Text pane in tree plots; A% and B% y-axis scales

Note how each node is now lettered so that information about the R value for that split can be displayed in the *text pane* underneath the tree, and also in the accompanying results window (right). The lettering size in the tree can be increased (as it has been here) by **Graph>General>Info font**. The lettering order looks a little haphazard but this is only because the tree has been rotated exactly as seen for the earlier dendrograms – by clicking on the horizontal lines – in order to allow a better comparison with the previous agglomerative clustering. (In fact, the SIMPROF tests again result in only four groups, largely similar to those found before). The text pane can be scrolled and dragged down or up to smaller or larger heights but it but does not serve a particularly strong function here and could be turned off altogether by unchecking the (✓Show text pane) box on the **General** tab. It comes into its own for the companion routine of *constrained* divisive clustering (LINKTREE) seen in Section 13. There the text pane will list, for example, the inequalities on environmental variables which are capable of 'explaining' each lettered division of the biotic communities. Note also that, as for agglomerative clustering, details are given in the text-based results window (UNCTREE1) of the π statistic and its significance level from the SIMPROF test at each node for which the test is performed. For example, the initial split A into groups B and I is highly significant ($p<0.1\%$) but that at B, into the group C and the single sample 9, only achieves a non-significant level according to the criterion for continuation set in the SIMPROF dialog ($p<5\%$). Thus no more tests are carried out on the nodes further down this branch (C, D, E, …), as can be seen in the results window.

The choice of *A%* as the *y*-axis scale above, evens out the spacing of steps down the binary tree in essentially arbitrary fashion, to give an uncluttered presentation – values of *A%* in different parts of the tree are not then quantitatively comparable (and a cophenetic correlation coefficient would make no sense). The alternative, originally described for the LINKTREE routine by Clarke KR, Somerfield PJ, Gorley RN 2008, *J Exp Mar Biol Ecol* 366: 56-69, is to take the (Vertical positions• B% – split quality) option in the UNCTREE dialog, in which average rank dissimilarities between groups on the original ranks (not re-ranked at each stage) are used to define a scale reflecting the magnitude of a division, in relation to the overall scale of variation (e.g. community change) across the full set of samples. The *B%* values are therefore comparable across different parts of the tree.

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