Current Trends in Ecology
Vol. 2, 2011

Original Communication

Measuring carabid beetle biodiversity quality: An example of setting baseline biodiversity indices

Alan Feest[1,*], Michael D. Eyre[2], and Timothy D. Aldred[3]

[1]Water and Environmental Management Research Centre, University of Bristol, 83 Woodland Road, Bristol BS8 1US, [2]Nafferton Ecological Farming Group, Nafferton Farm, University of Newcastle, Stocksfield, Northumberland, UK NE43 7XD, [3]24 Sion Hill, Clifton, Bristol, BS8 4AZ, UK

ABSTRACT

Carabid beetles meet the requirements of many ecological studies because they are found in almost all terrestrial ecosystems, are responsive to environmental variables, and satisfy the criteria for useful bioindicators. Carabid biodiversity studies are now active nationally and internationally, but sampling regimes are rarely standardized and are often costly and time-consuming. We describe how a pitfall sampling protocol for carabids that is simple and easily repeatable by non-specialists can be used for the rapid assessment of site biodiversity quality baselines for the detection of change. Using this methodology, change in carabid beetle biodiversity quality is revealed, which would not be detected by simple registration of species richness or the presence of rare species.

KEYWORDS: beetles, biodiversity quality, carabidae, standardized methodologies, biomass, species richness

INTRODUCTION

Invertebrates are numerically dominant in most ecosystems [1], yet their protection has traditionally been dependent on trends in larger, more accessible taxa [2]. Logistical setbacks with sampling, combined with the problems of hyperdiversity and the effort needed in time, money and taxonomic expertise to quantify invertebrate fauna has typically militated against their use in routine conservation planning [2, 3, 4, 5]. Increasingly, efforts are being made to integrate invertebrates into surveys, but a lack of common standards and incongruent sampling techniques gives rise to stochastic and patchy data. This prevents decision-makers from making reasoned comparisons between sites, which is a critical component of conservation actions such as reserve design and development compensation. However, the application of a standardized sampling method would foster uniformity of biodiversity values and allow site comparisons using unbiased data [6, 7, 8].

Post hoc statistical techniques such as rarefaction (editing of large data sets to match the size of the smallest sample) and regression models (extrapolating species richness for a given amount of effort invested) have been employed to correct for variation in sampling effort [9, 10, 11]. However, data loss from rarefaction invalidates large samples, and the errors inherent in both estimation systems could be avoided if standardized sampling techniques were available from the offset. Efforts to produce standardized sampling protocols have been made for a range of taxa, including butterflies [12], birds [13, 14], mammals [15], carabid beetles [16, 17], crayfish [18], ants [4], bats [19], termites [20], therophytes [21], frogs [22], epigean arthropods [6], dung beetles [23], spiders [24] and macrofungi [8]. However, a generalized application of the

*Corresponding author
A.Feest@bris.ac.uk

methodologies described is difficult because the criteria of standardization are contentious. Different authors operate in fixed currencies of: (i) number of sampling units [8, 25, 26]; (ii) time spent sampling [19]; (iii) total area covered [27]; (iv) number of observed individuals or species [28]; (v) percentage of total estimated species richness [29]; (vi) number of previously unencountered species [30]; and (vii) degree of sample variance [27]. From this, we can identify two distinct groups of standardization techniques: (a) those that stipulate limits on time, effort and expense beforehand (i-iii); and (b) those that involve sustained sampling until a predetermined threshold is reached (iv-vii). The former generates samples of varying completeness, while the latter is not conducive to rapid assessment and often validated post hoc.

How should biodiversity be measured?

Of the biodiversity characteristics used commonly, species richness is the most intuitive and most commonly used measure of biodiversity, yet it is strongly affected by inconsistencies in sample size [10]. A diverse range of indices emphasize other facets of biodiversity such as relative abundance or evenness of species [31] but there is no universal single index that meets the criterion of an unbiased biodiversity value [27]. This is the basis of a comment by Gaston and Spicer (2004) [32]: "it is clear that no single measure of biodiversity will be adequate. Indeed, given its great complexity, it would be foolish to believe the variety of life in an area, however small or large that area might be, could be captured in a single number". A dangerous choice can thus arise whereby one can be tempted to select an index that will support one's hypotheses most effectively [33]. For the purposes of this paper and following the research of Hooper *et al*. [34] and Petchey *et al*. [35], biodiversity is defined as the quality of a site that can be inferred from a number of measured species characteristics of the populations studied (*sensu* Feest [8]; Feest *et al*. [26, 36]).

A universal system for quantifying biodiversity has obvious practical value. Progression towards this goal includes initiatives such as the Global Earth Observation System of Systems, which aims to consolidate biodiversity-observing systems [8].

Our research hypothesis is therefore:

H1: A standardized sampling methodology will allow the creation of a number of biodiversity quality indices for establishing biodiversity baselines.

In this hypothesis standardized sampling aims to provide a methodology applicable to many different organism groups; biodiversity quality indices are used in the sense of Feest [8] and Feest *et al*. [26, 36] as individual biodiversity characteristics of the sample dataset; and biodiversity baselines are index values based on standardized sampling that can a) be repeated in the future to establish the probability of change; or b) be compared between sites for probability of difference.

Methodological considerations

Sampling parameters can influence the reliability, comparability and accuracy of data and carefully designed surveys are thus of over-riding importance. This was emphasized by de Solla *et al*. [22], who found that two different monitoring programmes for the same amphibian population produced results with opposing trends. In setting the standardized methodology, the following should be considered:

Sampling technique

Individual sampling methods do not collect all fauna equally [2, 37, 38] and species that are difficult to detect using one method may be collected abundantly with another [4]. This has cultivated the use of "shopping basket" methodologies, comprising a suite of techniques for optimal taxonomic coverage [2, 5]. By contrast, there is evidence that the use of just one or two sampling methods is sufficient if the aim is to maximize catches of particular target groups [5, 8, 38]. Lange *et al*. [38] clearly demonstrate that pitfall trapping is effective for surveying ground beetles (and spiders), but that the results depend strongly on the standardization of the individual traps.

Sample size

Problems with small samples are well articulated [2, 4, 10, 38], but it is not clear exactly what constitutes a small sample, because species richness depends on a number of locally dependent factors,

such as population density, ecological conditions, geography, altitude, microclimate, vegetation structure, season, activity levels and detectability. Melo *et al*. [10] use the term "rich" for tropical invertebrate inventories containing 30 or more species, which should be achievable with limited effort even in temperate regions.

Timescale

The activity and abundance of many animal species varies between seasons and between years, so if only one sample is to be taken, the time of year could vastly affect the results [3, 40, 41]. Leponce *et al*. [41] also note that the interpretation of single-sample inventories is complicated by questions such as (a) which proportion of the local fauna is represented; (b) whether "characteristic" species have been included; (c) whether the indices and biodiversity values were calculated from the data accurately; and (d) whether comparable results would be obtained at different times of year?

Spatial scale

The choice of the spatial scale of sampling can affect the precision of species richness estimates, particularly for invertebrates, whose spatial distribution varies between and within sites [42, 43]. For example, one might expect the species richness of a sample to increase in proportion with the distance between sampling stations because a larger surveyed area is likely to include more microhabitats containing unique assemblages. In support of this theory, Alexander *et al*. [43] found that insect species richness in agricultural landscapes was more accurately estimated by random, rather than structured, sampling.

What is a reasonable degree of sampling effort?

Measures of species richness are virtually meaningless without the context of associated sampling effort [44]. Survey designs need to consider practical and financial cost per unit effort, and satisfy timescales relevant to conservation, yet a huge amount of effort and expense is still devoted to hand-collection surveys and the hobbyist "stamp-collecting" paradigm of species inventories. This tendency to search for rare sampling opportunities can sometimes supersede rational, objective sampling [45] and may reflect local concerns, rather than international standards. Martikainen and Kaila [39] presented results from a ten-year study of beetles in two Finnish forests and showed that almost all common species had been detected after three years, so that additional expense, and a further seven years, were devoted entirely to the collection of rare and threatened species. They concluded that: (i) there were insufficient differences in species numbers between the two forests to provide a reliable ranking; (ii) "new" species collected later in the sampling regime could have been uncharacteristic vagrants; and (iii) management decisions based on the presence/absence of rare species should be made with caution. Similarly, Pearson and Cassola [46] found that 50 hours spent hand-collecting tiger beetles in nine sites in the Americas and Indian subcontinent uncovered 78-93% of the total fauna. An additional 5,000 hours of survey work added only two to five rare species. Studies such as this are important because they add credence to the logic behind minimum sampling effort - a concept committed to "replication rather than [further] identification" [47].

Species accumulation rate

Species accumulation declines considerably as sampling effort or area increases [48, 49]. The minimum sampling effort is defined as the point when additional effort is no longer justified by the marginal improvement in species accrual [20]. Many authors caution against the use of minimal sampling because detection of rare species (arguably the most important in conservation logic) usually requires great effort. For example, Martikainen and Kouki [2] stipulate that detection of rare beetle species in boreal forests requires a minimum sampling effort of 200 trapped species (or 2000 individuals) and at least double this effort before any reasonable probability of finding them exists. However, this does not take into account that some (many?) sites might not contain any species of notable rarity and should be assessed using other criteria.

The conflicting imperatives of minimizing sample size and generating data sets large enough to be representative clearly necessitates a compromise [20]. Inevitably, this compromise involves site

comparisons based on relative, rather than actual, differences [50]. Species accumulation curves can be used to estimate the minimum sampling effort required to obtain an efficient inventory and are defined as 'the cumulative number of species plotted against some measure of the effort it took to obtain that sample' [19]. Species accumulation rates are used for the estimation of true species richness [51] along with non-parametric methods (Chao 1 and 2 in Magurran [51]).

In this paper, we use a sampling protocol for carabid beetles in a homogenous grazed uplands habitat. The state of scientific knowledge of carabids is good - they have been studied intensively and are among the largest families of beetles known to science [52]. They are globally wide-ranging, ubiquitous in all ecosystems from the tropics to the boreal zone and sampled easily and cheaply by rudimentary methods. In particular, they are responsive to environmental variables including temperature, humidity, and vegetation, and have been used to assess forest fragmentation, management practices, site quality and classification of habitat type, as well as studies of urban ecology, insecticides, and effects of military hardware (Rainio and Niemelä [40] and references therein). Moreover, carabids satisfy almost every criterion for a useful bioindicator [16] and a National Carabid Classification system has been proposed as a tool for categorizing habitats in the same way that the National Vegetation Classification system is used to describe British plant communities [53].

Standardized pitfall sampling regimes have already been proposed for comparing carabid communities across local, regional and national scales in the UK [54-57]. There is now enough data from comprehensive studies throughout Europe [58, 59] to investigate the possibility of international site comparisons. An example of such a scheme is GLOBENET [16], based on a simple, repeatable pitfall trapping protocol that is used to detect carabid response to landscape changes caused by humans around the world. Responses are quantified by the same set of metrics (a combination of indices that produce a single statistic).

The aim of this paper is to investigate the applicability of a standardized methodology for carabids, and describe the measurement of site biodiversity "quality" based on familiar diversity indices. We discuss possible improvements for the legitimate use of carabid beetles in environmental assessments.

MATERIALS AND METHODS

We present here case study data donated by Dr. Michael Eyre (University of Newcastle upon Tyne) who used sampling methods that reflect the considerations above.

Redesdale is an upland hillside in the Rede Valley in Northumberland, UK. It rises from about 130m OD to about 240 m OD. It is mainly peat, with some mineral soils near the bottom of the hill. The vegetation is a mixture of sheep-grazed moorland grasses and heather.

Carabid communities were sampled by pitfall trapping at each site. Redesdale was sampled in 1989 and again in 1991 (the sampling procedure and position of traps was the same in both cases). At Redesdale, three parallel transects were installed along a hillside gradient. Each transect consisted of seventeen or more sampling stations with five traps per station (minimum 85 traps per transect).

Traps were polypropylene pots of 8.5 cm in diameter by 10 cm in depth, half-filled with 70% ethanol-5% ethylene glycerol solution. Each trap was sunk into the ground with the lip buried just below the soil surface, positioned in a straight line 1-2 m apart. Sites were sampled at monthly intervals from April to October (seven months) at each site, at which time traps were emptied and re-filled with fresh preservative. Contents of all traps at each sampling station were poured through a sieve and the retained material transferred to a polythene bag in the field.

Trap contents were sorted on white plastic trays under good light and any carabids were removed for storage in specimen tubes containing 70% alcohol. Each specimen was identified to species level (nomenclature follows Luff [60]). Species diversity was assessed by calculating species richness and diversity indices (Shannon-Weiner, Simpson's and Berger-Parker) generated by the computerized database Fungib (copyright Dr. Alan Feest). The software also calculated population

density, a species conservation value (rarity) index (SCVI) and biomass index (see below). The diversity indices were recalculated to reflect proportional biomass as well as proportional populations. Beetle sizes for the biomass index were supplied by Luff [61] and converted to biomass using the conversion factors given in Brady and Noske [62].

Following Magurran [51] estimated species richness was calculated using four methods: Chao1, Chao2, Bootstrap and Jacknife, thus combining non-parametric and rarefaction estimators.

Formulae for the calculation of Shannon-Weiner, Simpson's and Berger-Parker indices can be also be found in Magurran [51]. The remaining parameters were calculated as follows:

Population density

Total number of individuals which may be expressed as a standard input.

Species value index

Each species is assigned a value based on an arbitrary scale (see below) derived from national or regional occurrence statistics. The average of the summed values produces an index of average species commonness in the sample. Species are ranked as follows:

Abundant	2
Common	3
Frequent	4
Occasional/Local	5
Rare	10
Very Rare	20
Extremely Rare	100

Biomass index

This is the mg weight per species converted from the body length (Brady and Noske 2006) and per total sample.

RESULTS

Pitfall trapping at Redesdale yielded a total of 39 species from 3,461 collected specimens in 1989 and 47 species from 3,965 specimens in 1991. Samples were dominated by specimens of *Carabus problematicus* with high prevalence of *Pterostichus nigrita* and, to a lesser degree, *Pterostichus diligens*, *Patrobus assimilis* and *Loricera pilicornis*.

Results from Fungib treatment of a sampling transect at Redesdale (Redesdale 3/91) are presented in Figure 1, with species listed in the first column and sampling units represented in the first row. Presenting data in this way (as opposed to species lists) allows us to present species abundance and co-occurrence as well as a range of indices and is also useful for detecting sampling bias and seasonal or inter-annual variations. The indices compiled from sampling are given in Table 1.

Table 1 shows the complete Fungib-generated biodiversity indices dataset from the two samplings in 1989 and 1991, plus three sets of data where the indices are expressed as per pitfall trap or per individual.

The numbers of traps varied due to varying length of uniform habitat, but in all cases there were at least seventeen traps. The number of species per run of traps was not proportional to the number of traps and using the Species Richness estimators (Chao1 and 2, Bootstrap and Jacknife) showed that most species present were recorded (in most cases over 80% and always over 75%). Visual inspection of the species accumulation curves also showed that the species accrual rate was approaching the asymptote. Statistical testing (using t-tests) showed that there was no significant difference between any of the data from any of the trap lines, although species richness, SCVI, population and biomass were all higher on the second sampling (1991). In five of the six samples the number of species recorded was between 33 and 36. Two differences between years were of note:

1. The diversity indices all recorded differences between population-based estimates and biomass-based estimates, and in all cases the biomass-based estimates indicated lower diversity. This is due to an increased population of individuals of large-bodied species.

2. Mean biomass per trap, Mean biomass per individual was significantly higher in the second sampling ($p=<0.05$. t-Test) and the mean population per trap ($p=0.07$. t-Test), albeit comparing only two sets of three means (even if they are mean values of seventeen or more traps).

Redesdale 3
30/06/91

Samples used = 17

Species name	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	Sum	SCVI	BI
GPS easting	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
GPS northing	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
0: Amara communis	3																				3	3	16.131
1: Bembidion mannerheimi	2		1	1																	4	2	3.5
2: Carabus problematicus	11	25	51	28	55	17	15	43	7	4	8	17	31	8	8	12	6				346	2	24,088.521
3: Carabus violaceus	2	10	7		1	1	2	1	2	4	2	1	1		5	3	1				43	2	2,993.66
4: Pterostichus niger	1	1	1					2						1	6	15	5				32	2	838.4
5: Pterostichus rhaeticus	12	8	10	22	14	13	1	3	13	4	4	1		2	1		32				140	2	1,138.2
6: Pterostichus versicollor	3						1														4	2	26.52
7: Trechus obtusus	3																				3	2	1.17
8: Amara lunicollis		1	7		8		8	2					2		1	3	1				33	2	104.61
9: Carabus arvensis		2	2				1	2	1	1	1	1	8	2	2	8	2				33	4	811.47
10: Carabus glabratus		3	5						1				1	1	2	1	1				15	4	1,044.45
11: Carabus nemoralis		1	1	1	1		7	5			1	1									18	2	867.96
12: Patrobus assimilis		6	4	2	2	6	7	3	5	1	4	4	5	7	5	7	1				69	3	218.73
13: Pterostichus adstrictus		5	2	3	16	6	10	6	1	1	1	1	5	7	14	14	17				109	3	887.26
14: Pterostichus dilgens		6	4	6	2	4	6	3	6	11	10	15	2	1	3		6				85	2	141.1
15: Calathus melanocephalus			1					9		1					1	13					25	2	79.25
16: Loricera pilicornis			3	3	23	8	1	6	1		2		3	1	1		5				57	2	155.61
17: Pterostichus strenuus			2		1																3	2	4.98
18: Trichocellus placidus			1							1											2	3	1.78
19: Agonum fuliginosum				1	1	3				1	1					2					9	2	21.06
20: Nebria brevicollis				1		1		1													3	2	29.52
21: Nebria salina				2	24	7		7		1							2				43	2	385.71
22: Synuchus nivalis				1																	1	3	2.73
23: Bembidion bruxellense					1																1	3	0.7
24: Bembidion lampros					1	1															2	2	1.06
25: Dyschirius globosus						1			1												2	2	0.38
26: Leistus rufescens						1		2	7	9		8	3			2					32	2	74.88
27: Carabus nitens								2									1				3	5	56.28
28: Pterostichus aethiops									1						2	1					4	5	39.36
29: Notiophilus germinyi										1											1	3	0.89
30: Notiophilus aquaticus											2			1	3		1				7	2	7.84
31: Trichocellus cognatus														1	2	2					5	4	1.95
32: Bradycellus harpalinus																1					1	2	0.39
33: Bradycellus ruficollis																	1				1	3	0.28
34: Trechus quadristriatus																	1				1	2	0.39
Summary	37	68	102	71	150	69	59	97	46	40	36	49	61	32	56	84	83	0	0	0	1140	2.6	34,046.723

Species Richness = 35
Shannon-Wiener Index = 2.5175(1.2697)
Simpson Index = 7.3926(1.9489)
Berger-Parker Dominance Index = 0.3035(0.7075)
Density = 1.14 per sq.m.
Species Conservation Value Index = 2.6+/-0.8684
Biomass Index = 34046.7227

Chao1 (pop.) Richness = 41.0+/-5.2141
Chao2 (pres./abs.) Richness = 40.3333+/-4.1186
Bootstrap Richness = 41.1183+/-5.583
Jackknife Richness = 42.5294+/-11.4788

Figure 1

Table 1. Biodiversity quality dataset of three pitfall trap transect for 1989 and 1991.

	Redesdale 1/89	Redesdale 3/89	Redesdale 5/89	Redesdale 3/91	Redesdale 5/91	Redesdale 7/91
n =	20	17	19	17	19	17
1. Species richness	34	33	27	35	35	36
2. Shannon-Wiener/population	2.8	2.6	2.5	2.5	2.5	2.7
3. Shannon-Wiener/biomass	1.9	1.8	1.5	1.3	1.3	1.7
4. Simpson/population	11.8	9.5	8.9	7.4	6.8	9.9
5. Simpson/biomass	4	3.4	2.6	2	2	3
6. Berger-Parker/population	0.1	0.2	0.2	0.3	0.3	0.3
7. Berger-Parker/biomass	0.5	0.5	0.6	0.7	0.7	0.5
8. Population	1309	1053	1085	1140	1430	1376
9. SCVI	2.5	2.6	2.5	2.6	2.5	2.6
10. SCVI SD	0.8	0.9	0.8	0.9	0.9	0.9
11. Biomass	28402	22042	28627	34046	44140	44463
12. Chao 1	*	37	35	41	39.5	38
13. Chao 1 SD	*	4.3	8.3	5.2	4	2.2
14. Chao 2	46.3	39.3	36	40.3	41.1	42.1
15. Chao 2 SD	9.7	5.9	7.7	4.1	5	5
16. Bootstrap	38.4	37.1	30.8	41.3	40.7	41.5
17. Bootstrap SD	4	3.8	2.1	5.9	5.5	5.3
18. Jacknife	40.6	37.7	32.7	45.5	41.6	42.6
19. Jacknife SD	9.3	7.5	10.5	11.5	10.8	12.7
20. Mean Biomass per trap	1420	1296	1507	2002	2323	2615
21. Mean Population per tap	65.45	61.94	57.1	67.06	75.26	80.91
22. Mean Biomass per individual	21.7	20.93	26.38	29.86	30.87	32.3

n = number of traps. * = data not suitable for processing. 1 = Species Richness (number of species recorded in pit-fall traps of one transect); 2-7. Biodiversity indices based on either population numbers or relative biomass; 8. Population (number of individuals recorded in pitfall-traps of a transect); 9-10. Mean and Standard Deviation of Species Conservation Value Index; 11. Biomass calculated as in text; 12-19. Estimated Species Richness and Standard Deviation of the estimate for four different estimators; 20-22. Mean values of biomass and population per trap and per individual.

Legend to Figure 1. Survey results for carabid beetles in Redesdale Northumberland, United Kingdom (30/06/1991). Sampling units (five pitfall traps per unit) are represented in the first row and species identifications are listed in the first column with numbers of individuals recorded per sampling unit in the cells. Total individuals per sampling unit are represented in the bottom row and per species in the column marked “Sum”. The total number of individuals recorded in all sampling units is logged at the bottom of the “Sum” column. The SVI column = Species Value Index, with average value at the bottom. The BI column = Biomass Index, with total biomass at the bottom. Various other index values are indicated in the free text below the table. Data presented as per Fungib, copyright Dr. Alan Feest.

This second assessment confirms the first, in that whilst no significant increase in population or species richness can be demonstrated, we can show that there has been a significant increase in beetle biomass.

DISCUSSION

Testing the hypothesis

H1: A standardized sampling will allow the creation of a number of biodiversity quality indices for establishing biodiversity baselines

Clearly a number of baseline indices have been established and found to be testable statistically for simple probability of difference. That most of the baselines are not only similar in each of the three transects, but also similar two years later, allows confidence that they represent baselines. It is perhaps not unexpected that, with species turnover and habitat maturation, evidence is found of an increase in biomass of beetles between the years.

We have described a methodology based on pitfall trapping that allows assessment of carabid biodiversity quality to be represented by a range of indices and other numerical parameters. The technique is simple, cheap and easily repeatable and could therefore be applied widely to (i) gather information on poorly surveyed territories within a timeframe relevant to decision-makers; (ii) rank areas of conservation priority; or (iii) monitor changes at sites over time and carry out management impact assessments.

Although the use of pitfall trapping as a collecting method for carabids is the subject of relentless debate [38, 52, 63-67], it remains the most widely-used system because it is cheap, simple to use and traps can be left *in situ* for a length of time with almost no servicing required [7]. Furthermore, studies in forests have shown that the greatest number of invertebrate species occur at ground level and at least 75% of canopy species are also present on the ground [3, 68]. A key point to consider is that, regardless of the limitations of pitfall traps, a standardized sampling protocol is subject to the same constraints and the bias is constant wherever they are used (for example, although pitfall traps fail to reflect absolute abundance of species, all sites can still be compared on the basis of relative abundance/activity). Although relative abundance of species can fluctuate erratically between years [69], inter-annual composition of carabid populations has been found to not differ greatly in pitfall samples [70, 71]. Thus, pitfall trapping can provide a useful "comparative reference" [72, 73] and has been advocated as the best method for carabid surveys across large geographic areas [66]. Indeed, an exceptional amount of pitfall trapping data is already available for carabids across the world and some of it has been used very successfully in site comparisons [74]. Trapping efficiency needs to be as high as possible for minimal sampling programs and innovative designs have been suggested by some authors such as barrier-connected pitfall traps [75] and funnel-covered pitfall traps [38, 76], which markedly increase carabid detection success. Trap size, collecting fluid and vegetation structure can also affect ground beetle catches [77, 78] and should be standardized for optimum performance.

The data from Redesdale (Figure 1) resembles a species accumulation curve with a decreasing rate of species accrual as sampling effort increases. Although an asymptote is not reached, this is rarely possible because late detection of rare, displaced or vagrant species could potentially increase the species list *ad infinitum*.

In comparing all six 85+trap transects at Redesdale, there is high concordance between biodiversity values with no significant differences between parameters except in the case of biomass. We can conclude from these findings that a single "snapshot" transect of 85 traps at Redesdale will produce a reliable estimate of biodiversity quality. However, there appears to be year-to-year variation, albeit insignificant, between the three 85-trap transects in 1989 and the three in 1991, as deduced by synchronized differences in the data output (Table 1). There is strong evidence in the literature for inter-annual variation in carabid beetle assemblages [52, 76, 79] and this has particular relevance to short-term snapshot assessments. Nevertheless, so long as data are explained in plain terms and the limitations of sampling surrogacy are communicated to policy-makers, it is possible to make informed management decisions in context [30, 80].

Literature records describe minimal sampling programs employing as few as five to thirty-five sampling units, which produce reliable "snapshots" of invertebrate faunas even in the tropics [4, 6, 20, 41, 81, 82]. It should also be noted that species accumulation at Redesdale begins to diminish at about six sets of traps (30 individual pitfall traps; see Figure 1). Vennila and Rajagopal [81] determined that 25-35 pitfall traps left open for four months was optimal for measuring carabid diversity in tropical forest. Leponce *et al.* [41] indicated that 25 litter "traps" were also the best compromise for tropical ants, even when compared with results from an eight-fold oversampling campaign and Feest [8] estimates that 20 samples are sufficient for macrofungi communities. However, small samples such as these are often met with skepticism [83-86] and critics express concern that year-to-year variation could produce different snapshots of the same assemblage [52]. However, Blake *et al.* [53] note that a "visually homogenous plant community may be equivalent to sampling a correspondingly homogenous beetle community" and much therefore depends on the determination of what are the limits of sampling site.

Research on coastal dune carabids in Belgium [79] showed that more than half the species recorded in a five-year pitfall trapping study were vagrants rather than members of the locally breeding population. This could be the result of species being displaced from surrounding habitats by coastal winds and thereby reaching dunes. It also highlights the impact that immigrating species can have on biodiversity assessments (Desender [79] cites other research from grasslands in Belgium where vagrants also comprise 50% or more of sampled species). This provides a further justification for reducing sampling effort in biodiversity assessments.

Measuring biodiversity

Species richness and Simpson's measures are good discriminating factors for site quality, but biomass is sensitive to natural variation in numbers of trapped individuals and varies significantly even within sites. Downie *et al.* [87] indicate that it may be possible to quantify stochastic variation and thus apply a correction factor to the data output, but the validity of this technique remains to be tested.

The other parameters we have measured are numerically constrained in such a way as to prevent valid statistical analysis (the Berger-Parker index always falls between 0 and 1; the Shannon-Weiner usually falls between 1.5 and 3.5; and the Species Conservation Value index is averaged from a list of numbers that are, in this case, nearly all the same, regardless of the site). Magurran [51] argues that "an ecologist confronted by [Shannon index] values of H' = 2.35 and H' = 2.47 may have little idea whether the two sites in question have similar diversities or are substantially different". The raw form of the Simpson's index also has a range of 0-1 but the Simpson's Reciprocal Index used by the Fungib program is less constrained. It has a numerical ceiling, as determined by the number of categories (in this case, number of species) but we were still able to detect a statistical difference with this index. It is therefore recommended that alternative forms of other commonly-used indices are investigated.

It has been argued that biodiversity indices are not appropriate for carabid research or impact assessments, because they are not sensitive enough to habitat change, do not respond in a consistent way, and can yield contradictory results [11, 72, 88]. Furthermore, Luff [57] concludes that they do not take account of the rate of movement of species and thereby neglect the relationship between actual density and pitfall catch. In the same study, however, Luff explains that rate of movement is correlated with body size and the latter measurement could be used to "correct" pitfall catches and generate alternative indices. In theory, these indices could be more sensitive to differences among carabid assemblages and further investigation is recommended.

We argue that the *balance* of numerical parameters generated from sampling can be used to assess biodiversity *quality* of sites (*sensu* Feest *et al.* [26]). The facets of biodiversity measured are individually well understood so that the method is attractive for a wide range of ecological studies. Various authors have stressed the importance of factors such as endemism [89], species sensitivity [27], typicality [54] and rarity [38], and the lattermost of these is represented in this paper by the Species Conservation Value Index.

This approach is not new since other authors have developed rarity indices such as "species quality factor", "rarity quality factor" and "importance value index" based on the same principle [6, 16, 54, 56, 90] but it provides an example of how rarity can be expressed in quantitative terms, rather than the commonly-used qualitative description. Although in this study the SCVI was not significantly different between sites, it recognizes rare species accurately as a minority: only one index grade 5 species was detected in our data (*Pterostichus aethiops*) and the single specimen was not enough to affect the mean substantially. The SCVI becomes more responsive if the standard deviation is incorporated – the Fungib software calculates this automatically. It would also be interesting if relative abundance of species was factored into the SCVI, because nationally uncommon, scarce or even rare species can occur at high densities in certain sites even if they are found nowhere else. For example, an index grade 5 species, *Pterostichus aethiops*, occurs frequently at Redesdale.

We are not suggesting that qualitative descriptions of biodiversity factors such as rarity do not still have a role to play (the numerical parameters described here are insensitive to species identities), but by themselves they are not appropriate comparative references. The tabular data output of the Fungib program (Figure 1) illustrates the importance of other factors, such as patterns of occurrence, co-occurrence, species abundance and rarity.

CONCLUSIONS

Standardized sampling protocols need to be informative, reliable and broad-spectrum, and perform equally well in sites with high and low biodiversity. It is therefore advisable to first establish the minimum sampling effort needed at sites with high species richness. This will help to assure the performance of the methodology across the board. Equally, restricted sampling programmes should coincide with the period of optimal activity in the target [19, 41] to avoid the risk of underestimating biodiversity. For most temperate epigean arthropods, activity peaks during the spring and summer, although there is evidence that some carabid beetles do not exhibit seasonal variations and can be used for realistic diversity estimates in short-term studies [73]. It is important that there is minimal laxity when following standardized protocols, since even minor deviations in sampling method can bias the results [57, 76].

Where a comprehensive species list is required at a site, there is no substitute for intensive surveys and criteria for sufficient sampling should, therefore, reflect the aims of the project [4]. However, carabids meet the requirements of ecological studies where economy of resources is a priority, because they can be trapped in large numbers with less effort than vertebrate taxa. We have shown that pitfall trapping is a valid technique for carabid studies and has the advantage that other arthropod taxa such as rove beetles (Staphylinidae), spiders, collembola and water beetles [74, 91] can be collected with the same technique. If a standardized methodology for carabids performed equally well for these other taxa, it would have the distinct benefit of broadening the applicability of the technique and providing additional levels of discrimination between sites.

Taxonomy of invertebrates remains a problem because it requires skill and training, yet the minimal sampling protocol we suggest means that identification and sorting can occur within weeks, rather than years (as is customary for long-term arthropod surveys).

We suggest that it is possible to economise on sampling effort for carabids by: (i) ensuring sampling is in homogenous sites if the aim is to assess the biodiversity quality of a particular habitat type; (ii) taking a single sample over the summer months when temperate epigean arthropod activity peaks if possible; and (iii) restricting sample size to as little as 20 traps in spatially homogenous sites. Extrapolation of these results to other communities is speculative and warrants further investigation. A broad spectrum of habitats and taxonomic groups needs to be considered before a general approach can be developed and promulgated.

The value of this information will remain dependent on the importance with which arthropods are considered by resource managers and policy-makers,

but it is hoped that these developments will lead to consistent and representative monitoring techniques for terrestrial biodiversity.

ACKNOWLEDGEMENT

We thank Katrin Jedamzik for her assistance with the data manipulation and entry.

REFERENCES

1. Myers, N., Mittermeier, R. A., Mittermeier, C. G., da Fonseca, G. A. B., and Kent, J. 2000, Nature, 403, 853-858.
2. Martikainen, P. and Kouki, J. 2003, Biodiv. Conserv., 12, 1815-1831.
3. Oliver, I. and Beattie, A. J. 1996, Ecol. Appl., 6, 594-607.
4. Fisher, B. 1999, Ecol. Appl., 9, 714-731.
5. Kitching, R. L., Li, D., and Stork, N. E. 2001, Biodiv. Conserv., 10, 793-813.
6. Borges, P. A. V., Aguiar, C., Amaral, J., Amorim, I. R., André, G., Arraiol, A., Baz, A., Dinis, F., Enghoff, H., Gaspar, C., Ilharco, F., Mahnert, V., Melo, C., Pereira, F., Quartau, J. A., Ribeiro, S. P., Ribes, J., Serrano, A. R. M., Sousa, A. B., Strassen, R. Z., Vieira, L., Vieira, V., Vitorino, A., and Wunderlich, J. 2005, Biodiv. Conserv., 14, 2029-2060.
7. Lott, D. A. and Eyre, M. D. 1996, Eyre, M. D. (Ed.), Environmental monitoring, surveillance and conservation using invertebrates. EMS Publications, Newcastle Upon Tyne, UK, pp. 9-13.
8. Feest, A. 2006, Restor. Ecol., 14, 112-122.
9. Elphick, C. S. 1997, Ibis, 139, 189-190.
10. Melo, A. S., Pereira, R. A. S., Santos, A. J., Shepherd, G. J., Machado, G., Medeiros, H. F., and Sawaya, R. J. 2003, Oikos, 101, 398-410.
11. Buddle, C. M., Beguin, J., Bolduc, E., Mercado, A., Sackett, T. E., Selby, R. D., Varady-Szabo, H., and Zeran, R. M. 2005, Can. Entomol., 137, 120-127.
12. Pollard, E. and Yates, T. J. 1993, Monitoring butterflies for ecology and conservation, Chapman and Hall, London.
13. Marchant, J. H. 1994, Brit. Birds, 87, 26-28
14. Watson, D. M. 2003, Austral. Ecol., 28, 515-525.
15. Wilson, D. E., Cole, F. R., Nichols, J. D., Rudran, R., and Foster, M. S. 1996, Measuring and monitoring biological diversity: standard methods for mammals. Smithsonian Institution Press, Washington, D. C.
16. Niemelä, J. 2000, Ann. Zool. Fenn., 37, 307-317.
17. Eyre, M. D., Lott, D. A., and Garside, A. 1996, Ann. Zool. Fenn., 33, 157-163.
18. Edsman, L. and Soderback, B. 1998, Freshwater Crayfish, 12, 705-713.
19. Moreno, C. E. and Halffter, G. 2000. J. Appl. Ecol., 37, 149-158.
20. Jones, D. T. and Eggleton, P. 2000. J. Appl. Ecol., 37, 191-203.
21. Kluth, C. and Bruelhide, H. 2004. J. Biogeogr., 31, 363-377.
22. De Solla, S. R., Shirose, L. J., Fernie, K. J., Barrett, G. C., Brousseau, C. S., and Bishop, C. A. 2005, Biol. Conserv., 121, 585-594.
23. Larsen, T. H. and Forsyth, A. 2005, Biotropica, 37, 322-325.
24. Jimenez-Valverde, A. and Lobo, J. M. 2005, J. Arachnol., 33, 33-42.
25. Smith, K. L. and Jones, M. L. 2005, Can. J. Fish. Aquat. Sci., 62, 1580-1588.
26. Feest, A., Aldred, T. D., and Jedamzik, K. 2010, Ecological Indicators, 10(6), 1077-1082.
27. Valdecasas, A. G. and Camacho, A. I. 2003, Biodiv. Conserv., 12, 1113-1117.
28. Willott, S. J. 2001, J. Appl. Ecol., 38, 484-486.
29. Thompson, G. G., Withers, P. C., Pianka, E. R., and Thompson, S. A. 2003, Austral. Ecol., 28, 361-383.
30. Watson, R. 1999, J. Appl. Ecol., 36, 1-10.
31. Stirling, G. and Wilsey, B. 2001, Am. Nat., 158, 286-299.
32. Gaston, K. J. and Spicer, J. I. 2004, Biodiversity: An introduction, Blackwell, Australia.
33. Huhta, V. 1979, Oecologica, 41, 11-23.
34. Hooper, D. U., Chapin, III, F. S., Ewel, J. J., Hector, A., Inchausti, P., Lavorel, S., Lawton, J. H., Lodge, D. M., Loreau, M., Naeem, S., Schmid, B., Setala, H., Symstad, A. J., Vandermeer, J., and Wardle, D. A. 2005, Ecological Monographs, 75(1), 3-35.

35. Petchey, O. L. Hector, A., and Gaston, K. J. 2004, Ecology Letters, 5, 847-857.
36. Feest, A., van Swaay, C., Aldred, T., and Jedamzik, K. 2011, Ecological Indicators, 11, 669-675.
37. Wikars, L. O., Sahlin, E., and Ranius, T. 2005, Can. Entomol., 137, 304-324.
38. Lange, M., Gossner, M. M., and Weisser, W. W. 2011, Methods in Ecology and Evolution, 2, 185-190.
39. Martikainen, P. and Kaila, L. 2004, Biol. Conserv., 120, 171-181.
40. Rainio, J. and Niemelä, J. 2003, Biodiv. Conserv., 12, 487-506.
41. Leponce, M., Theunis, L., Delabie, J. H. C., and Roisin, Y. 2004, Ecography, 27, 253-267.
42. Su, J. C. and Woods, S. A. 2001, Entomol., 30, 400-408.
43. Alexander, C. J., Holland, J. M., Winder, L., Woolley, C., and Perry, J. N. 2005, Ann. Appl. Biol., 146, 361-370.
44. Gaston, K. J. 1996, Gaston, K. J. (Ed.), Biodiversity, A Biology of Numbers and Differences, Blackwell Science, Oxford, pp. 77-113.
45. Rocchini, D., Butini, S. A., and Chiarucci, A. 2005, Global Ecol. Biogeogr., 14, 431-437.
46. Pearson, D. L. and Cassola, F. 1992, Conserv. Biol., 6, 376-391.
47. Beattie, A. J. and Oliver, I. 1994, Trends Ecol. Evol., 9, 488-490.
48. Keating, K. A., Quinn, J. F., Ivie, M. A., and Ivie, L. L. 1998, Ecol. Appl., 8, 1239-1249.
49. Dolphin, K. and Quicke, D. L. J. 2001, Biol. J. Linn. Soc., 73, 279-286.
50. Hammond, P. M. 1994, Phil. Trans. R. Soc. Lond. B, 345, 119-136.
51. Magurran, A. E. 2004. Measuring Biological Diversity, Blackwell Science, Oxford.
52. Niemelä, J. 1996, Ann. Zool. Fenn., 33, 1-4.
53. Blake, S., McCracken, D. I., Eyre, M. D., Garside, A., and Foster, G. N. 2003, Ecography, 26, 602-616.
54. Eyre, M. D. and Rushton, S. P. 1989, J. Appl. Ecol., 26, 159-171.
55. Luff, M. L. and Woiwood, I. P. 1995, Harrington, R. and Stork, N. E. (Eds.), Insects in a Changing Environment. Academic Press London, pp. 399-422.
56. Eyre, M. D. 1996, Eyre, M. D. (Ed.), Environmental monitoring, surveillance and conservation using invertebrates, EMS Publications, Newcastle Upon Tyne, UK, pp. 48-52.
57. Luff, M. L. 1996a, Eyre, M. D. (Ed.), Environmental monitoring, surveillance and conservation using invertebrates, EMS Publications, Newcastle Upon Tyne, UK, pp. 42-47.
58. Turin, H., Alders, K., den Boer, P. J., van Essen, S., Heijerman, Th., Laane, W., and Penterman, E. 1991, Tjidschrift voor Entomologie, 134, 279-304.
59. Maelfait, J. P., Desender, K., and Dufrene, M. 1994, Desender, K., Dufrene, M., Loreau, M., Luff, M. L., and Maelfait, J. P. (Eds.), Carabid Beetles: Ecology and Evolution. Kluwer Academic Publishers, Dordrecht, pp. 319-323.
60. Luff, M. L. 1998, Provisional atlas of the ground beetles (Coleoptera, Carabidae) of Britain, Biological Records Centre, Huntingdon.
61. Luff, M. L. 2007, Key to British Carabidae (ground beetles), Handbooks for the Identification of British Insects, 4(2) RES, St Albans, UK.
62. Brady, J. C and Noske, R. A. 2006, Australian Journal of Entomology, 45, 187-191.
63. Luff, M. L. 1975, Oecologica, 19, 345-357.
64. Adis, J. 1979, Problems of interpreting arthropod sampling with pitfall traps, Zool. Anz., 202, 177-184.
65. Topping, C. J. and Sunderland, K. D. 1992, J. Appl. Ecol., 29, 485-491.
66. Spence, J. R. and Niemelä, J. K. 1994, Can. Entomol., 126, 881-894.
67. Hawthorne, A. 1995, Toft, S. and Riedel, W. (Eds.), Arthropod natural enemies in arable land. I. density, spatial heterogeneity and dispersal. Acta Jutl., 70, 61-75.
68. Stork, N. E. 1988, Biol. J. Linn. Soc., 35, 321-337.
69. Kempton, P. A. and Taylor, L. R. 1976, Nature, 262, 818-820.
70. Baars, M. A. 1979, Oecologica, 41, 25-46.

71. Luff, M. L., Eyre, M. D., and Rushton, S. P. 1992, J. Environ. Manage., 35, 301-315.
72. Penev, L. 1996, Ann. Zool. Fenn., 33, 49-63.
73. Jukes, M. R., Peace, A. J., and Ferris, R. 2001, Forest Ecol. Manag., 148, 271-286.
74. Lott, D. A. 1996, Eyre, M. D. (Ed.), Environmental monitoring, surveillance and conservation using invertebrates, EMS Publications, Newcastle Upon Tyne, UK, pp. 36-41.
75. Winder, L., Holland, J. M., Perry, J. N., Woolley, C., and Alexander, C. J. 2001, Entomol. Exp. Appl., 98, 249-258.
76. Luff, M. L. 1996b, Ann. Zool. Fenn., 33, 185-195.
77. Work, T. T., Buddle, C. M., Korinus, L. M., and Spence, J. R. 2002, Environ. Entomol., 31, 438-448.
78. Koivula, M., Kotze, D. J., Hiisivouri, L., and Rita, H. 2003, Entomol. Fennica, 14, 1-14.
79. Desender, K. 1996, Ann. Zool. Fenn., 33, 65-75.
80. Maelfait, J. P. and Desender, K. 1990. Stork, N. E. (Ed.), The Role of Ground Beetles in Ecological and Environmental Studies, Intercept, Andover, pp. 217-226.
81. Vennila, S. and Rajagopal, D. 1999, Curr. Sci., 77, 281-283.
82. Brose, U. 2002, Pedobiologica, 46, 101-107.
83. Preston, F. W. 1948, Ecology, 29, 254-283
84. Hairston, N. G. 1959, Ecology, 40, 404-416.
85. Hurlbert, S. H. 1971, Ecology, 52, 577-586.
86. Southwood, T. R. E. and Henderson, P. A. 2000, Ecological Methods 3rd Edn. Blackwell Science, Oxford.
87. Downie, I. S., Wilson, W. L., Abernethy, V. J., McCracken, D. I., Foster, G. N., Ribera, I., Murphy, K. J., and Waterhouse, A. 1999, J. Insect Conserv., 3, 273-286.
88. Dritschilo, W. and Erwin, T. L. 1982, Ecology, 63, 900-904.
89. Stattersfield, A. J., Crosby, M. J., Long, A. J., and Wege, D. C. 1998. Endemic Bird Areas of the World: Priorities for Biodiversity Conservation, BirdLife Conservation series No.7. BirdLife International, Cambridge, UK.
90. Foster, G. N. 1987. Luff, M. L. (Ed.), The Use of Invertebrates in Site Assessment for Conservation, Agricultural Environment Research Group, University of Newcastle Upon Tyne, UK, pp. 8-17.
91. Foster, G. N. 1996, Eyre, M. D. (Ed.), Environmental monitoring, surveillance and conservation using invertebrates, EMS Publications, Newcastle Upon Tyne, UK, pp. 33-35.