Avoiding strict label matching

The best policy to avoid confusion is to use precise, unique species and sample labels (typically, the sample label would be a conglomeration of all the different study design factors and a replicate number). However, conflicting desirable criteria can sometimes arise, e.g. when the pattern of sites from year 1 is to be compared with the pattern in year 2, using the RELATE test (Section 14) on the two separate similarity matrices, *identical* sample (site) labels are ideally needed in both arrays, so they can be matched. But, as just pointed out, a Merge of the two data sheets underlying these similarities (so that both year 1 and 2 sites can be seen on the same *n*MDS say) requires the sample labels to be *different*. Thus, PRIMER is not dogmatic about label matching: several routines, which include **Merge** and **RELATE**, are able to 'fudge' the matching and provide a natural alternative. In **Merge**, this is shown above, using the •Join (rename duplicates) option, used either for Samples or Variables (or possibly both, to create a block diagonal matrix, though this is unlikely to be needed). For Tasmania nematodes v4 and Tasmania copepods v4 sheets to be placed one under the other, even though they share species labels, take **Tools>Merge** >(Variables•Join(rename duplicates)) and defaults for the other options, i.e. (Samples•Merge(strict names)), and there should be no combined or new cells. The copepods are labelled 1(2), 2(2), …, to distinguish them from nematodes 1, 2, … Save the workspace Tasmania ws and close it.

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