

Analysing between variables

The introduction above of the concept of ‘distances’ among species raises the issue of how best to compute *species similarities* – or more generally *variable associations* – taking the menu option of **Analyse>Resemblance>(Analyse between•Variables)**. Several significant new developments in PRIMER 7 (see Section 10 and Chapter 7 of CiMC) on *shade plots* and *coherent species curves* concern better display and analysis techniques for characterising responses of individual (or groups of) species across the samples in space, time or over a changing environment. Two species are considered perfectly similar if they co-occur across samples – with numbers or biomass in strict proportion, for quantitative data. As with sample similarities, the issue of how to treat joint absence is often relevant here too – it would often be appropriate to regard the absence of two species at a particular site as uninformative (a clay-living and a gravel-living species are not similar because neither are found at sandy sites). A measure which captures this biological constraint well is the Whittaker Index of Association (IA), met earlier in this section. As remarked then, this will give the same outcome as standardising species (by total) and applying Bray-Curtis on the species. The (implicit) standardisation however will come unstuck with all-blank species, which must certainly be removed, and it is also almost always a good idea to remove all the ‘occasional’ species, rarely observed and with low abundances when they do occur. The various options for reducing to the ‘most important’ species were covered at the end of Section 3, and for standardising species near the start of Section 4; these options would not usually apply when calculating sample similarities, but are important to eliminate wildly erratic, and not meaningful, similarities among rare species.

On the **Groundfish density** matrix, **Select>Variables>(•In at least n samples where n is: 10)**. To see how many species are retained (61, in fact), click on the sheet’s final row which displays this in the status bar at the foot of the PRIMER desktop. Take **Analyse>Resemblance>(Measure•Index of association) & (Analyse between•Variables)** to create the species similarities (*Resem4* perhaps). Show that the same outcome is produced (*Resem5*) by putting the selected species from **Groundfish density** through **Pre-treatment>Standardise>(Standardise•Variables) & (By•Total)**, followed by **Analyse>Resemblance>(Measure•Bray-Curtis similarity) & (Analyse between•Variables)**.

The screenshot displays the PRIMER 7 software interface. The 'Select Variables' dialog is open, showing the 'In at least n samples where n is' option selected with a value of 10. A 'Select' menu is open, highlighting 'Variables'. The 'Resemblance' dialog is also open, with 'Index of association' selected as the measure. The 'Resem4' window shows the results for 'Groundfish NW European shelf' with a similarity matrix.

Select Variables Dialog:

- Variable numbers: []
- Indicator levels: Indicator name: Class# Levels: []
- Use n-most important where n is: 1
- Use those that contribute at least: 5 %
- In at least n samples where n is: 10

Resemblance Dialog:

- Measure:
 - Bray-Curtis similarity
 - Euclidean distance
 - ☒ Index of association
 - Other
- Analysed between:
 - Samples
 - ☒ Variables
- Add dummy variable: [] Value: 1

Resem4 Window:

Groundfish NW European shelf
Similarity (0 to 100)

Variables	Raja nae	Raja und	Raja clav	Raja micr
Raja naevus				
Raja undulata	0			
Raja clavata	5.8475	5.8114		
Raja microocell	1.9481	9.4202	8.1165	
Raja brachyura	17.892	10.278	21.361	22.191

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