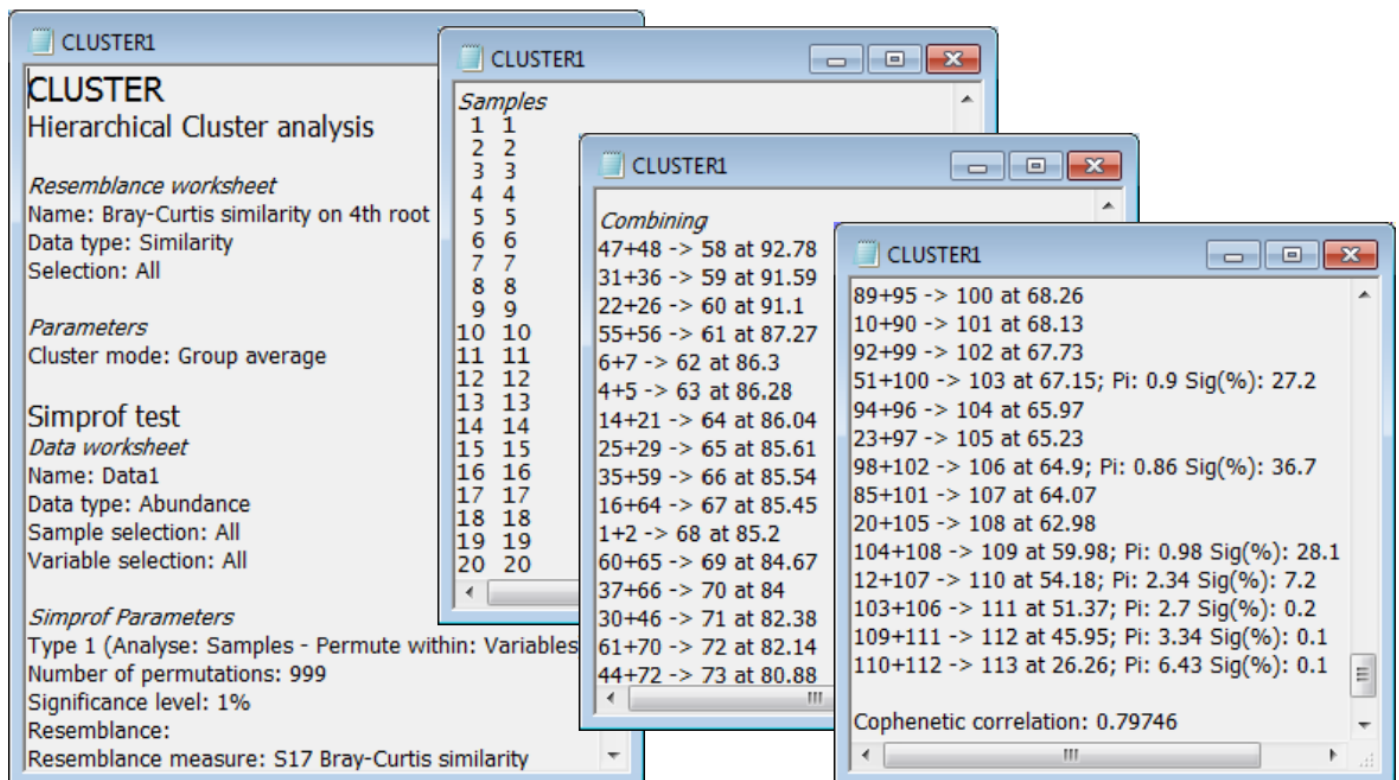# CLUSTER results window

In addition to the dendrogram plot itself, **Analyse>CLUSTER** (like all analysis routines) produces a separate Results window (here CLUSTER1) which firstly lists the conditions under which the analysis was run (e.g. whether on a selection of the matrix, with what linkage option etc.), and then outputs text-format information. For succinctness, the Results windows will often use the sample numbers (1-57) rather than the sample labels (stations 1-29, 31-58, confusingly, since station 30 was not sampled!), so a listing is initially given of the numbers and their corresponding labels (the last label here, of sample 57, thus being station 58). Then the results specify, numerically, how the dendrogram is constructed, just in case the precise numbers are needed for another purpose: sample numbers 47 & 48 (stations 48 & 49) are the first to group, at similarity 92.78, with the new group labelled 58, then 31 & 36 group at 91.59, ..., 16 & 64 (i.e. 16 & 14 & 21) at 85.45 etc. Likely to be most useful here, however, are the SIMPROF test results. These are read from the bottom upwards: π=6.4 (p<0.1%, its most extreme value for 999 permutations) for a test that all samples are from the same assemblage; and π=3.3 & 2.7 (p<0.1% or 0.2%) for the successive splits, at 46.0% and 51.4% similarity, of the three right-hand groups. Site 12 is borderline for splitting from the rest of the left-hand group, at 54.2% similarity (π=2.3, p<7%), but there is no evidence for the apparent division of the second group into two at 60.0% similarity (π=1.0, p<28%), or any of the other groups. Tests of finer-level structure are not carried out, if the differentiation of the coarser level structure is not significant, so only seven tests are needed here. Note that the choice of threshold significance level (p<1%) for rejecting the null hypothesis of 'no structure' is not at all critical here – p<5% or p<0.5% would have led to the same set of decisions – and such robustness is common.