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Biodiversity Quality: a paradigm for biodiversity

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Biodiversity quality: a paradigm for biodiversity

Summary

A statistically-based assessment of biodiversity that allows biodiversity, and change in biodiversity, to be measured.

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Summary

The balance of biodiversity indices derived from *de novo* or metadata analysis of standardised biodiversity sampling allows a picture of **biodiversity quality** to be formed. This is an advance on the international definition of biodiversity, where it is referred to as the variability of genes, species and ecosystems, but where the precise meaning of the word 'variability' is not defined. This new approach, which expresses biodiversity as a series of numerical indices relating to functionality or quality, makes biodiversity open to statistical analysis for estimation of probability of difference over time, or between sites or taxonomic groups. The relationship to functional biodiversity is also discussed.

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Abstract

The internationally accepted definition of biodiversity creates difficulty in measuring difference and change. The authors suggest that well-sampled data can be used to generate a range of numerical indices reflecting species group characteristics/functionality (Species Richness, Simpson's Index, Population Density, Biomass and Species Conservation Value) that can be viewed in combination to create a picture of **Biodiversity Quality**. This overall approach has considerable advantages over the currently accepted Convention on Biological Diversity definition, based on the "variability" of genes, species and ecosystems, since the numerical expression of the indices allows the probability of difference between biodiversity quality trends and values over time, and between sites or taxonomic groups, to be assessed for statistical inference of difference.

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Introduction

The Convention on Biological Diversity defines biodiversity as follows: "**the VARIABILITY [**our capitals**] among living organisms from all sources including, *inter alia*, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems**". This definition hangs on the use of the word 'variability', in that this is at three levels: within species (genetic); between species; and between ecosystems. At the same time, 'variability' implies that a list of the different genes, species and ecosystems will describe the biodiversity. There are two major problems in this approach:

1. Two of the three levels of biodiversity present practical problems in their assessment:

i. Genes often require specific technical equipment and expertise to be studied fully, and due to the large number of variations of genes, only either very small populations, or clearly defined genetic variants (such as are demonstrated in domestic animals) can reasonably be studied. It is therefore impractical to study the large populations of many organisms at this level, as many individuals would be genetically different in some way from each other at some of the reference loci!

ii. **Ecosystems** suffer from a scale effect because they can be studied at landscape scale (e.g. a rainforest basin), locally (e.g. a woodland) or

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microscopically (e.g. the composition of a soil particle). At what arbitrary scale do we measure ecosystem biodiversity, and why?

Most ecologists have taken the practical and sensible route of studying biodiversity at the species level (species are generally far easier to define), rather than attempt the more difficult gene or ecosystem elements. Observations of species biodiversity will also have implications for the understanding of genetic and ecosystem biodiversity.

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2. The use of the word “variability” carries a problem in that, whilst it encompasses “difference”, it does not help in the measurement of biodiversity. Common practice is to measure Species Richness (the number of species in a unit area) [1.] This has been a useful approach because changes in Species Richness at a site can be recorded easily; but Species Richness is an indiscriminate statistic that, whilst relatively easy to sample, conveys very little information [2]. How does one compare changes in Species Richness? Are all species equal? Is a tiger equal to a domestic cat? Obviously not.

The practical solution to these problems has been to use an indicator approach, for example the EU 2010 countdown process [3] has a proposed 26 indicators (mostly indicating pressures on biodiversity). However, this approach also has problems because an indicator is just that: a proxy for the real thing. An estimation of the reliability of the indicator is needed, but in most cases this reliability is unknown or just not considered. Indicators are therefore rarely (if ever) validated against what they are supposed to indicate.

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For example, one would assume it was safe to conclude that predatory birds are good indicators of avian biodiversity (well-studied, large, countable, charismatic, top predators). Predatory birds in the UK have had a considerable renaissance and numbers and distribution are the best for at least thirty years or more. So is the avifauna of the UK thriving? No, there has been a disastrous decline of the smaller farmland birds and also some woodland birds, with some populations declining over 90% in the last twenty years [4]. Predatory birds would have not indicated this fact.

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So what is the way forward? We suggest that, at a time when change in biodiversity is of global concern, a new approach that allows easy statistical assessment of change in biodiversity is needed. We suggest that this approach can be accommodated in the CBD definition as a clarification of the word “variability”. For example: ‘Variability is expressed as a range of biodiversity-related indices’.

Hooper *et al.* [5] approached the problem of biodiversity from a theoretical basis. They assessed different measures of functional diversity and considered this term to include composition, richness, evenness and interactions. Searching for a pragmatic presentation of biodiversity that would be of utility to ecological consultants and their clients, Feest [6] considered biodiversity to consist of species richness, evenness/dominance, biomass, population and rarity/intrinsic value and proposed ways of measuring these elements. It can be seen that these two approaches have come to similar conclusions in attempting to take biodiversity beyond the current definition.

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Macrofungi: the worst case

In our own studies we have, in the past, been asked to do macrofungal surveys (Agaricales, Boletales and Gasteromycetales) as part of the biodiversity baseline monitoring of sites threatened by development or of particular conservation interest.

It was obvious to us that a new approach was required to provide a meaningful survey methodology and biodiversity data information. We also assumed that any methodology that could solve the problem of macrofungal biodiversity recording might also be useful for other species groups. Our methodology allows the key role played by fungi to be integrated into community studies in a way that avoids several inherent problems [7]. The following analysis also illustrates some of the problems of the current macrofungal biodiversity survey methodologies:

1. Historically, records have been collected in a random way (people with varying taxonomic expertise "walking about") so that they are the result of an unknown skill, effort or time input. These records are often in the form of a site species list, which is not standardized in its compilation, nor does it have a methodology for determining when a species can reasonably be considered no longer present. Lists therefore grow and grow and represent cumulative historical input rather than current biodiversity levels. Tofts and Orton [8] recorded fungal species present on a site for 25 years. At the end of that time they were recording new species at the same rate as when they started; *ergo,*

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it could be concluded that there was an infinite number of species at the site!. In our macrofungal methodology, the input effort is standardised and the species lists for each survey are therefore comparable. If required, a cumulative species list can be compiled for a site with an indication of the number of surveys contributing to the list and over what timescale.

2. Historically, the only records available are of fruiting bodies, but at any one time most of the fungi present are not fruiting. Ectomycorrhizal species can be recorded by the examination of mycorrhizal fine roots, but often not to the species level and the effort required is considerable. Given that we now know [9, 10, 11] that the situation below ground is highly dynamic, how reliable will this information be? It has now also been demonstrated that the incidence of mycorrhizal species occurrence on tree roots varies considerably and may be seasonal [12]. Our methodology samples the fruiting species as representing part of the whole species set. The root assessment technique does not, of course, deal with the occurrence of saprophytic fungi or those that vary in activity according to the prevailing conditions.

3. Mass fruit bodies may represent a single cloned individual, singular individuals or a mixture of both. What is to be counted? Our methodology assesses the biomass and therefore the relative biomass proportions of each species can be inferred as a component of biodiversity [13].

4. Fruit body production is seasonal, so records are of those fruit bodies present at the time of the survey (date often not recorded!). Fruit body

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production is also influenced by weather conditions, so the right weather is also a prerequisite of a survey. Our methodology partially addresses this problem as although population/biomass and species richness will vary with fruiting conditions, the other indices might not.

The Methodology

The methodology that was devised to solve the problem of macrofungal biodiversity recording was described fully in Feest [6] and in essence consists of recording numbers of fruit bodies in twenty standardised 4m radius circles (≈1000 m^2) along a line transect and then calculating a variety of indices as follows:

Species Richness: the number of species in a unit area; 1000 $m^{2;}$

Even-ness/Dominance: Shannon-Wiener, Simpson and Berger-Parker indices, based on both numbers of fruit bodies and relative species biomass;

Density/population: total number of individual fruit bodies in 1000m^2;

Relative Biomass: calculated from the area of the cap of the fungus multiplied by the number of individuals (see [13]);

Species Conservation Value Index (SCVI): calculated as a mean number representing the commonness/rarity of the species recorded and referenced from authoritative identification handbooks [14]. The standard deviation is also presented, so that the presence of a rare species will be indicated by the SD even if its presence is concealed in the mean value of the larger number of more common species.

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A review of the existing data from other biodiversity recording schemes showed that the devised methodology contained the same elements as that of Pollard and Yates [15] butterfly survey, which is well accepted and fully validated. To test the broadness of the method, data collected for the Dutch Butterfly Monitoring Scheme (de Vlinderstichting) was subjected to the above treatment to see if it added further value to the data. Biomass was assumed to be proportional to wing width [16] but the difference between the largest and smallest species is much less than for macrofungi, so in essence biomass and population density are related for butterflies

The above methodology is based on the counting of individuals, but it is not possible to record all organisms in this way, so we also applied the technique to survey data of Bryophytes, recorded as presence or absence (1 or an empty cell) within twenty 4m radius circles. The biomass input was obviously not used in this analysis.

To speed up the processing of data, a simple computer programme (Fungib) was created that presented the data in such a way that not only were the indices calculated and presented, but also the species accumulation curve shown, so that one can estimate crudely when most easily-detected species have been recorded and further sampling effort is probably not justified.

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Results

The results of the analysis of examples of three species groups (Macrofungi, Butterflies and Bryophytes) are given in Figures 1, 2 and 3 (the latter two to be found in Appendices 1 and 2?).

Figure 1:

Shows a site (Lower Woods: East Stanley Coppice, Gloucestershire UK)[surveyed for fungi. The calculated biodiversity indices are presented in the left hand corner. Note that the SD of the mean SCVI is presented and that the evenness/dominance indices are calculated based on individuals and also biomass; the latter is presented in parentheses. The species accumulation curve indicates that after sample sixteen, only two further species are recorded and that therefore the Species Richness of 47 is close to the total number of species present at the time of the survey. (Species Richness modelled Chao 1 = 57+/-6 and Chao 2 = 65+/-9)

Figure 2 (?Appendix 1):

Shows a survey of butterflies on Dutch site (169/03) in the Vlinderstichting scheme. Species richness of 23 is probably close to the actual because no new species are recorded after plot twelve (Species Richness modelled Chao 1 = 23 and Chao2 = 25) and the SCVI SD of 3.56 indicates the presence of a rare species.

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Figure 3 (Appendix 2?):

Shows bryophytes recorded simultaneously with the fungi in the plots in Fig.1 indicated by presence (1) or absence (empty cell). The sum column indicates proportional incidence out of twenty. It is clear that the Species Richness is much lower than for macrofungi, indicated by the species accumulation curve. The steepness of the curve also shows that an estimation of the total species richness close to the actual is reached quickly.

Figure 3 shows that bryophytes are a good example of taxa that are not possible to count as individuals but can still yield information on a presence/absence basis.

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These figures show that indices can be calculated *de novo* or retrospectively on well surveyed data and even such difficult groups as macrofungi can provide information.

The stability of some of these values despite the differences in the actual species recorded is an unlooked-for element. For macrofungi Feest [17] reported several sites that had been surveyed over a number of years where the data of some indices (especially SCVI) remained very stable over time despite differences in weather each year (see Table 1).

Table 1: Macrofungal data for 1995 and 1997 at Pratt's Wood, Somerset, UK

Statistic	1995	1997	t-test
SCVI	3.19	2.97	P=0.45
Mean pop	11.7	7.15	P=0.20

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Biomass	175	538	P=0.14
Species Richness	26	34	
Total Species List		51	

Only nine (<20%) species occurred in both years and yet the SCVI is very similar in both years. The biomass is different (but not quite significantly), illustrating that the years probably did differ in respect of the macrofungal fruit body yield of the site, even if the rarity of the species did not

Feest [6] reported the macrofungi records from two sites: East End Wood, New Forest, Hampshire UK, and Weston Big Wood, Somerset, UK, where it was shown clearly how the sites differed statistically. F-tests of the SCVI, Fruit Body Density and Biomass showed the two sites are significantly different ($p = 0.05$). In Feest's paper, he also shows how the data is amenable to more complicated statistical analysis with a Principle Component Analysis of seventeen years of butterfly data in the Netherlands against nitrogen Critical Load Exceedence (see below) .

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Discussion

By assessing the balance between a range of indices and their relative magnitudes, we can ascertain the 'biodiversity quality' of a site. Using numerical values to represent the pattern of Biodiversity Quality, it becomes possible to compare sites statistically over time or spatially (see [6] and [18] for examples) both by the T-test and F-test (for mean values and variance).

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Thus, in a comparison we can prioritise sites, depending on the objective of the prioritisation, for an individual statistic (e.g. Species Richness or Biomass), or for biodiversity quality, based on a suite of statistics [18]. The latter option satisfies the criticism by Gaston & Spicer [19] that biodiversity cannot be encapsulated by a single number. A range of indices representing the various qualities of the biodiversity being studied is much more informative and open to interpretation and agrees with Hooper *et al*. [5] who prefer a "wide" definition of biodiversity that encompasses varying functional properties.

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For example, a site may have a biodiversity quality that is dominated by the high biomass of a few species (low species richness), in contrast to another site where the opposite prevails. Under these circumstances, the biodiversity quality of the two sites is very different and the better value of one site over the other might be expressed by a third index such as SCVI.

A more practical example comes from research commissioned by the European Environment Agency, where Feest, van Swaay and Hinsberg [20] were asked to link two of the proposed 2010 biodiversity indicators, namely: butterfly populations and nitrogen deposition (as expressed by the nitrogen critical load exceedence or CLE) (also reported in [18]). The data was supplied by the Dutch Butterfly Conservation Society (de Vlinderstichting) who had a seventeen-year run of well-sampled standardized data for a large number of sites. These data were then allied with CLE data for the sites and a Principle Components Analysis (PCA) of all indices plus a created nitrogen sensitivity index (SNVI) produced the following result:

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Species richness was not a suitable indicator of a linkage (whereas the other indices were) since the nitrogen-sensitive species were being replaced by the nitrophilic/generalist species. The usual way of equating biodiversity with species richness would have therefore missed the other linkages.

A further benefit of the Biodiversity Quality approach is that different taxonomic groups (fungi and bryophytes as in figs 1 and 3 above, or, for example, spiders and beetles) can be compared in terms of their Biodiversity Quality, thereby facilitating assessment of the 'biodiversity importance' of sites.

What is proposed here does not create any new individual indices or values for biodiversity and follows the recommendations of Hooper *et al.* [5]. The approach of viewing these in combination is new and, it is suggested, adds significantly to the study of biodiversity and changes occurring now as a result global climate change, habitat alteration, nutrient enrichment[21] and development pressures.

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What emerges from this recommendation is a more complex picture of biodiversity, beyond political or economic interpretations, which reflects the situation far better and reduces the risk of misleading results that beleaguers the current approaches. The clarification of the word "variability" in the CBD definition through this biodiversity quality paradigm should assist ecologists in relating biodiversity to the socio-economic context that the CBD also recognises as important in the achievement of the 2010 aim of reducing the

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rate of loss of biodiversity. The disciplines will be communicating in the same numerical terms something which is currently not possible and is impeding progress.

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Figure 1.

Fungib program printout of a biodiversity survey of macrofungi in East Stanley Coppice, Lower Woods Gloucestershire, UK. Species are listed down the left-hand column and the occurrence of macrofungi in the 20 plot samples are given across the figure. The three right-hand columns give the total number of fruit bodies recorded for each species, their relative conservation value and their relative biomass. The calculated biodiversity quality indices are given in the left hand corner. The species accumulation curve can be seen to come to an asymptote at around plot 18.

Figure 2.
Fungib program printout of a butterfly survey conducted by de Vlinderstichting. Details as for figure 1.

Figure 3.
Fungib printout of a bryophyte survey conducted simultaneously with the macrofungal survey shown in Figure 1. Details as for Figure 1.

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Species name	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	Sum	BM	BI
GPS starting	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
GPS starting	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
0:41 Erpobdella nigra	6	2	1																		9	20	20
1:19 Planorbis planorbis	2	2	3	1			2	2	1				1	1	1						15	4	144
2:30 Planorbis corneus	17	12	11	1	1	4	13	3	5	6	5	3	11	5	4	3	1	2			105	2	840
3:41 Planorbis carinatus	6	4	5	3	5	5	12	2	2	4	1	2	3	10	10	2	1	5			85	2	445
4:33 Anisus vortex	1	2	6		1	5	1							1							15	3	60
5:03 Bathyomphalus contortus	23	4	7			1	4	33	28	24	28	19	3	7	18	16	17	33			294	3	844.8
5:36 Valvata piscinalis	1		1	2					2										1		7	2	42
7:00 Valvata cristata	2	3	1	1	2		1	2	2		1	2	1	2	3	2	2	6			33	2	198
8:02 Lymnaea stagnalis	8	3	5				5			1			4	3				1			26	3	156
8:10 Menetus dilatatus	55	27	35	6	5	6	19	26	24	16	29	26	29	30	26	16	26	22			461	3	2,005
10:7 Gyraulus laevis		1												2	2						5	3	15
11:29 Physa fontinalis	1	3						3	3				3	4	1		1	15			35	2	150
12:11 Lymnaea peregra	1												1								2	3	7.8
13:23 Ischnura elegans			3	5	2	1	2		1	3	2		7	11	2		1	4			44	2	264
14:56 Aphelocheirus aestivalis				16	19	21	2	2	1	1	3	4	4		6	10	8	10			86	3	488
15:19 Anacaena limbata						1				1											2	3	6
16:26 Gyraulus crista								1													1	4	5
17:39 Hydroporus palustris									1												1	5	5
18:58 Haliplus ruficollis										1											1	3	3
19:14 Polycelis nigra/tenuis												1	1	2							4	3	12
20:10 Agabus bipustulatus														1							1	2	4.5
Summary	95	62	84	36	35	46	55	70	70	61	61	60	67	62	73	49	53	90	0	0	1159	3,667	5,409.8

Species Richness = 21
Shannon-Wiener Index = 2.8878 (2.1887)
Simpson Index = 0.0418 (5.1936)
Berger-Parker Dominance Index = 0.2466 (0.3798)
Density = 1.159 per sq.m.
Species Value Index = 1.8888+3.7531
Biomass Index = 5408.8889

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Lower Woods East Stanley Bryophytes
01/11/08

Species name	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	Sum	Bit	Bit
QPP sampling	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
QPP counting	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
15: Brachythecium rivulicum	1	1	1	1	1	1	1	1	1	1	1	1		1	1	1		1	1	1	17	4	0
1: Calypogeia fissa	1	1							1		1										4	3	0
2: Eurhynchium striatum	1	1	1	1	1	1	1		1	1	1			1	1		1	1	1	1	17	3	0
3: Eurhynchium praelongum	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	20	2	0
4: Fissidens bryoides	1	1	1	1			1	1	1	1	1		1						1		11	3	0
5: Hypnum cupressiforme	1	1	1	1			1	1	1	1	1		1						1		11	3	0
6: Isothecium myosuroides	1											1				1	1				4	3	0
7: Mnium hornum	1	1	1		1	1	1	1	1	1	1		1	1	1	1	1	1	1	1	16	2	0
8: Neckera complanata	1				1					1							1				4	3	0
9: Orthotrichum affine	1	1	1	1	1	1		1	1		1		1	1	1	1	1			1	15	3	0
10: Plagiomnium undulatum	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			1	14	3	0
11: Plagiothecium denticulatum	1	1			1	1	1	1	1	1	1	1	1	1	1	1	1				15	3	0
12: Thamnobryum alopecurum	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	20	3	0
13: Ulota crispa	1		1		1				1	1	1			1	1		1				9	4	0
14: Fissidens dubius		1	1			1			1	1	1		1	1	1		1		1	1	12	3	0
15: Leptodictyum riparium		1											1			1			1		4	3	0
16: Rhytidiadelphus squarrosus	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	18	3	0
17: Thuidium tamariscinum				1			1		1				1			1	1		1	1	8	3	0
18: Homalia trichomanoides				1					1	1							1				4	4	0
19: Brachythecium velutinum							1										1	1			3	3	0
20: Leptodictyum riparium							1														1	3	0
21: Cirriphyllum heterophyllum								1													1	4	0
22: Hamatocaulis vernicosus													1								2	3	0
23: Mnium hornum																1	1				2	2	0
24: Pseudocalliergon lycopodioides																	1				1	3	0
25: Rhizomnium punctatum																			1		1	3	0
Summary	14	14	12	11	10	11	11	11	16	15	11	4	12	12	11	17	17	8	13	10	231	2.78	0

Species Richness = 26
Shannon-Wiener Index = 2.884(Ln)
Simpson Index = 16.845(0.0)
Berger-Parker Dominance Index = 0.0866(0.0)
Evenness = 0.291 per sp.m.
Species Value Index = 2.7082+4.0.0000
Blossom Index= 0.0

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