analyses*** – clustering and ordering options for axes of the new shade plots; new testing methods (SIMPROF Type 3) producing coherent variable curves; segmented bubble plots.
8	***Non-parametric tests*** – ANOSIM (ordered or unordered factors), RELATE (including tests for seriation and cyclicity), BEST (finding combinations of environmental variables which together create distances to match biotic dissimilarities).
9	***PERMANOVA, part 1*** – ANOVA as a partitioning; extend to a multivariate dissimilarity-based geometric approach, with tests (p-values) by permutation.
10	***PERMANOVA, part2*** – Multi-factorial designs – nested vs crossed; fixed vs random; expectations of mean squares; components of variation; PCO; distances among centroids
11	***PERMDISP*** – Tests for homogeneity of multivariate dispersions; permutation of residuals; analyses of beta diversity.
12	***Other topics in biodiversity*** – Taxonomic diversity, functional diversity, phylogenetic diversity, taxonomic distinctness (AvTD, VarTD), taxonomic dissimilarities, cophenetic distances.
13	***DISTLM*** – Dissimilarity-based linear models; multivariate multiple regression; diagnostics and model selection criteria (R^2, adjusted R^2, AIC, AICc, BIC) and procedures (forward, backward step-wise and "best").
14	***DISTLM and dbRDA*** – fitting sets of predictor variables; categorical predictors; constrained ordination.
15	***CAP, part 1*** – canonical analysis of principal coordinates; discriminant analysis based on distances; classification of new samples using canonical models.
16	***CAP, part2*** – Predicting positions along a known gradient; monitoring programmes; canonical correlation analysis.
17	***Synthesis*** – overview of methods; example application of multiple complementary methods learned across the PRIMER/PERMANOVA+ suite of tools.
18	'Own-data' analysis session, in consultation with the presenter/lecturer.

PROVISIONAL TIME-TABLE – ADVANCED PRIMER/PERMANOVA WORKSHOP

The time-table 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.

	Monday	Tuesday	Wednesday	Thursday	Friday
Session 1 08:30 – 10:15	(**1**) Introduction; mini-review; wizards	(**5**) nMDS; diagnostics; animations; cluster overlays	(**9**) PERMANOVA; geometric partitioning	(**13**) DISTLM; diagnostics; model selection	(**17**) Synthesis; overview of methods
Coffee Break 10:15 – 10:45					
Session 2 10:45 – 12:30	(**2**) Diagnostics on multivariate data	(**6**) mMDS; tmMDS; fix collapse; bootstrap averaging	(**10**) PERMANOVA; multi-factorial designs; PCO	(**14**) DISTLM; dbRDA	(**18**) 'Own-data' session
Lunch 12:30 – 13:30					
Session 3 13:30 – 15:15	(**3**) Cluster analysis; flexible beta, SIMPROF	(**7**) Species analyses, SIMPROF; coherent variable curves	(**11**) PERMDISP; beta diversity;	(**15**) CAP; discriminant analysis; predictive models	(**18**) 'Own-data' session (cont'd)
Coffee Break 15:15 – 15:45					
Session 4 15:45 – 17:30	(**4**) UNCTREE; kRCLUSTER; LINKTREE	(**8**) ANOSIM ordered and multi-factor; RELATE; BEST	(**12**) Taxonomic, functional & phylo-diversity	(**16**) CAP; gradients; canonical correlation	(**18**) 'Own-data' session (cont'd)

Throughout, participants will be given real data sets to analyse, but they may also wish 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 should take every opportunity during labs and breaks to discuss their data with the presenter, prior to Friday as well as in the final 'own-data' session.