Quantitative measures on P/A data; Unravelling resemblances; Scatter plots

It is instructive to draw the other links between quantitative coefficients and the presence/absence measures they reduce to, when calculating them on a P/A matrix. Pure distance measures such as D_1, D_6, D_7 and D_{10}, which are not averaged in some way over the number of species, clearly cannot reduce to the dimensionless ratios in the P/A similarity definitions above. Similarly, D_{15}, D_{16}, S_{15} and S_{19} are not of interest in this context because they are not just functions of a, b, c, d for the two samples but bring in species for all other samples, in their species standardisations. However, the other quantitative measures mainly reduce to simple monotonic functions of four P/A similarities: S_1 (simple matching), S_7 (Jaccard), S_8 (Sørensen) and S_{14} (Ochiai P/A). Of course, as defined, the relationships will be between D and $(1 – S/100)$. To be precise: D_2 reduces to the square root of the complement of $S_1/100$; both D_3 and D_{17} go to the square root of $2(1 – S_{14}/100)$, D_4 to $\cos^{-1} (S_{14}/100)$ and S^{Och} to S_{14}; D_8 reduces to the complement of S_7, D_{11} to the square root of that complement, and S^{Can} to S_7. As noted earlier, S_{17} reduces to S_8 and, finally, S_{18} goes to S_{13}.

In less technical description: average Euclidean distance (squared) is the natural counterpart of simple matching (they are both functions of the number of joint absences); chord, geodesic and Hellinger distance, and naturally quantitative Ochiai, all have an affinity to the P/A form of Ochiai; Czekanowski’s mean character difference, the divergence coefficient and Canberra similarity all relate to Jaccard; Bray-Curtis reduces to Sørensen and, unsurprisingly, the quantitative and P/A forms of the Kulczynski coefficient converge, e.g. as strong transforms force the data towards P/A.

Demonstrate one of these points for the Ekofisk abundance data in the Ekofisk ws – which should still be open – by calculating Hellinger distance (D_{17}) on the presence/absence data produced from the macrofauna sheet, and comparing this with the Ochiai P/A coefficient (S_{14}). Thus:

a) With Ekofisk macrofauna counts as the active window, **Pre-treatment>Transform(overall)**> (Transformation: Presence/absence) to produce the P/A matrix, then renamed P-A (forward slash is not a permitted symbol in the Explorer tree, since these may sometimes be filenames);

b) On P-A, **Analyse>Resemblance**>(Measure•Other: D17 Hellinger distance) & (Analyse between •Samples), renaming the *Resem* sheet to Hell on P-A. [Do not take ‘Add dummy variable’ here – or routinely (always think carefully about it first!). It will have negligible effect here on relative distances because there are no denuded samples at all. However, the option is permitted with all measures and could make sense, in the presence of blank or near-blank samples (which are then required to have zero or near-zero distances/dissimilarities), for all those coefficients identified above (as ratios). This is essentially anything with a y term or p_{12} in the denominator,

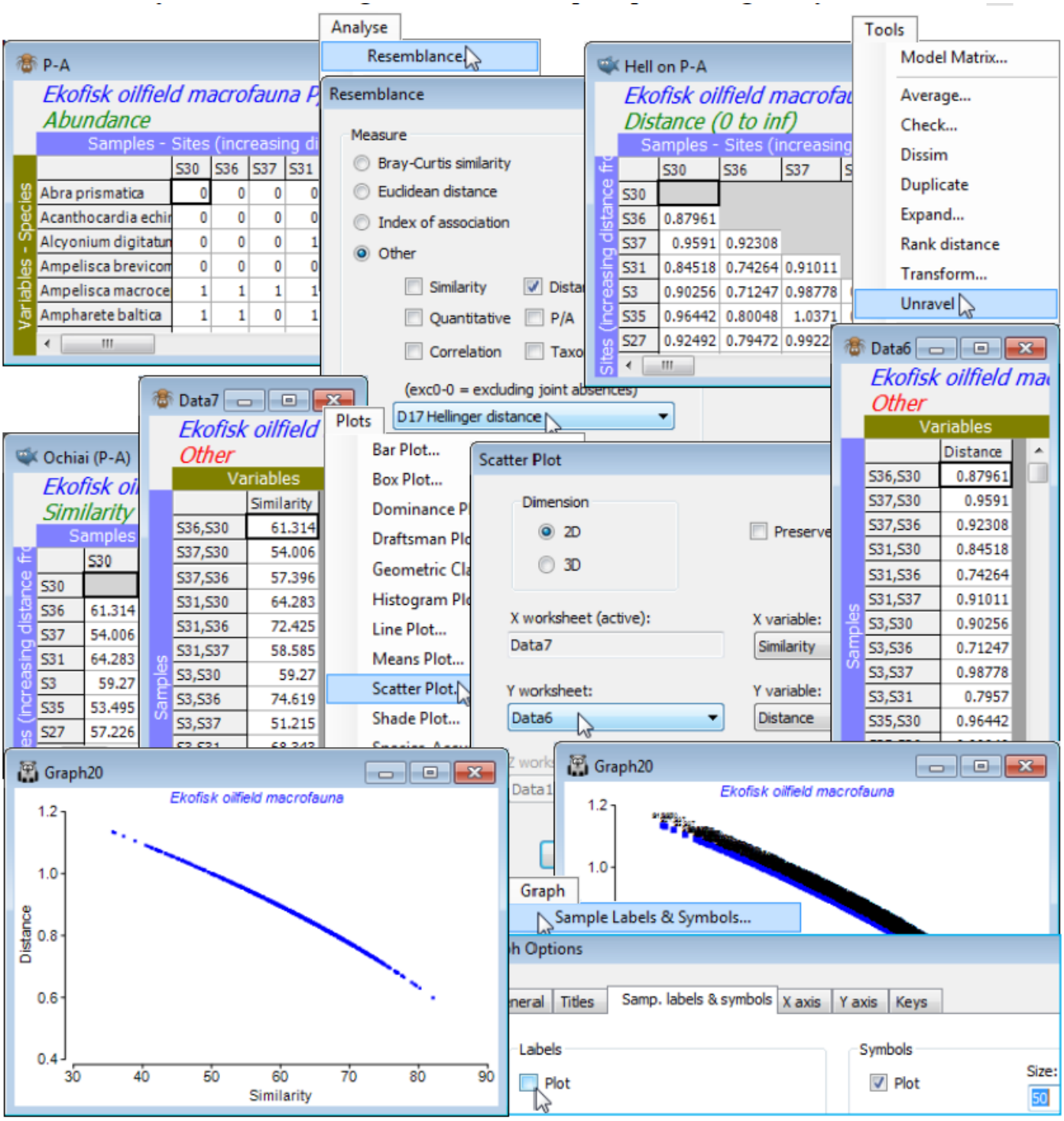
since these give an Undefined! resemblance entry for blank samples. The pure distance measures D_1, D_6, D_7 and D_{10} will be unchanged with an added dummy, as will the species-standardised S_{15} (which promptly has to remove the just-added dummy variable since its range R_i over samples is zero!)]

c) On Ekofisk macrofauna counts take **Analyse>Resemblance**>(Measure•Other:S14 Ochiai(P/A)), renaming the result to Ochiai (P/A).

To view the relationship between these matrices, exploit two of the new features in PRIMER 7:

d) **Run Tools>Unravel** on both Hell on P-A and Ochiai (P/A), to turn these triangular matrices into long single columns (unravelling the rows), possibly now called Data6 and Data7.

e) With Data7 (say) as the active sheet, take **Plots>Scatter Plot**>(Dimension•2D) & (X variable: Similarity) & (Y worksheet: Data6) & (Y variable: Distance) – of course the X worksheet is the active Data7 – to see that Hellinger distance (on P/A data) is a decreasing function (near-linear here) of Ochiai similarity. The unnecessary sample labels can be removed by **Graph>Sample Labels & Symbols**, unchecking Labels✓Plot, and perhaps reducing the Symbols to Size: 50.



Revision #12
Created 7 June 2024 21:02:35 by Arden
Updated 15 January 2025 02:14:41 by Abby Miller