Label matching

Alternatively, the same endpoint could have been achieved by Adding three new blank factors to the copepod sheet and copying and pasting the contents of the *Blk*, *Trt* and *Blk-Trt* columns from the nematode factor sheet. If importing entries from an external source, such as an Excel column, this approach may sometimes be necessary but it is only appropriate when the samples are in the same order in the two data sets (as they are here). In contrast, **Import** operates by matching up the sample labels in the two files and can therefore re-order the factor levels appropriately when the samples are in a different order. This is a general feature of PRIMER 7 – a lot of use is made of label matching across data sets in this way, which is why it is vital that labels are defined uniquely within a set and carefully checked for consistency of spelling across sets. Of course, if the two sets of sample labels are not identically defined, but do refer to the same set of samples, in the same order, then a copy and paste of the factor content is the only way of transferring the factors.

Revision #1
Created 19 May 2024 22:55:32 by Arden
Updated 19 May 2024 22:57:44 by Arden