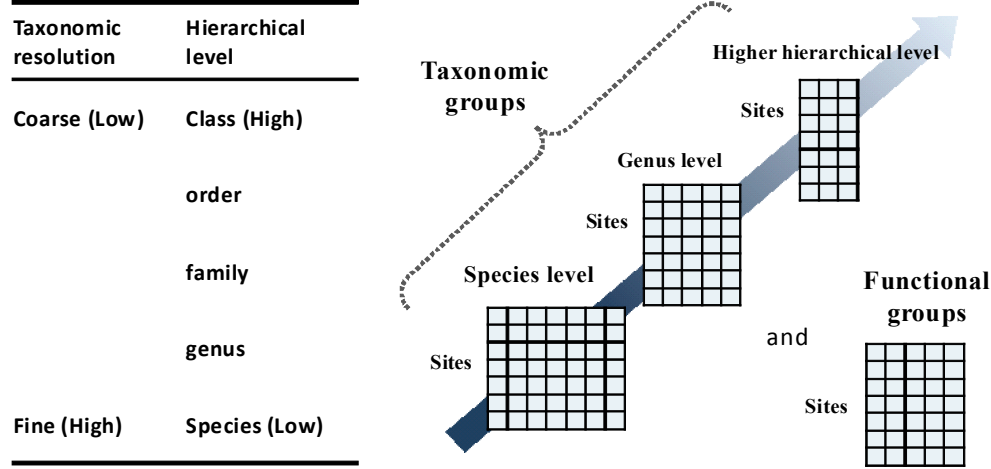


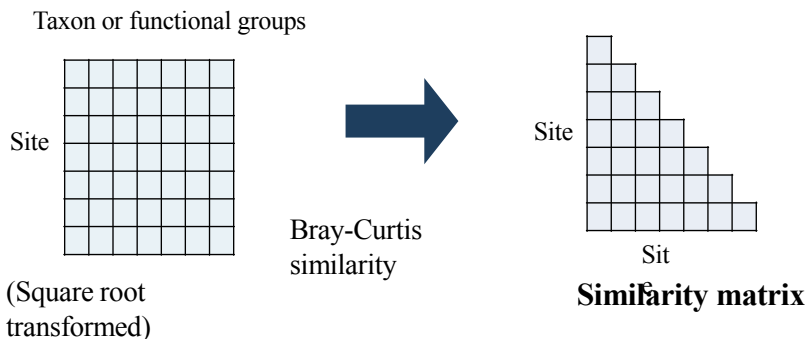
Step 1. Hierarchical level of assemblage dataset



圖一、流程一需將不同分類解析度的生物群集資料建檔，分類階層越高，分類解析度越低（資料來源：本研究繪製）

Fig. 1. Biological dataset identified by hierarchical level was constructed in first step. More coarse taxonomic resolutions mean a lower hierarchical level in taxonomy. Each dataset composited of column (sampling unit as single site) and raw (taxonomic groups) represented the hierarchical level of assemblage.

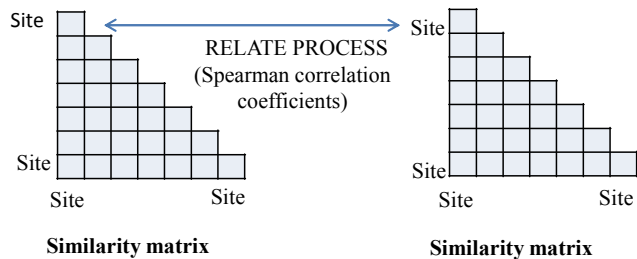
Step 2. Similarity matrix formation



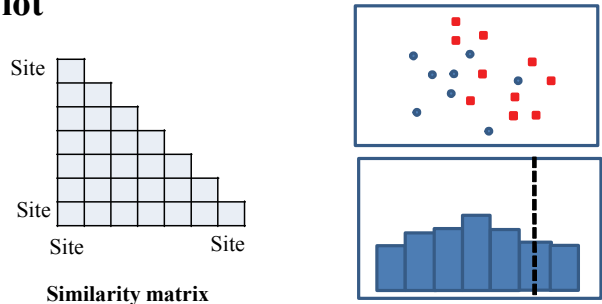
圖二、流程二以不同分類階層生物群集資料形成相似性矩陣（資料來源：本研究繪製）

Fig. 2. Biological similarity matrix was formed from assemblage dataset in second step. Bray-Curtis similar distance between sampling units.

Step 3-1. Correlation measurement among Similarity matrix



Step 3-2. Significance testing of ANOSIM and NMDS plot



圖三、流程三以多變量工具計算不同分類解析度：3-1.相似性矩陣間的相关性； 3-2.環境影響因子之分群檢測（資料來源：本研究繪製）

Fig. 3. Multivariate was used in third step for: 3-1. The correlations among similarity matrix 3-2 Significance testing and NMDS plot of environmental factor.