Multiple selections

It is important to note the effect of this second selection on WA fish diets %vol; it produces a sheet of all samples from these three *Sillago* species. The prior exclusion of samples A9, B3 and B4 has been ignored – each new selection is a fresh operation on the full data array that is held in that worksheet. If, as seems likely, a compounding of the two selections was required, then that is easily achieved, in at least two ways. One would be to take the current selection (all B, E and G samples), highlight everything displayed (e.g. by clicking in the blank, left corner box), dehighlight B3 and B4, by clicking on their column labels, then **Select>Highlighted**. (This is logically sound because all the omitted A, C, D, F samples from the first selection are not highlighted at that point.) This would retain the single copy of WA fish diets %vol in the Explorer tree. A more general option though, which would be more relevant to a complex multiple sequence of selections, is simply to **Tools>Duplicate** the sheet after every selection, then do the next selection on the new sheet. So, if the above selection of the *Sillago* samples had taken place on Data2, samples B3 and B4 would automatically have been excluded. Note, however, that if the two selections are on different axes (selecting a subset of both samples and variables) then they will not interfere with each other, i.e. when sequentially taking **Select>Samples**>•Factor levels and **Select>Variables**>•Indicator levels.

A third option for repeated selection of samples, with the outcome of multiple selection being a single worksheet (rather than a series of copies), is to create a compound factor (with **Factors> Combine**), which will allow simple selection of one (or more) of its levels.

To illustrate this, save and close down the above workspace, as WA fish ws(.pwk), and re-open the previous workspace, C:\Examples v7\Tasmania meiofauna\ Tasmania ws. Here there are only 16 samples, which helps for illustrative purposes (though in the real context would make selections quickest by simple highlighting). The study design has two crossed factors: *Trt* (disturbed, D, and undisturbed, U, sediment patches), and *Blk* (4 areas of sand-flat, B1 to B4), with 2 replicates in each combination. An example of 2-factor selection for the Tasmania nematodes sheet would be to select distinct sand patches within each treatment, say blocks 1 and 3 for D, and blocks 2 and 4 for U (which would make the data sheet 2-factor nested rather than crossed). Use the *Blk-Trt* combined factor created in the previous section to **Select>Samples**>•Factor levels>(Factor name: Blk-Trt)> **Levels**, leaving B1-D, B3-D, B2-U, B4-U in Include and moving the others back to Available.

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