3.1 Compare example output

PERMANOVA *vs* 'adonis2'

It is instructive to look at a particular example. Let's compare the results we get using a routine in R and a routine in PRIMER that should (on the face of it) do the same thing.

We'll compare:

- PERMANOVA (a routine in the PERMANOVA+ add-on package for PRIMER) *versus*
- 'adonis2' (a function in the 'vegan' package for R, Oksanen *et al.* (2022))

These are both (purportedly) designed to do PERMANOVA . More specifically, they should do the following:

1. Perform a partitioning of multivariate variation in the space of a chosen resemblance measure in response to a multi-factor ANOVA-type study design.
2. Construct a test of significance for each term in the ANOVA model using a (pseudo) F-ratio test-statistic , and
3. Calculate a p-value for each term empirically, using permutations.

For details regarding the PERMANOVA methodology, see Legendre & Anderson (1999) , McArdle & Anderson (2001) , Anderson (2001a) and Anderson (2017) . For details regarding correct construction of the test-statistic and estimation of components of variation using expectations of mean squares, see Cornfield & Tukey (1956) , Hartley (1967) , Rao (1968) , Searle (1971) , Hartley *et al.* (1978) and Searle *et al.* (1992) . For details regarding permutation methods, see Anderson & Legendre (1999) , Anderson (2001b) and Anderson & ter Braak (2003) .

Example data

We will consider an example dataset of assemblages colonising holdfasts of the kelp *Ecklonia radiata* in a 3-factor hierarchical experimental design. There were $n = 5$ holdfasts collected from each of 2 areas (tens of meters apart) at each of 2 sites (hundreds of meters to kilometers apart) from each of 4 locations (hundreds of kilometers apart) in rocky reef habitats along the northeastern coast of New Zealand (Anderson *et al.* (2005a) , Anderson *et al.* (2005b)).¶

There were 351 taxa from 15 different phyla quantified in this study. Here, we shall focus only on the phylum Mollusca (105 taxa).

Our interest lies in quantifying the degree of turnover in the identities of mollusc species at different spatial scales, as measured by the Jaccard resemblance measure. This a fully hierarchical

sampling design with three spatial factors, as follows:

- Locations (random with 4 levels: Berghan Point, Home Point, Leigh and Hahei)
- Sites (random and nested in Locations, with 2 sites per location)
- Areas (random and nested in Sites, with 2 areas per site)

Areas are therefore also (necessarily) nested in Locations.

For a detailed set of steps you can take to analyse these data in PRIMER with PERMANOVA+, see Chapter 7 'Run a PERMANOVA' in the online resource 'A Quick Guide to PRIMER'.

¶ *These data are provided as an example with the PERMANOVA+ add-on for PRIMER in the file called hold.pri in the folder named 'HoldNZ' inside the 'Examples add-on' folder. This folder can be downloaded directly from inside PRIMER with PERMANOVA+ by clicking Help > Get Examples add-on....*

Revision #28
Created 13 May 2024 23:31:16 by Marti
Updated 15 May 2024 02:52:47 by Marti