The biodiversity quality of butterfly sites: A metadata assessment

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ABSTRACT

1. Recent political agreements mandate that the current rate of biodiversity loss is reduced by 2010 (the 2010 target). In Europe one of the 26 indicators given for this assessment is butterfly biodiversity which therefore requires butterfly biodiversity to be measured. Feest et al. (2010) advocates that this can be done using the concept of "Biodiversity Quality".

2. "Biodiversity Quality" measurement requires data analysis based on a series of indices examined both independently and jointly, rather than the use of a single measure such as species richness or a single composite index. We show that, where the theoretical base of sampling is sound, data collected with a simple analytical procedure in mind, can generate far more information than envisaged initially. An example of the compilation of "Biodiversity Quality" indicators is given for a site in the Dutch butterfly monitoring scheme (de Vlinderstichting) and two sites are compared for difference.

3. A scheme showing how changes in the different indices might be interpreted to show change in biodiversity quality is given.

4. These butterfly data are important from the perspective of the 2010 targets because:

(i) they represent invertebrates, which comprise over half of all terrestrial species;
(ii) they are based on relatively long time series; and
(iii) they provide a model against which similar programmes can be designed for other taxonomic groups.

1. Introduction

The parties present at the 2002 Convention on Biological Diversity (CBD) pledged "to achieve, by 2010, a significant reduction of the current rate of biodiversity loss at the global, regional and national levels" (CBD, 2004). This represents a major opportunity for politically-endorsed conservation, but challenges the disciplines of conservation and ecology themselves. Assessing how rates of biodiversity loss have changed from earlier levels by 2010 requires measurements that are accurate, reliable and transparent, yet ecologists cannot agree on how biodiversity should be defined, let alone quantified.

Species statistics such as richness, abundance or evenness are used commonly (Rousseau and Van Hecke, 1999; Gotelli and Colwell, 2001; Stirling and Wilsey, 2001), but most definitions of biodiversity also recognise ecosystem and genetic components (Humphries et al., 1995). With this in mind, a number of new indicators have entered the ecological arena (see Balmford et al., 2005 for an overview). The scope of these measures is ambitious, including attempts to encapsulate, in a single number, the extent of global ecosystems (e.g. the index of coral cover, Côté et al., 2005), and nationwide or even global taxonomic diversity (e.g. the UK Wild Bird Index discussed by Gregory et al., 2005, and the Living Planet Index discussed by Loh et al., 2005). Hooper et al. (2005) indicated that a wider concept of biodiversity cannot be achieved without considering the full functional nature of biodiversity, and that the use of species richness as a measure of biodiversity is misleading and conveys little information.

Whilst we recognise the convenience of such composite indices in the sense that they can be communicated easily to non-scientists, their use is not supported by those who argue that biodiversity cannot be captured by a single number (Pielou, 1993; Gaston and Spicer, 2004; Buckland et al., 2005). Moreover, analysis of the dis-aggregated data is often more useful (Reyers et al., 1998; Kang et al., 2002) and can be used to guide policy.

We reason, therefore, that any attempt to quantify biodiversity and its rate of change should reflect the multifaceted nature of the term, necessitating a broad range of data. Therefore, we define species biodiversity as a quality/characteristic represented by a number of properties that can be measured (Feest, 2006; Feest et al., 2010). It is the picture created by the relationship between these properties that defines the biodiversity of a species group for a site. In the case of butterflies, the biodiversity of a site might be represented by a few species, and high numbers of individuals might be present of those species, giving the site a high butterfly population and biomass. This might contrast with another site where there are few species and only a few individuals of each (low population and biomass), but the species might all be rare. Since these properties can be represented by numerical indices, change can be measured and statistical significance of change inferred. This paper assesses the viability of this approach, based on the creation of indices from previously surveyed butterfly populations and is founded on practical experience of performing surveys and having to compare different sites over time. In a parallel development, and working from a theoretical basis, indices that describe the functional properties of butterfly biodiversity (Hooper et al., 2005; Petchey et al., 2004) e.g. population, biomass, number of species, rarity, and evenness/dominance of species, are the same as those developed by ourselves and Feest (2006) and Feest et al. (2010).

1.1. Butterfly monitoring schemes

Insects are particularly suited for biodiversity quality analysis as they face a high extinction risk (Thomas et al., 2004; Dunn, 2005), and they provide the majority of ecosystem services (Rohr et al., 2007). Butterflies are one of a few insect groups for which annual abundance monitoring has been possible (Brereton et al., 2006) and butterfly monitoring networks, based on a standardized and validated sampling protocol (Pollard and Yates, 1993; Pannekoek and Van Strien, 2001), exist in at least fourteen countries in Europe (Brereton et al., 2006). Some of these schemes have produced data on decadal time scales (e.g. the UK monitoring scheme, which began in 1976).

Seventeen years of data from two differing sites in the Dutch monitoring scheme (de Vlinderstichting), which began in 1990, are presented here and analysed for evidence of suitability for creating a picture of site butterfly biodiversity quality, assessing difference and a possible trend analysis of these data.

This paper therefore tests the following hypotheses:

- H_1: Butterfly population monitoring data can be converted to biodiversity quality/characteristic indices.
- H_2: Biodiversity quality/characteristic indices can show trends in butterfly populations for a site, which may not be revealed by assuming species richness and biodiversity are similar.
- H_3: Butterfly biodiversity quality/characteristic indices can be tested for statistical significance to show difference, trends and relationships.

2. Methods

The field method is based on the use of transects first applied in the British Butterfly Monitoring Scheme (Pollard and Yates, 1993)—a detailed description can be found in van Swaay (2005). There are several deviations from the British scheme, the biggest being that each transect is divided into 50 m sections, with a maximum of 20 sections (1 km in total). Each section must have homogenous vegetation structure.

From April to September all butterflies 2.5 m to the left and right of the recorder and 5 m in front and above are counted weekly along a transect under standardized weather condition requirements. At the end of the recording season, participants submit their data on standard paper forms or via an online web application. Data are checked by specialists in Dutch Butterfly Conservation, and Statistics Netherlands (CBS) performs standardized computerized checks to detect typing and other errors. Transects that are not counted enough times during the flight period of a particular species are omitted. Calculations reflecting the functional diversity concepts of Hooper et al. (2005), and Petchey and Gaston (2002) are made. Values for species richness, population density, biomass, Berger–Parker, Shannon–Wiener, and Simpson's indices (so-called biodiversity indices) and the Species Conservation Value Index (SCVI) were generated for the two sites and analysed using the computerized database "Fungib" (copyright Dr Alan Feest and available free on request from ecosulis ltd.). All of these indices, except SCVI, are used commonly and are fairly easy to calculate. SCVI was first suggested by Feest (2006) and can be calculated where data relating to butterfly numbers exists. The Fungib programme is a tool for assembling these indices together, along with a presentation of the species accumulation curve and species incidence. Mathematical formulae for the calculation of Shannon–Wiener, Simpson's and Berger–Parker indices can be found in Magurran (2004). In practice these three "biodiversity indices" show a strong relationship therefore any statistical analysis including all three would be compromised by this relationship so we have used the Simpson index alone because (a) it has the widest amplitude of the three and gives therefore the greatest discrimination and (b) Magurran (pages 101 and 130) considers this the more accurate of the three indices.

The remaining indices are defined as follows:

Biomass Index we have interpreted as the cumulative wingspan per species and per total sample (Miller, 1977). For the Dutch Lepidoptera, wingspans were obtained from Sterry and Mackay (2004). In moths, for example, the significant difference between the adult body forms of Geometrids and Noctuids would require an adjustment of this measure. This index therefore does not represent actual weight but rather a proportional relationship.

Density is the total number of individuals in a completed survey and may be expressed per unit of area if that is the basis of the sampling (Feest, 2006).

Species Conservation Value Index (SCVI) is the mean "conservation value" score for all species in the sample. Each species is assigned a score, based on national occurrence statistics (derived from previous surveys by de Vlinderstichting) following the scale devised by Feest (2006), which accentuates the value of rarity. It is expressed as the mean value and the Standard Deviation; the latter of these two will register the presence of rarer species in a species rich habitat and populations can therefore be compared by a simple F test.

The Fungib programme presents the data (see Figs. 1 and 2) so that on the left-hand column the butterfly species are listed as they are recorded along the length of the transect. The columns identified as 1–20 of the table refers to the 50 m sections of a whole transect that is 18–20 sections (900–1000 m) long. This cross-table format makes it easy to derive more information than the simple number and identity of species. It also shows patterns of occurrence, co-occurrence, species abundance, dominance and rarity very clearly. On the right-hand side, three columns show the total number of individuals recorded of each species; the SCVI of each species and their calculated Biomass Index. At the bottom the total population, mean SCVI and total Biomass Index are given. The full set of indices is presented in the bottom left-hand corner with the indices in brackets being the results of calculations based on biomass indices, rather than population numbers. In butterflies the differences in size are not great, so these indices do not differ