

Relatedness supplied as resemblances

Note the alternative means of supplying the variable information, to these dissimilarity measures and the biodiversity indices of Section 15, which is now available in PRIMER 7. In the Variable Relationship dialog box, Type•Resemblance>**Details** now requires specification of a numeric among-species resemblance matrix which could be constructed from genetic, functional, etc. data, but is illustrated here by first creating a species distance matrix through the Linnean tree with **Analyse>Similarity** when the aggregation file **Groundfish taxonomy** is the active window. This takes you to a similar Taxonomy dialog box as above and creates sheet **Resem2** of among-species distances 20, 40, 60, 80, 100. The Linnean tree could be viewed by **Analyse>Cluster** (next section) on **Resem2**, or in alternative format by **Tools>Tree** on **Groundfish taxonomy**. When **Resem2** is supplied as the Variable resemblance worksheet from **Details**, the same γ^+ matrix results, naturally.

The image displays several overlapping windows from the PRIMER 7 software interface, illustrating the process of creating a resemblance matrix from taxonomic data.

- Groundfish density**: Shows a table of abundance data for groundfish species across samples S79 to S82.
- Groundfish taxonomy**: Shows a table of taxonomic data for the same species, including Genus, Family, Order, and Class.
- Variable Relationship**: A dialog box where 'Type' is set to 'Resemblance' and 'Details' is clicked.
- Taxonomy (Master)**: A dialog box showing 'Variable info. worksheet (taxonomic)' as 'Groundfish taxonomy' and 'Current level of sample data' as 'Species'.
- Variable simil...**: A dialog box showing 'Master taxonomy' and 'Variable info. worksheet: Grou...'.
- Resem2**: A window showing the resulting 'Taxonomy for NW European shelf Dissimilarity (0 to 100)' matrix.
- Resem3**: A window showing the resulting 'Groundfish NW European shelf Dissimilarity (0 to 100)' matrix.
- Tree**: A window showing a hierarchical tree structure of the taxonomy data.

