Pre-treatment of data

Pre-treatment of the data (sometimes in more than one way) is usually desirable. For assemblage data, transformations will reduce the dominant contribution of abundant species to Bray-Curtis similarities. Though not usually needed for controlled (‘quantitative’) sampling, standardising of samples to relative composition (so sample totals are all 100%) can be achieved, with Fal nematode abundance active, by **Pre-treatment>Standardise**>(Standardise•Samples) & (By•Total) – the Wizard default was not to standardise but it did give that option, where % composition is desired.

Transformation of all values (which should be after standardisation, if the latter is appropriate) is obtained by, for example, **Pre-treatment>Transform (overall)**>(Transformation: Square root). A more severe transform would have been by Fourth root or Log(X+1) or by the ultimate in severity of transformation – reduction of the quantitative data to purely Presence/absence of each species. Since the purpose of transforming is to avoid the ensuing analysis becoming dominated by just one or two species with very large abundances, and bring more species into the definition of similarity of two assemblages – whilst at the same time avoiding giving sporadic, singleton species too much weight – the effects of competing choices can be assessed by running the second **Wizards** item.

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