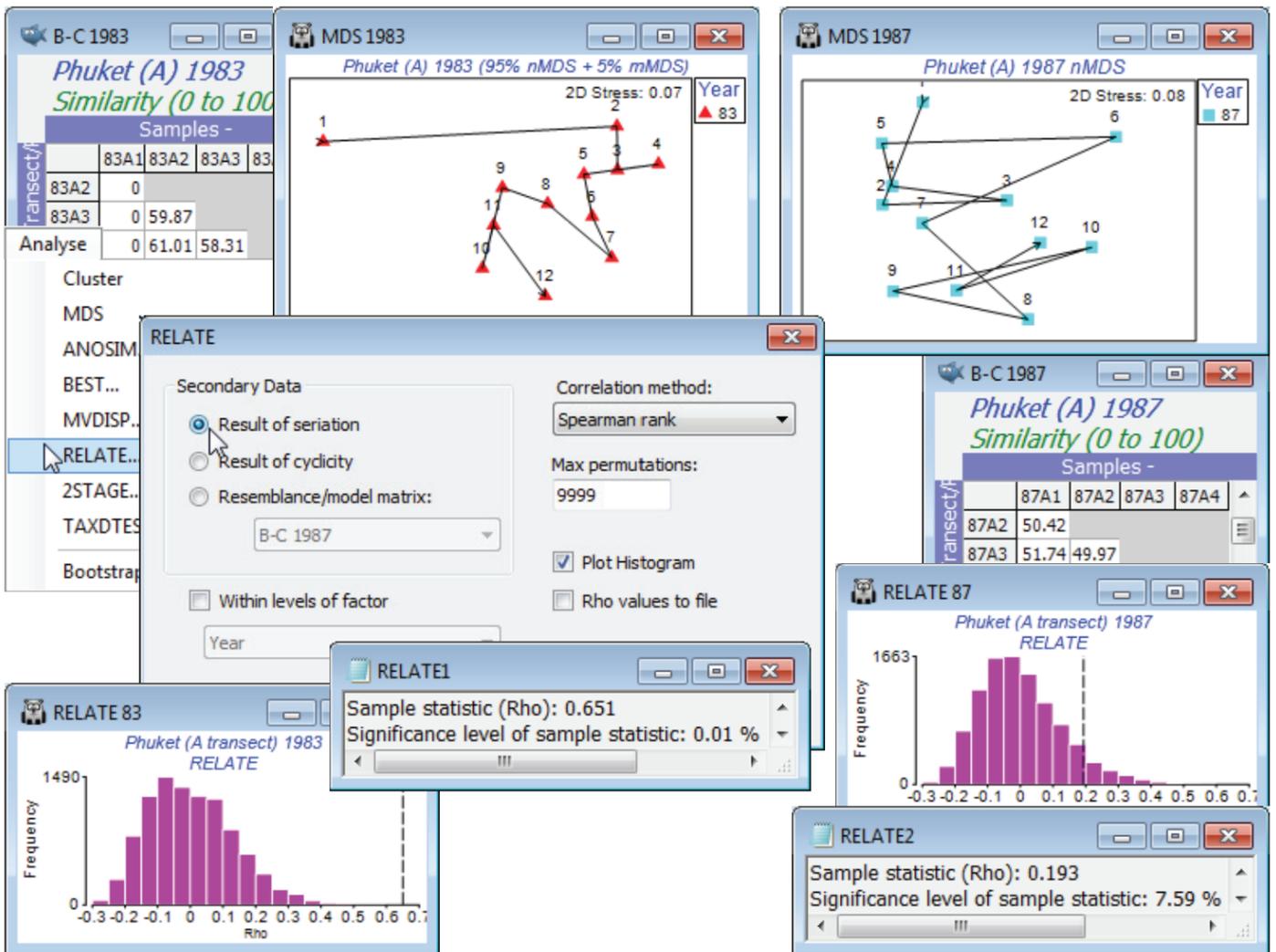


Seriation (Phuket coral transects)

The Phuket coral-reef assemblages at equi-spaced positions down an onshore-offshore gradient (transect A) from Phuket Island, were seen previously in Sections 8, 9 and 11. Open the workspace **Phuket ws**, or if not available open just **Phuket coral cover 83-87** from C:\Examples v7\Phuket corals, square-root transform, calculate similarity and create *n*MDS plots such as that of Section 8, separately for the two years 1983 and 1987. Do this by selecting the 12 samples along the transect in 1983, with **Select>Samples>(•Factor levels)>(Factor name: Year>Levels>(Include: 83)** - note that **Select** works in just the same way on a resemblance matrix as a data sheet - then take **Tools>Duplicate** to make a copy of this smaller resemblance matrix, renaming it **B-C 1983**. **Analyse>MDS>Non-metric MDS** with default options, except (Fix collapse)>(Metric proportion: 0.05). This is needed to avoid the collapse of the *n*MDS plot because of the outlying first point on the transect (as seen in Section 8). With **Graph>Special>Overlay>(✓ Overlay trajectory)>(Numeric trajectory factor: Position)**, the serial change in coral community over the transect positions is clear. Repeat these steps for 1987, giving resemblance **B-C 1987**. The choice of (Fix collapse) is not necessary here but if you run the *n*MDS with and without this option you will see that it makes no difference at all to the outcome - the metric proportion of the minimised combined stress function is so small that it cannot influence the plot unless there really is no non-metric information to use, as for Position 1 in 1983, when the metric stress kicks in. (You may want to use the Procrustes routine, **Graph>Align Graph** on one of these plots, specifying the other as the (Configuration Plot:) to match to - see Section 8) **Align graphs automatically** - to see they are indeed identical).



The serial change along the transect in 1983 has largely disappeared in 1987, with sedimentation impact from nearby dredging for a deep-water port. This is reflected in the RELATE tests shown above, with ρ declining from 0.651 to 0.193, e.g. on B-C 1983, **Analyse>RELATE** >(Secondary Data•Result of seriation) & (Max permutations: 9999), with defaults for the other choices, gives a histogram and results window with observed $\rho = 0.651$ greater than for any of the 9999 simulated values, so the null hypothesis of no seriation at all ($\rho \approx 0$) is decisively rejected, $p < 0.01\%$. Note that the strong outlier has not wrecked this test, though it somewhat degrades the match to a model of equi-stepped change, as is seen by ρ rising to 0.75 if this first transect position is omitted. [Since we have not provided the factor **Position** when using the (•Result of seriation) option, the routine has to assume that samples are in the desired equi-stepped serial order – a different order, or a wish to fit unequal steps, perhaps by omission of an intermediate transect sample, must be handled by a Model Matrix.] The $\rho = 0.193$ for 1987 is more in the body of the null distribution however, and there is no clear evidence in the RELATE test for any serial structure ($p \approx 7.5\%$). In this simple case, there is a very close link with the ordered, unreplicated 1-way ANOSIM test on factor **Position** (see Section 9), with R (not ρ) statistics of $R^{\{Os\}} = 0.655$ ($p < 0.01\%$) and 0.194 ($p \approx 7.0\%$) for 1983 and 87.

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