# 17.10 Concluding remarks on taxonomic distinctness

Early applications of taxonomic distinctness ideas in marine science can be found in Hall & Greenstreet (1998) for demersal fish, Piepenburg, Voss & Gutt (1997) for starfish and brittle-stars in polar regions, Price, Keeling & O'Callaghan (1999) for starfish in the Atlantic, and Woodd-Walker, Ward & Clarke (2002) for a latitudinal study of pelagic copepods. An early non-marine example is the work of Shimatani (2001) for forest stands. Over the last decade the index has become very widely used and cited. A bivariate example is given by Warwick & Light (2002) who use 'ellipse' plots of expected ($\Delta ^ +$, $\Lambda ^ +$) values, from live faunal records of the Isles of Scilly, to examine whether easily sampled bivalve and gastropod 'death assemblages' could be considered representative of the taxonomic distinctness structure of the live fauna.

Too much should not be claimed for these methods. It *is* surprising that anything sensible can be said about diversity at all, for data consisting simply of species presences, and arising from unknown or uncontrolled sampling effort (which usually renders it impossible to read anything into the relative size of these lists). Yet, much of the later part of this chapter suggests that not only can we find one index (AvTD) which is comparable across such studies, capturing an intuitive sense of biodiversity, but we can also find a second one (VarTD), with equally good statistical properties, and which may (sometimes at least) capture a near independent attribute of biodiversity structure.

Nonetheless, it is clear that controlled sampling designs, carried out in a strictly uniform way across different spatial, temporal or experimental conditions, must provide additional, meaningful, comparative diversity information (on richness, primarily) that $\Delta ^ +$ and $\Lambda ^ +$ are designed to ignore. Even here, though, concepts of taxonomic relatedness can expand the relevance of richness indices: rather than use *S*, or one of its variants (see Chapter 8), total taxonomic distinctness (TTD) or total phylogenetic diversity (PD), see page 17.4, capture the richness of an assemblage in terms of its number of species *and* whether they are closely or distantly related.

**Sensitivity and robustness**

Returning to the quantitative form $\Delta^*$, the Ekofisk oilfield study suggested that such relatedness measures may have a greater sensitivity to disturbance events than is seen with species-level richness or evenness indices ( Warwick & Clarke (1995a) and Warwick & Clarke (1995b) ). This suggestion was not borne out by subsequent oil-field studies ( Somerfield, Olsgard & Carr (1997) ), particularly where the impact was less sustained, the data collection at a less extensive level and hence the gradients more subtly entwined with natural variability. But it would be a mistake to claim sensitivity as a rationale for this approach: there is much empirical evidence

that the best way of detecting subtle community shifts arising from environmental impacts is not through univariate indices at all, but by non-parametric multivariate display and testing (Chapter 14). The difficulty with the multivariate techniques is that, since they match precise species identities through the construction of similarity coefficients, they can be sensitive to wide scale differences in habitat type, geographic location (and thus species pool) etc.

Though independent of particular species identities, many of the traditional univariate indices have their own sensitivities, to habitat type, dominant species and sampling effort differences, as we have discussed. The general point here is that robustness (to sampling details) and sensitivity (to impact) are usually conflicting criteria. What is properly claimed for average taxonomic distinctness is not sensitivity but:

a) *relevance* – it is a genuine reflection of biodiversity loss, gain, or neither (rather than recording simply a change of assemblage composition), and one that appears to respond in a monotonic way to impact;

b) *robustness* – it can be meaningfully compared across studies from widely separated locations, with few (or even no) species in common, from different habitats, using data in presence/absence form (and thus not sensitive to dominant species), and with different sampling effort. This makes its natural use the comparison of regional/global studies and/or historic data sets, and it is no surprise to find that many of the citing papers address such questions.

**Taxonomic artefacts**

A natural question is the extent to which relatedness indices are subject to taxonomic artefacts. Linnean hierarchies can be inconsistent in the way they define taxonomic units across different phyla, for example. This concern can be addressed on a number of levels. As suggested earlier, the concept of mutual distinctness of a set of species is not constrained to a Linnean classification. The natural metric may be one of genetic distance (e.g. Nei (1996) ) or that from a soundly-based phylogeny combining molecular approaches with more traditional morphology. The Linnean classification clearly gives a discrete approximation to a more continuous distinctness measure, and this is why it is important to establish that the precise weightings given to the step lengths between taxonomic levels are not critical to the relative values that the index takes, across the studies being compared. Nonetheless, it is a legitimate concern that a cross-phyletic distinctness analysis could represent a simple shift in the balance of two major phyla as a decrease in biodiversity, not because the phylum whose presences are increasing is genuinely less (phylogenetically) diverse but because its taxonomic sub-units have been arbitrarily set at a lower level. Such taxonomic artefacts can be examined by computing the (AvTD, VarTD) structure across different phyla in a standard species catalogue, and Warwick & Somerfield (2008) show that the 4 major marine phyla do not suffer badly from this problem, though rare phyla with few species *do* have substantially lower AvTD. The pragmatic approach, as here, is to work within a well-characterised, taxonomically coherent group.

**Master species list**

Concerns about the precise definition of the master list (e.g. its biogeographic range or habitat specificity) also naturally arise. Note, however, that the existence of such a wide-scale inventory is not a central requirement, more of a secondary refinement. It is not used in constructing and contrasting the values of $\Delta ^ +$ for individual samples, and only features in two ways in these analyses:

1. In the funnel plots (Figs. 17.8, 17.12, 17.14), location of the points does not require a master species list, the latter being used only to display the background reference of the mean value and limits that would be expected for samples drawn at random from such an inventory. In Fig. 17.12, in fact, the limits are not even that relevant since they apply to *single* samples rather than, for example, to the mean of the tens of samples plotted for each sea area. The most useful plot for interpretation here is simply a standard *means plot* of the observed mean $\Delta ^ +$ and its 95% confidence interval, calculated from the replicates for each sea area (see Rogers, Clarke & Reynolds (1999) and Warwick & Clarke (2001) ).

2. In Table 17.1 and Fig. 17.3, the master species list is employed to calculate step lengths in a revised form of $\Delta ^ +$ – weighting by taxon richness at the different hierarchical levels. The existence of a master inventory makes this procedure more appealing, since if the taxon richness weighting was determined only by the samples to hand, the index would need to be adjusted as each new sample (containing further species) was added. The message of this chapter, however, is that the complication of adjusting weights in $\Delta ^ +$ for differences in taxon richness is unnecessary. Constant step lengths appear to be adequate.

The inventory is therefore only used for setting a background context, the theoretical mean and funnel limits. Various lists could sensibly be employed: global, local geographic, biogeographic provinces, or simply the combined species list of all the studies being analysed. The addition of a small number of newly-discovered species to the master inventory is unlikely to have a detectable effect on the overall mean and funnel for $\Delta ^ +$. If these are located in the taxonomic tree at random with respect to the existing taxa (rather than all belonging to the same high or low order group) they will have little or no effect on the theoretical mean $\Delta ^ +$. This, of course, is one of the advantages of using an index of *average* rather than *total* taxonomic distinctness.

It also makes clear what the limitations are to the validity of $\Delta ^ +$ comparisons. Whilst many marine community studies seem to consist of the low-level (species or genera) identifications which are necessary for meaningful computation of $\Delta ^ +$, there are always some taxa that cannot be identified to this level. There is no real difficulty here, since $\Delta ^ +$ is always used in a relative manner, *provided* these taxa are treated in the same way in all samples (e.g. treated as a single species in a single genus, single family, etc., of that higher taxon). The ability to impose *taxonomic consistency* is clearly an important caveat on the use of taxonomic distinctness for historic or widely-sourced data sets. Where such conditions can be met, however, we believe that these and similar formulations based on species relatedness, have a useful role in biodiversity assessment of biogeographic pattern and widescale change.

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