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Beyond maps: a review of the applications of biological records

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Biological records are one of the most important sources of data for a large number of research areas. For example, their application has made valuable contributions to climate change ecology, where they are used to monitor species range shifts; to conservation ecology, where they are used to assess species' Red List status; and to biogeography, where they are used to highlight hotspots of biodiversity. A major benefit of biological records is the large spatial extent of the coverage combined with the fine spatial precision of the data: this combination is essential for any ecologist hoping to address large-scale questions about biodiversity and environmental change. Because most biological records are collected by a vast pool of volunteer recorders, studies utilizing biological records have the advantage of large-scale long-term data that it would otherwise be unfeasibly expensive to collect. We review the application of biological records by focussing on four key areas of biodiversity research: biogeography, trend assessments, climate change ecology, and conservation biology. We showcase the diversity of insights that biological records have delivered, which in turn illustrates the contribution of the voluntary recording community to our understanding of biodiversity science. © 2015 The Linnean Society of London, *Biological Journal of the Linnean Society*, 2015, **115**, 532–542.

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INTRODUCTION

Knowledge of the spatial and temporal distribution of species is vital to many areas of research. Biological records are one of the most important sources of data contributing to this knowledge globally (Hochachka *et al.*, 2012), and the UK is probably the best-recorded country on earth [almost one-eighth of the records on the Global Biodiversity Information Facility (GBIF) originate from the UK; https://code.google.com/p/gbif-occurrencestore/wiki/IndexDataAnalysis, accessed 27/11/2014]. Biological records originate from a variety of sources, including targeted research projects, although most records are collected by a vast number of volunteer recorders. One of the major advantages of biological records data is the large spatial extent of the coverage (i.e. national) combined with the fine spatial precision (most records are collected at 1 km^2 or finer): this combination describes the 'holy grail' of datasets that ecologists need to address large-scale questions about biodiversity and environmental change (Beck *et al.*, 2012). Therefore, studies that utilize biological records have the advantage of large-scale long-term data that would be unfeasibly expensive to collect without the effort of volunteer recorders. In the last 10 years, 12 atlases and over 200 research articles have been published using UK biological records alone.

Biological recording has grown markedly in recent decades (Isaac & Pocock, 2015), partly as a result of the technological developments that have made species identification and submitting records accessible to wider public participation (August *et al.* 2015). With these improvements, the size and taxonomic breadth of species distribution datasets are expected to rise (Silvertown, 2009; Dickinson *et al.*, 2012; Miller-Rushing, Primack & Bonney, 2012). This

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*Corresponding author. E-mail: gary.powney@ceh.ac.uk growth in data collection highlights the importance of recording schemes and organizations that host online portals that increase data accessibility, such as the National Biodiversity Network Gateway (NBN Gateway; http://www.nbn.org.uk/) and GBIF (http://www.gbif.org/). Additionally, this growth has been accompanied by a broadening of the taxonomic basis of studies using biological records, from the well-studied birds, butterflies, and vascular plants (Thomas *et al*., 2004a) to ladybirds (Roy *et al*., 2012), woodlice (Purse *et al*., 2012), pollinating insects (Carvalheiro *et al*., 2013), and Odonata (Powney *et al*., 2014).

Here, we review the application of biological records in four areas of biodiversity research: biogeography, trend assessments, climate change ecology, and conservation biology. We showcase the diversity of insights that biological records have delivered and celebrate the achievements of the voluntary recording community.

BIOGEOGRAPHY AND MACROECOLOGY

Biogeographical and macroecological studies require large-scale distribution data and have therefore benefited from the increase in availability of biological record data. A key response variable in biogeographical studies is species richness. Biological records are frequently used to estimate species richness, although it can also be estimated from expert-drawn species range maps. To extract richness from range maps, a spatial grid can be overlaid onto a series of extent of occurrence maps, with richness estimated as the cumulative number of species ranges that fall within each cell. Richness based on biological records is simply a count of the number of species occurring in each grid cell. Both techniques have strengths and weaknesses that tend to be scale-dependent: range maps tend to overestimate richness (a greater level of false presences), whereas gaps in biological record data lead to an increase in false absences and therefore an underestimation of richness (Hurlbert & White, 2005; Hurlbert & Jetz, 2007). Species richness has been mapped for a variety of taxonomic groups across a range of geographical regions. Rahbek & Graves (2001) mapped species richness patterns of the avian fauna of South America, which was extended to the global scale by Orme *et al*. (2005). Global richness maps are also available for amphibians and mammals (Stuart *et al*., 2004; Grenyer *et al*., 2006). More recently, Rouse, Spencer Jones & Porter (2014) mapped the richness of marine bryozoans off the coast of Scotland using data that were partly extracted from the NBN Gateway. Richness maps are usually static and estimated for a distinct time period; however, by using long-term data, some studies have estimated temporal change in richness; for example, Ball-Damerow, M'Gonigle & Resh (2014) examined change in Odonata richness of California and Nevada over the last century, finding that dragonfly richness had declined across all sites. Recently, Carvalheiro *et al*. (2013) used biological records to show that declines in the species richness of pollinating insects have slowed in recent years.

Richness is one of many metrics of biodiversity that are frequently derived from biological records; others include beta, phylogenetic, and functional diversity (Magurran & McGill, 2011). As with species richness, these other metrics of biodiversity can be estimated using a variety of functions. Essentially, each of these metrics measures turnover between species communities (Magurran & McGill, 2011), with beta diversity based purely on species composition and phylogenetic diversity incorporating evolutionary history into the measure, whereas functional diversity is based on the ecological characteristics of a species (Petchey & Gaston, 2002; Flynn *et al*., 2011; Srivastava *et al*., 2012). Biological records are often used to identify spatial turnover in species composition across a gridded landscape (Lennon *et al*., 2001); consequently, they can be used to highlight regions of conservation interest (more details are provided further below).

A potential limitation of the use of biological records for estimating richness and diversity patterns is that spatial variation in recorder effort can lead to spatial bias in distribution maps (i.e. areas that have been intensely surveyed are likely to have higher richness, whereas poorly studied regions will have a higher level of false absences) (Isaac & Pocock, 2015). When using a large dataset of plant observations to estimate plant richness in South Africa, Robertson & Barker (2006) noted a spatial bias in the data and used the relationship between climate and richness to map under-surveyed regions. Hill (2012) outlined an approach to highlight and account for poorly recorded regions based on the frequency of common 'benchmark' species within local neighbourhoods. Finally, species distribution models (SDMs) have been used to predict species richness in poorly studied regions (Elith *et al*., 2006; Thuiller *et al*., 2009). These models identify species-specific associations with various environmental variables (usually climate and habitat) and then use these associations alongside various gridded environmental layers to produce a suitability surface/predicted distribution for each species. These predicted distributions are treated as presence absence data and are summed to create a corrected/predicted richness for each grid cell. Newbold *et al*. (2009) used a SDM approach to create corrected richness maps for the mammal and butterfly fauna of Egypt, finding that richness tended to be higher within protected areas. Vasconcelos, Rodríguez &

Hawkins (2011) fitted SDMs to data from GBIF to identify richness patterns in New World Amphibians. They found that the models performed well at predicting richness patterns compared to expert opinion, and concluded that the SDM approach is a useful macroecological tool for investigating broad-scale richness patterns. The SDM approach has several important assumptions and limitations, which means that derived richness values tend to be overestimated (Vasconcelos *et al*., 2011). Thus, raw biological records and SDMs set the lower and upper bounds on the likely number of species in any grid cell.

Understanding the processes that drive the spatial patterns in species richness and diversity is a popular area of research for biogeographers. Several studies have examined environmental correlates of species richness, generally finding that, at the broad-scale, climate variables tend to be key drivers of richness (Currie, 1991; Field *et al*., 2009). Blackburn & Gaston, (1996) found that New World bird richness was related to solar radiation and primary productivity, whereas Powney *et al*. (2010) found that lizard richness was highest in the hot, dry regions of Australia. Using data from GBIF, Giannini *et al*. (2013) found that bee and plant richness in South America was positively associated with precipitation and, in areas of lower precipitation, the interactions between bees and plants tended to be more specialized. Other studies have used gridded distribution data to test macroecological rules, such as Rapoport's rule (Kerswell, 2006).

A variety of research areas require detailed species level trait data, and some of these traits can be directly derived from biological records. A simple trait frequently extracted from biological records is species range size. This can be estimated simply as the combined area of all occupied grid cells, although more complicated methods, such as α-hulls and localized convex hulls (Burgman & Fox, 2003; Getz & Wilmers, 2004; Getz *et al*., 2007; Maes *et al*., 2015) attempt to fill in data gaps and therefore produce more accurate results (although genuine gaps can be mistakenly filled). Range size is an important metric of species' rarity (Gaston, 2003), it is an essential component of extinction risk (Purvis *et al*., 2000), and it has been used in a huge number of studies (Blackburn & Gaston, 1996; Jetz & Rahbek, 2002; Botts, Erasmus & Alexander, 2012).

Climate and habitat associations are regularly derived from biological records. Species climate indices have been estimated as the mean temperature/rainfall of all occupied grid cells (Devictor *et al*., 2008; Powney *et al*., 2013). Binomial logistic regression has also been used to estimate species climate and habitat associations (Lundy, Montgomery & Russ, 2010). Oliver *et al*. (2009) estimated the preferred habitat of butterfly species as the habitat type containing the highest density of records. They then used the ratio of records in the preferred habitat and subordinate habitat as a measure of habitat specificity. A method known as ecological niche factor analysis (ENFA) combines species presence records and habitat layers to estimate the difference between a species habitat requirement and that of a given landscape (Hirzel *et al*., 2002). ENFA compares the species niche breadth in multivariate space to the niche breadth of the overall study region, with the difference between the two forming the marginality score (the higher the marginality score, the more marginal the niche breadth of the species relative to the study region). A related approach is to use species co-occurrences to identify biogeographical boundaries. Finnie *et al*. (2007) used biological records to identify 'floristic elements' in Europe; this approach was later refined using biological records in Britain and Ireland (Preston, Harrower & Hill, 2011; Preston *et al*., 2013). Wilson *et al*. (2004) highlighted fractal dimension (FD) as a measure of fragmentation of a species distribution, suggesting that aggregated distribution patterns reflect range expansion, whereas a fragmented distribution is characteristic of the process of range decline. The FD of a species distribution was calculated as the slope of the relationship between the log of the area of occupancy at the 10-km and 100-km scales plotted against the log of the length grid cell at each scale. More recently, FD has been superseded by more sophisticated techniques for measuring the shape of a species distribution, and these have been applied to biological records data on plants (Azaele *et al*., 2012) and dragonflies (Barwell *et al*., 2014).

This section illustrates that, through their application in the mapping of diversity patterns and their use in deriving species level trait data, biological records have made a major contribution to several areas of biogeographical and macroecological research.

ESTIMATING SPECIES TRENDS

Trends in species' status are a key currency for measuring biodiversity loss and responses to environmental change. The long-time span covered by biological records makes them an excellent data source for estimating trends, although the semi-structured nature of the recording process presents many challenges to trend estimation (Hill, 2012; Isaac *et al*., 2014; Isaac & Pocock, 2015).

Trend estimation from biological records can be traced back to Perring, (1970) who examined threatened plant species in Britain. Consecutive atlases have been a popular source for trend estimation, an early example of such comes from the publication of the *New Atlas of Breeding Birds in Britain and Ireland 1988–1991* (Gibbons, Reid & Chapman, 1993). By comparing the number occupied grid cells with the original atlas (Sharrock, 1976), it was possible to reveal large changes in the distribution of many bird species over two decades. The *New Atlas of Breeding Birds* was followed by the *Millennium Atlas of Butterflies in Britain and Ireland* (Asher *et al*., 2001) and the *New Atlas of the British and Irish Flora* (Preston, Pearman & Dines, 2002), both of which included sections on species trends. Thomas *et al*. (2004a) used the three atlas pairs to compare losses and gains across these taxonomic groups in a study that is frequently cited with regard to the global extinction crisis.

In recent years, statistical ecologists have developed a suite of methods for estimating robust trends from biological records at the same time as accounting for uneven recording intensity (Szabo *et al*., 2010; Hill, 2012; van Strien, van Swaay & Termaat, 2013; Isaac *et al*., 2014). A feature common to many newer techniques is the use of fine spatial and temporal resolutions (e.g. per km^2 and year) for modelling, rather than aggregated to atlas-type resolution, which means that trends can be reported over shorter time periods (e.g. per decade) and without the need for repeat atlases. These modern trend-estimating techniques have been used in recent British atlas publications for ladybirds (Roy *et al*., 2011), hoverflies (Ball *et al*., 2011), bryophytes (Blockeel *et al*., 2014), and dragonflies (Cham *et al*., 2014) and invertebrates of early successional habitats (Thomas *et al*., 2015). Robust trend estimates from biological records are an important resource in both pure and applied ecology. Trends for individual species form a critical component of the assessment process for International Union for Conservation of Nature (IUCN) Red Lists (Maes, 2015). Aggregate trends across species are a major component of biodiversity indicators (JNCC, 2013; WWF, 2014) and have provided some of the best evidence for large-scale biodiversity losses (Thomas *et al*., 2004a; Burns *et al*., 2013; Dirzo *et al*., 2014).

We have highlighted the vital role that biological records play in the estimation of species trends. Such species level trends are crucial for determining species' conservation status and for helping research that aims to identify the main drivers of such trends.

CLIMATE CHANGE ECOLOGY

Anthropogenic climate change is a major threat to biodiversity as it is responsible for species range shifts, phenological changes, and declines in abundance (Parmesan *et al*., 1999; Willis *et al*., 2008; Gregory *et al*., 2009; Bellard *et al*., 2012). Much of this evidence is based on knowledge gained through analyses of biological records. Contributions to climate change ecology are some of the most important applications of biological records and, with the continued rise in greenhouse gas emissions, the impact of climate change is likely to persist and intensify (IPCC, 2013).

Climate limits species distribution patterns, with the upper and lower thermal tolerance of a species forming the boundaries of its temperature niche. There is a wealth of evidence suggesting that species distributions are shifting polewards to track the shift in their climatic niche (Thomas & Lennon, 1999; Crozier, 2004; Walther *et al*., 2007; Chen *et al*., 2011; Mason *et al*., 2015). This evidence has been observed from shifts in species range margins (Parmesan *et al*., 1999; Hickling *et al*., 2006; Franco *et al*., 2006; La Sorte & Thompson, 2007) and from temporal changes in the thermal preference of communities (Devictor *et al*., 2008) and has also been observed in species of terrestrial and marine environments (Perry *et al*., 2005; Sorte, Williams & Carlton, 2010). Additionally, SDMs have been used to predict range shifts under future climate scenarios (Jones *et al*., 2013). However, evidence suggests that predictions from SDMs should be interpreted with caution because their predictive accuracy tends to be poor (Rapacciuolo *et al*., 2012). Altitudinal range shifts have also been found in response to climate warming. Using data from GBIF, Feeley *et al*. (2010) found upward shifts in tropical Andean tree species in response to elevated temperatures, becoming one of the first studies to document such shifts in tropical plant communities.

The intensity, and in some cases direction, of these range shifts is not uniform within or between taxonomic groups (Thomas *et al*., 2004b; Lenoir *et al*., 2008; Hill & Preston, 2015). The potential impact of this variation on community structure and in turn the functioning and resilience of ecosystems is a cause for concern (Lenoir *et al*., 2008; Walther, 2010), with evidence showing that change in community structure can result in mismatch between trophic and functional groups (Edwards & Richardson, 2004; Lauzeral *et al*., 2010; Thackeray *et al*., 2010; Schweiger *et al*., 2012).

Changes in phenology, the timing of key ecological events, have been observed in response to climate change (Menzel *et al*., 2006; Thackeray *et al*., 2010; Walther, 2010). Analyses based on the long-term trend in the date of the annual first appearance of a species often provide useful insights into the impact of climate change on biodiversity. Using abundance data collected by a vast number of volunteer recorders, Roy & Sparks, (2000) reported significant advancement in the first appearances of most butterfly species in the UK. These changes were measured over a 20-year period, leading to the conclusion that they were a result of climate warming. A similar pattern was discovered in the flight dates of British and Dutch Odonata (Hassall *et al*., 2007; Dingemanse & Kalkman, 2008). Related to first appearance, the arrival dates of 18 common migratory bird species in North America have advanced over time, based on an analysis of eBird data (Hurlbert & Liang, 2012; eBird: http://ebird.org/content/ebird/). Phillimore *et al*. (2010) used biological records of the common frog (*Rana temporaria*) to show that spawning dates were related to local climate conditions and predicted that the species would need to advance their spawning date by 21–39 days to track projected climate warming. The value of biological records was highlighted by Bishop *et al*. (2013) who found phenological events estimated from opportunistic biological records can accurately predict those extracted from more robust structured surveys. Menzel *et al*. (2006) reviewed numerous phenological studies, including many studies based on biological records, finding that climate-driven phenological shifts are occurring without doubt. The concerns surrounding phenological changes mirror those for variation in species range shifts, in that changes may lead to trophic and functional groups mismatches (Edwards & Richardson, 2004; Lauzeral *et al*., 2010; Thackeray *et al*., 2010; Schweiger *et al*., 2012).

APPLIED ECOLOGY AND CONSERVATION BIOLOGY

Biological records are vitally important to applied ecology and conservation biology. Their use has made significant contributions to conservation prioritization, the planning and assessment of protect area networks, the study of invasive species, estimating species trends, and the subsequent understanding of the drivers of such trends.

The limited resources available for conservation, and the consequent need to maximize the efficiency of conservation efforts, is the basis of conservation prioritization research. Conservation prioritization tends to focus on spatial aspects of biodiversity and, as highlighted above, biological records are frequently used to map spatial patterns of diversity. These maps play an important role in conservation prioritization, where they are used to highlight hotspots of biodiversity (Myers *et al*., 2000; Moilanen, Wilson & Possingham, 2009). Furthermore, species can be grouped in such a way that the resulting maps reflect the spatial patterns of species of conservation concern (e.g. endemic species, priority species: Orme *et al*., 2005; Grenyer *et al*., 2006). Additionally, species complementarity algorithms can be used to efficiently select the optimal set of cells that capture the majority of species (Grenyer *et al*., 2006; Thomas *et al*., 2013). A limitation of this approach is that it leaves little buffer for future biodiversity loss. Losses as a result of stochastic events can be intensified and the priority patches are often isolated and therefore vulnerable to the negative impacts of habitat fragmentation (Fahrig, 2003; Wiegand, Revilla & Moloney, 2005). Furthermore, the results of such studies tend to fall short of being implemented practically but, instead, act as a call to arms for biodiversity conservation. Although the application of biological records to conservation prioritization has tended to focus on spatial aspects of biodiversity, it has also been applied at the species level. A key example of species level prioritization is Red Listing (Maes, 2015), with a recent example being the plant Red List for England (Stroh *et al*., 2014). Dolman, Panter & Mossman (2012) presented a form of biodiversity auditing, which combines biological records with autecological information to create spatially-informed evidence-based conservation management priorities.

Spatial conservation prioritization has clear links to protected area design and management. A key question for conservation science and natural resource agencies is whether protected areas are effective. Biological records have contributed to our understanding of this issue because recent evidence from biological records has shown that UK protected areas contain a disproportionate amount of wildlife (Gillingham *et al*., 2014) and provide stepping stones for species to shift their distributions in response to climate change (Thomas *et al*., 2012). As noted above, SDMs have been used to predict future species distribution patterns under various climatic projections. These future predictions can be related to the current protected area network to estimate the future coverage and potential mismatches between the protected area network and projected hotspots of biodiversity (Araújo *et al*., 2004). This approach was employed by Araújo *et al*. (2011) to examine projected plant and terrestrial vertebrate distributions in Europe, and Jones *et al*. (2013) to examine the project distributions of 17 marine vertebrates. Both conclude that the policy surrounding reserve design needs to consider future changes in species distributions and that SDMs are a valuable tool in this regard.

By combining two of the applications of biological records above: ‘species’ trend assessments’ and ‘deriving traits from biological records’, it is possible to gain valuable insights in to some of the main drivers of such trends. Responses to environmental change are not uniform across all species (Parmesan *et al*., 1999; Angert *et al*., 2011; Polce *et al*., 2011), and this variation in species response can be partly explained by variation in species trait characteristics (Purvis *et al*., 2000; Reynolds, Webb & Hawkins, 2005; Angert *et al*., 2011; Newbold *et al*., 2013). Comparative trait-based studies that link trends with species' traits has allowed researchers to move beyond statistical descriptions of changes in species' status, towards a deeper understanding of the mechanisms driving biodiversity loss (Fisher & Owens, 2004; Cardillo *et al*., 2005; Cowlishaw, Pettifor & Isaac, 2009). A classic example is provided by Fuller *et al*. (1995) who examined trends in British birds: they found that 86% of farmland bird species declined in distribution between 1970–1990 compared to just 51% of nonfarmland species, revealing the devastating effect of agricultural intensification on bird populations. Similarly, habitat loss has also been implicated as the major force driving changes in the British flora, with habitat specialists and species with lower competitive ability declining most rapidly (Preston *et al*., 2002; Powney *et al*., 2013). A suite of species traits predict long-term trends in the distribution of British moths, with strong regional variation reflecting both climate change and habitat loss as drivers of change (Fox *et al*., 2014). Biesmeijer *et al*. (2006) showed that the species richness of wild bees declined in Britain and the Netherlands, with specialized species declining fastest. This is important given that the status of pollinating insects is currently an issue of major concern among scientists and policy makers (Klein *et al*., 2007; POST, 2010; Potts *et al*., 2010; Garratt *et al*., 2014). Biological records have provided some of the most compelling evidence on the status of wild pollinators. Despite the decline in wild bees, the news is not all gloomy because hoverfly species richness generally increased in both countries (Biesmeijer *et al*., 2006), and more recent evidence suggests that some declines, particularly wild bees, may have been reversed subsequent to 1990 (Carvalheiro *et al*., 2013).

Invasive species are alleged to be a key cause of biodiversity loss (Hooper *et al*., 2005), although evidence linking invasions to species declines has been limited (apart from on pristine island ecosystems; MacDougall & Turkington, 2005). Invasive and nonnative species have been historically under-recorded, although the arrival of the harlequin ladybird, *Harmonia axyridis*, in northern Europe was the stimulus for one of the first online recording schemes, established in Belgium in 1999 and in Britain in 2005. The result is an unusually rich source of data on the spread of *H. axyridis* and its impact across two countries, which has revealed a direct link between the arrival of *H. axyridis* and declines in a majority of common native ladybird species (Roy *et al*., 2012). Recently, SDMs have been applied to predict future hotspots for biological invasions, finding that the distributions of terrestrial and aquatic invasive invertebrates are likely to substantially expand (Bellard *et al*., 2014).

The value of biological records for conservation biology is clear. With their large spatial coverage and fine-scale spatial precision, they are essential for conservation prioritization, monitoring the threat of invasive species and understanding the main drivers of biodiversity loss. Crucially, they enable ecologists to examine large-scale processes that would unfeasibility expensive to address without the voluntary contribution of recorders.

CONCLUDING REMARKS

Our review has highlighted the enormous breadth of scientific questions for which biological records have provided answers. The growth of citizen science means that datasets of biological records are likely to grow even faster, providing a wealth of research opportunities for ecologists and conservation biologists. Additionally, with the recent adoption of hierarchical Bayesian techniques by ecologists, uneven recording effort can be modelled explicitly (van Strien *et al*., 2013; Beale, Brewer & Lennon, 2014; Isaac *et al*., 2014), thus greatly expanding the potential scientific uses of biological records data.

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