

# 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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