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Correcting for variation in recording effort in analyses of diversity hotspots

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Abstract. Interpretation of large-scale faunal and floral survey data is often frustrated by the bias caused by variation in recording intensity. Using distribution data for Odonata and Hepaticae from the Biological Records Centre, a technique for correcting this bias is described. The method is used to locate species-rich hotspots for the two taxa and comparisons are made with uncorrected data.

Key words. Recorder effort, hotspot, rarefaction, Odonata, Hepaticae, British Isles.

INTRODUCTION

For conservation practitioners, the idea of clearly delimited areas with unusually large concentrations of species has particular appeal. Considerable attention has been paid to the pinpointing of such hotspots (Phipps & Cullen, 1976; Blondel, 1990; Crowe, 1990), particularly in the tropics (Myers, 1990; Gentry, 1992; Pearson & Cassola, 1992) and claims made that if hotspots can be identified then a disproportionately large fraction of a regional biota could be conserved by protecting relatively small areas.

Hotspots can be defined in several ways, all legitimate, depending on theoretical and practical objectives. They may be defined simply in terms of absolute species richness on say, a national or continental scale. Alternatively species may be weighted by taxonomic criteria, hotspots with many endemic or phylogenetically isolated species being regarded as more important than those made up of many closely related species (Williams, Humphries & Vane-Wright, 1991). Hotspots may also be defined relative to the species richness of small geographic areas within national boundaries—so called local hotspots (Lawton, Prendergast & Eversham, in press). This paper is concerned with national and local hotspots in Britain, defined in terms of species richness, unweighted by taxonomy.

From a conservation standpoint, the location of national hotspots focuses attention on those areas where unusually species-rich sites exist for the taxon in question. Clearly, such sites will warrant serious consideration by national conservation decision-makers. Local hotspots, on the other hand, are areas which outperform their immediate neighbours and will be of interest to bodies such as the U.K. county wildlife trusts. In either case, at the scale of sampling employed here (10 km) it is likely that, rather than an entire square being exceptionally species-rich, it will be a site or a combination of sites within it which is of particular interest.

The apparently simple task of identifying hotspots is, however not without difficulties. Even in Britain, arguably the best-recorded country in the world, the variability of species’ distribution data confounds uninforme attempted to interpret species richness maps (Lawton et al., in press). The problem is a particular case of the general problem of determining the optimal sample size for diversity measurement (for a concise review see Magurran (1988)) and stems from the fact that for virtually all large-scale floral and faunal surveys, volunteer recorders are the main source of data. Variation in the distribution and behaviour of recorders (Figs 1 and 2) creates data sets which may be heavily biased in favour of recorder, rather than species, distributions. The problem, widely known as the recorder effort problem, or the collecting effect (Levins, 1991), recurs as a confounding variable in many large-scale surveys (Sharrock, 1977; Lack,
Fig. 1. National maps for Hepaticae (liverworts) showing the distribution of recorders and records in each 10 km square since 1960. Symbols represent, in increasing size:
Recorders: 0, 1–2, 3–4, 5–6, 7–8, 9–10, 11–12, 13–15, 16–20, >20.
Fig. 2. As Fig. 1., but for Odonata (dragonflies and damselflies). Note that in both cases that the areas with the highest number of recorders do not necessarily have the highest number of records.
Based on data from the Biological Records Centre (BRC) at Monks Wood, (Lawton et al., in press) we use two highly disparate taxonomic groups, dragonflies & damselflies (Insecta, Odonata) and liverworts (Plantae, Hepaticae) (Fig. 3), on the British mainland and Western Isles to illustrate a technique to reveal hotspots of species richness corrected for variation in recording effort. The method will not be useful unless the data are of high quality; when they are, the

Fig. 3. Three representative taxa: (a) Aeshna cyanea ♂; (b) Libellula depressa ♀; (c) Conocephalum conicum.
method described can be used to standardize recorder effort to reveal hotspots at all scales from national to local.

**DATA AND DEFINITIONS**

BRC species distribution data are mapped in 10x10 km squares (so-called 10 km squares) of the Ordnance Survey, n=2876 in the British Isles excluding Ireland (Harding & Sheal, 1992). To eliminate many early records for which no visit data exist or which are questionable we used 1960 as a baseline. We also removed any records where the identity of the recorder or the date of visit was not supplied, resulting in 2235 squares with data for Odonata and 2070 for Hepaticae. Data are extracted from the BRC Oracle database in the form of a list of all the separate visits to each square, and for each visit the identities of all species revealed are similarly listed.

We define **diversity** as the number of species recorded per 10 km square. **Hot spots** (local or national) are defined by comparing diversity in any one square with diversity in surrounding squares (local) or in all British squares (national). Classifying squares as hotspots (or, conversely, coldspots) is arbitrary. We have chosen to designate the top and bottom 5% of squares as hot and coldspots respectively.

We term the square under examination during this procedure the **reference square** and a **neighbourhood** as the block of squares (neighbours) in which the reference square occupies the central position. Any size of block may be used to define a neighbourhood; for national hotspots we have used a neighbourhood size of 100x100 squares (which covers the entire British Isles) and for local hotspots a 5x5 block has been chosen for illustrative purposes only (Using the method described below, local hotspots can be defined for any arbitrarily sized block. A 5x5 block covers and area of 2500 km²; the furthest point from the centre of the reference square 35.35 km away).

Measuring the amount of recorder effort devoted to each square presents difficulties. Input from recorders usually contains no indication of the amount of time spent in a square or of other factors such as the weather at the time of recording (particularly important for flying insects). Modern recording cards address these questions directly but most of the records in the BRC database, extending back several decades, contain no such information. We have chosen to use recorder visits to a square as a measure of **recorder effort**. We define a **visit** as a submission which differs from all

![Graph](https://via.placeholder.com/150)

**Fig. 4.** Hypothetical species discovery curves for four 10 km squares labelled 1–4, illustrating the method by which species richness is compared between squares (see text). Pairwise comparisons are made between the reference square and each other square at the highest number of visits possible without extrapolating. \( r_{ij} \), the index of relative richness for the pair of squares \((i,j)\) is simply the ratio of the expected number of species in each square at the same visit level. If square 2 has three neighbours (1,3 and 4) then three comparisons are made to calculate \( r_{21}, r_{23}, r_{24} \) (For example \( r_{21} \) is calculated from \( E_d(v_2)/E_d(v_1) \), labelled on the figure.) The relative richness index \( R_i \) is then \( R_i = \exp(\log r_{1i} + \log r_{2i} + \log r_{3i} + \log r_{4i}/3) \).
others for that square in at least one of the following criteria: recorder identity, date, site name or grid reference. We have yet to develop a reliable way to determine the relative merits of each visit, and for the present purpose, therefore, all visits are treated as being equal in terms of species discovery power. The extent to which this assumption holds true is likely to vary between data sets.

METHODS

The procedure adopted is based on the rarefaction method of Sanders (1968). Sanders used rarefaction to estimate the number of species expected from a sample in a sub-sample of a given number of individuals. It has here been adapted to estimate the number of species to be expected when the species-pool for each square is sampled (i.e. visited) a given number of times (Fig. 4).

If square j has v_j visits the expected number of species observed in a random sample of n visits can be obtained as follows, provided n≤v_j.

1. Choose n visits at random, without replacement, from the set of all v_j visits to the square; count the number of separate species observed in these n visits, say S_n.

2. Repeat step 1 k times to obtain k values of S_n (where the value for the m\textsuperscript{th} repeat is S_n\textsuperscript{(m)}). The number of species expected in square j after n visits is then

\[ E(n) \approx \frac{1}{k} \sum_{i=1}^{k} S_n^{(i)}. \]  
\text{Eq. 1.}

3. Note that E(v_j) is the total number of species recorded in square j to date. A pairwise measure of relative species richness, corrected for recorder effort, for any pair of squares, is

\[ r_{ij} = \frac{E(v_j)/E(v_i)}{E(v_j)/E(v_j)} \quad v_i \leq v_j \]  
\text{Eq. 2.}

where i and j are two squares being compared. Notice that r_{ij} = 1/r_{ji}. Notice also that the pairwise comparisons made for each i,j maximize v for each pair, in this way the maximum use is made of available information and recourse to extrapolation of the rarefaction curves is avoided (Fig. 4).

4. This pairwise measure can then be repeated and averaged over all the squares in the neighbourhood of each reference square. Let \( \varphi \) be the set of squares in the neighbourhood of i, but excluding the \( i^{th} \) square, and suppose that \( \varphi \) has \( p \) elements which have been visited by recorders and so \( \sum_{j} \) represents all the squares, \( j \), which are members of the set \( \varphi \). We define

\[ R_i = \exp \left( \frac{1}{p} \sum_{j \in \varphi} \log r_{ij} \right) \]  
\text{Eq. 3.}

as an index of relative species richness, independent of recorder effort. Note that the geometric mean is employed for the averaging.

In the work reported here, for local hotspots, the regions defining \( \varphi \) and used to calculate \( R \) are squares of 50 km side, centred on square \( i \). For national hotspots the region size used to calculate \( R \) is expanded to squares of 1000 km side, thus encompassing the entire country for each reference square. All squares which are members of neighbourhoods but which fall entirely outside the coastline of Britain are ignored in all pairwise comparisons.

The method is implemented in Pascal (efficient code is available from the authors) and random number generation for the multiple sub-sampling performed using the routines of Press et al. (1989). The value for \( k \) was set at 100. (Increasing this value improves the reliability of the estimate of \( E(n) \) but at the expense of computing time).

It is possible to calculate the expected species number in Step 2, \( E(n) \), by applying the formula which derives rarefaction curves (see, for example, Muller-Scharer, Lewinsohn & Lawton (1991)), but only if species occur independently. The slightly less elegant but more robust method employed here does not rely on this assumption.

Different taxa are subject to different recording practices for a variety of reasons (Harding & Sheail, 1992); it is useful therefore to evaluate the degree to which species richness has been corrected for recorder effort for both groups, using equation 3. For each reference square a simple correction index is:

\[ C_i = \frac{R_i - B_i}{B_i} \]  
\text{Eq. 4.}

where \( R_i \) is defined in Eq. 3. and \( B_i \) is the number of species recorded in square \( i \), uncorrected for recorder effort, divided by the mean uncorrected number of species per square in the neighbourhood.

RESULTS

Discovery curves

Figs 5 and 6 show families of species discovery curves for four arbitrarily selected reference squares for both
Fig. 5. Families of actual species discovery curves for Odonata for four randomly selected groups of 10 km squares. For clarity, only the curves for eight squares are shown in each family, and the named reference square plotted with asterisks in each case. The remaining seven curves relate to squares with data immediately adjacent to the reference square. The national grid reference number of the reference square within each group of eight is given above the diagram.
Fig. 6. As Fig. 4, for Hepaticae. These plots typify the problem of uneven recording, some squares having been visited many more times than their neighbours.
Fig. 7. (a) National hotspot map for resident Odonata, plotted using raw data from the BRC database. In this and all subsequent maps, large symbols represent hotspots (top 5% of squares in terms of $R_i$ (corrected maps) or $B_i$ (uncorrected maps)), small symbols are coldspots (bottom 5%) and an intermediate symbol is inserted into all other squares from which records have been received. (b) National Odonata hotspots, corrected for recorder effort.
FIG. 8. 
(a) National Hepatic hosts, uncorrected, displaying a reversed national gradient compared to that of Odonata. 
(b) National Hepatic hosts, corrected.
Table 1. The percentage of uncorrected national and local hot and coldspots reclassified as hotspots, coldspots or intermediate by the correction algorithm. For example, 47.5% of the national Odonata hotspots originally identified in the uncorrected data remained as hotspots after correction for recorder effort, whilst 52.5% were ‘downgraded’ to the intermediate class.

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taxa. The differences in recorder behaviour between the taxa are revealed in the shape of the curves (see Discussion). Mean national species yields per visit were: Odonata 5.79, Hepaticae 9.91.

Distribution of national and local hotspots

Comparison of Fig. 7a and b illustrates the effect of the correction process on national hotspots. On the corrected map the majority of Odonata hotspots are still shown to be in the south of England although some are lost from this region whilst several previously unrecognized hotspots are revealed in Devon and Cornwall, Hertfordshire and Cambridgeshire and Scotland. Similarly, for the Hepaticae (Fig. 8a and b) the extreme aggregation of hotspots in the west of Scotland is seen to be the result of heavy recording to some extent and some of these are replaced by squares in England and Wales.

As expected, local hotspots are distributed throughout Britain (Figs. 9 and 10). Using 5x5 square neighbourhoods, both Odonata and Hepaticae have hotspots in most parts of the country although Wales is notable for its lack of local liverwort hotspots as is the Midlands for Odonata. Also as expected, some squares are found to be both nationally and locally important.

Degree of correction

The frequency distributions of correction indices (Eq. 4) for both taxa are shown in Fig. 11. For both groups, most have values of C in the range −1 to +1 with a modal interval of 0 to −0.2 for Odonata and −0.2 to −0.4 for Hepaticae. Odonata are relatively well recorded and it is reassuring to see that nearly half the squares have required virtually no correction at all. Hepaticae have generally been given less attention in most squares, although in some areas recording has been heavy. Estimates of relative diversity for liverworts have therefore been quite markedly altered in many squares by correcting for recorder effort. The extent to which apparent national and local hotspots and coldspots in the uncorrected data move to new categories when corrected for recorder effort is shown in Table 1.

DISCUSSION

It is first worth considering the families of species discovery curves in Figs 5 and 6 to appreciate the implications of the recorder effort problem and why the present correction method is considered appropriate. All eight graphs illustrate clearly variation in the extent to which different squares in the same neighbourhood have been sampled. Furthermore, none of the squares depicted in either group, appears to have yet reached an asymptote. This precludes direct comparison of any squares at their final visit level, which is what uncritical use of the uncorrected species-richness values per square amounts to. Nor can we compare squares by using the mean neighbourhood level of recording because it is not uncommon for one square in a neighbourhood to be much more heavily sampled than the others — it may, for example, be the habitual haunt of a particularly enthusiastic recorder (a possible example is shown in 18/95 for Odonata, Fig. 5). The unusually intensively sampled squares may elevate the neighbourhood mean level of sampling beyond the final level for all or most of the squares in the neighbourhood,
Fig. 9. (a) Local Okonoina hotspots, uncorrected. (b) Local Okonoina hotspots, corrected.
Recorder effort and diversity hotspots
making comparisons at the mean recording level for the set of squares impossible. (In the example the mean level is twenty visits and five squares in the group fail to reach this level). To circumvent this complication by adopting a lower standard intensity of sampling, say three visits, is also problematic since, as the graphs illustrate, discovery curves may cross over as they are developed — species richness ratios at low levels of sampling are not a reliable indicator of those at higher levels. For this reason we also rejected methods of standardization that depended upon extrapolation beyond the limits of the data.

The method described, by virtue of its comparative approach and the scale of the BRC mapping grid, is suitable for the identification of hotspots corrected for sampling effort at the 10 km scale. It is possible to repeat the procedure at larger scales by treating blocks of 10 km squares as squares themselves. However, in modern Britain there are few areas, except perhaps northern Scotland, where habitats are continuous at greater than a 10 km scale so this limitation does not present great difficulties. Of more value would be the application of the procedure at a smaller scale since most habitat fragments are now far smaller than 100 km². Unfortunately data at such resolution exists only for a very limited taxa and regional coverage.

The correction process we describe has been designed to reveal squares which are species rich when compared to their neighbours. Effectively, it reveals squares which have yielded a larger number of species than their neighbours at varying increments of sampling. This may not always mean that the square is indeed very species rich. It may, for instance, reflect some other characteristic of its recorders or those of its neighbourhood. A very efficient and skilled observer may record a large number of species in a few visits, creating an apparent local or regional hotspot where none exists. We therefore regard our process as a necessary first step in any analytical treatment of species richness but acknowledge that further scrutiny of the data may be required to establish whether the pinpointed squares are indeed highly diverse for the taxon under examination.

This point is well illustrated by reference to Figs 5, 6 and 11. The species discovery plots show that for Odonata, many squares have had a high number of
visits and that species addition takes place relatively slowly after the first few visits. For the liverworts, however, most squares have had few visits, often by specialist recorders, with many species revealed on each. Those occasional squares which have also had a few visits but only one or two species revealed on each therefore are subjected to considerable (possibly excessive) upgrading by the method. The longer right tail on the Hepaticae correction index distribution is evidence of this effect and that results must be considered carefully. These caveats notwithstanding, the elucidation of species richness hotspots via this pairwise comparison method is likely to facilitate a variety of analytical work on species distribution in Britain and, if suitable data can be made available, in other parts of the world. Indeed, perhaps the most important general message to emerge from these analyses is the degree to which apparent hotspots of species richness may be influenced by recorder effort. Even in the British Isles, where data on species distribution are among the best in the world, there are clearly major differences in the efficiency of recorder effort in different parts of the country, and these differences may make the identification of local and regional hotspots a more difficult problem than has generally been acknowledged.

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