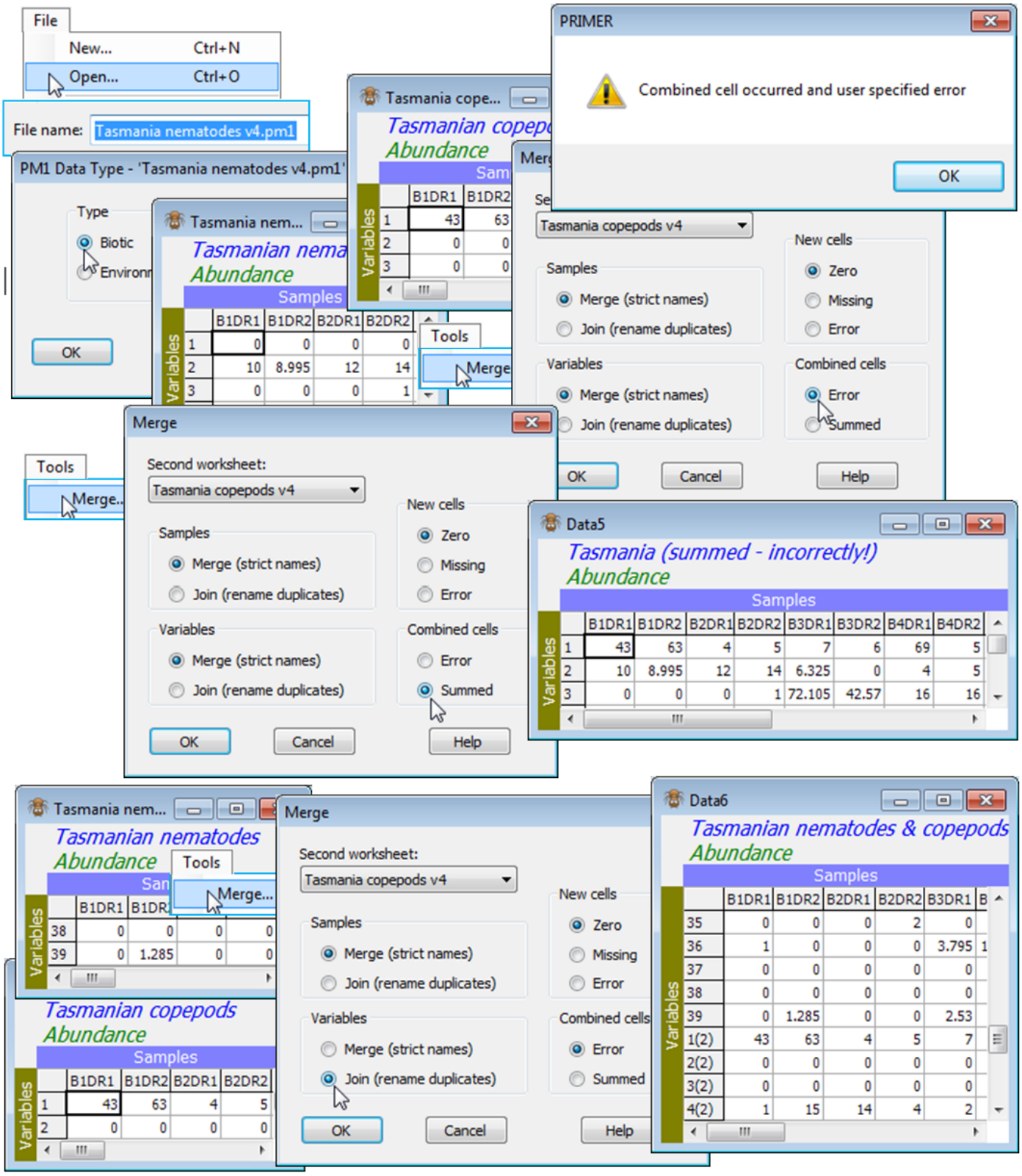
Combined cells in Merge

Occasionally, use of strict label names does not give the this desired outcome, and the default behaviour can be changed to force PRIMER to consider an identical label, but in a different matrix, to be treated as a different name. For example, this might be needed when species names have not been provided for either set, and the variable labels are just the numbers 1, 2, 3, …. Species 1 in the first set is not to be taken as the same variable as species 1 in the second set, and the default options in **Merge** will cause difficulty in this case. Equally possible is the opposite case where the species names match in the two matrices, but the same sample labels are repeated, though should not be equated. Samples collected in year 1 might be labelled by their site identification. A second matrix of data from those sites in year 2 might use exactly the same set of sample labels, i.e. without reference to the year. This causes no confusion if the matrices are to be analysed separately, but a **Merge** under the default of strict name-matching would place the two matrices on top of each other (because they have exactly the same row and column labels!). The two options given in such a case are (Combined cells•Summed) or (Combined cells•Error). The first literally adds the two matrices, element by element. Very often though, this is not the desired behaviour, so the default is the second option: if a **Merge** instruction results in an attempt to combine two cells, an error results.

In the same workspace, take **File>Open** on the data files Tasmania nematodes v4 and Tasmania copepods v4 (in *.pm1 format, from the old DOS-based PRIMER4), which should be read in as Type•Biotic. These are the same nematode and copepod matrices as their *.pri counterparts except that PRIMER v4 held species lists as separate files so both the *.pm1 files have variables numbered just 1, 2, 3, …, though the species are different in the two matrices. A **Tools>Merge** on them, with the default of (Variables•Merge (strict names)) will potentially give combined cells. Try this with both (Combined cells•Error) in place, to note the error message and the fact that execution then stops. Then repeat with (Combined cells•Summed) – those cells with the same species and sample numbers *are* then simply added together. This may occasionally be a useful option, e.g. it would allow for easy collation of data for the same samples by several different observers (though it must be debatable whether such a piecemeal approach to data matrix construction – losing information on potential observer differences – is often desirable). Taking nematode species 1 to be the same taxon as copepod species 1 and adding the two counts is clearly nonsense in this context, however. The solution, if it is easier to join the arrays in PRIMER and then rename the variable labels later, is next described (the Join option) – this forces the arrays to be placed one after the other.



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