

### JNCC Report No: 488

## Trends in the Distribution of UK native species 1970-2010 Preliminary report to JNCC

Isaac, N. J. B., August, T. A., Harrower, C. & Roy, D.B.

May 2013

© JNCC, Peterborough 2013

ISSN 0963 8901



## For further information please contact:

Joint Nature Conservation Committee Monkstone House City Road Peterborough PE1 1JY www.jncc.defra.gov.uk

### This report should be cited as:

Isaac, N.J.B., August, T.A., Harrower, C. & Roy, D.B. Trends in the Distribution of UK native species 1970–2010: Preliminary report to JNCC. *JNCC Report No 488* 

## Acknowledgement

Biological Records Centre, NERC Centre for Ecology & Hydrology, Crowmarsh Gifford, Wallingford, OX10 8BB, UK

# **Contents**

1	Introduction	1
2	Methods	1
3	Results	2
4	Conclusions	3
5	References	3

### 1 Introduction

The partnership between the Joint Nature Conservation Committee (JNCC) and Biological Records Centre (BRC) is a research program to analyse and interpret biological records data. A key strategic aim of this work is to derive quantitative and robust measures of trends in species' status over policy-relevant time-periods.

Biological records are observations of species in a known place in space and time. Most records are made by volunteer recorders and whilst these data may be collected following a specific protocol, the majority of records in these datasets are opportunistic. The intensity of recording varies in both space and time (Isaac, 2012), which is a challenge for estimating robust quantitative trends.

Fortunately, a range of methods now exists for producing such trends using unstructured biological records data. Computer simulations show that some of these methods are robust to the biases in biological records data (Isaac, 2012). Here we apply three such methods to estimate preliminary trends in the status of over 1300 native species of plants and animals in well-recorded groups. The summary statistics provide a broad overview of changes in the status of native biodiversity for a much wider range of taxa than has previously been possible (Thomas *et al* 2004).

### 2 Methods

We used datasets from four recording schemes (Table 1) covering well-studied taxa. We restrict our analyses to the period 1970-2010, since few data are available prior to this period.

Taxon	Source	Number of	Number of
		records	species
Bryophytes	British Bryological Society	2,281,525	1,371
Coccinellidae	UK Ladybird Survey	107,392	61
Hymenoptera	Bees, Wasps & Ants Recording	362,819	548
	Scheme		
Moths National Moth Recording Scheme		10,985,245	1,033

Table 1 – Datasets used in these analyses. Sample sizes are for the period 1970-2010.

Many candidate methods exist for estimating trends from biological records data and we lack a coherent view on which method is best. Preliminary results from computer simulations (Isaac, 2012) suggest that three methods show sufficient promise to warrant serious consideration. These are List Length (Szabo *et al*, 2010), the 'mixed model' (Roy *et al*, 2012) and Frescalo (Hill, 2011). The first two of these use data at the level of a 'visit', defined as a unique combination of date and 1km², and produce an estimated change in occurrence per year (i.e. a linear trend). Frescalo uses data aggregate into two time-periods with a spatial resolution of the 10km grid cell (henceforth referred to as a 'hectad'). We used time periods of 1970-1989 & 1990-2009 for all datasets.

We applied all three methods to the records data for each species for which there were not known taxonomic issues and for which records existed in a minimum of 20 hectads with at least one hectad in England (following the method in Hickling *et al*, 2006). For the mixed model, we restricted the data to a subset of well-sampled grid cells: we selected only those visits in which at least four species were recorded, and used only the grid cells for which at least three visits meet this criterion (c.f. Roy *et al* 2012, who used a threshold of two

species). Some models from the mixed model and list-length approaches gave fitted probabilities of 0 or 1 due to small numbers of observations: these were excluded from further analysis. For Frescalo, we used the default parameterization recommended in Hill (2011). For all methods, we separated the Hymenoptera dataset into Bees, Wasps and Ants, since the three constituent groups tend to be recorded separately.

We then combined the results to obtain a consensus view of the change in distribution of each species. Each method estimates a trend in a different way, but all three return a Z-value as a measure of statistical significance. For each species we calculated the mean Z-value across methods (sensu Whitlock, 2005). The result indicates whether the consensus across methods was that the species was significantly increasing (Z > 1.96), significantly decreasing (Z < -1.96) or in between. For the purpose of summarizing the results, we separate those species with small but non-significant increases ( $0 < Z \le 1.96$ ) or decreases (0 < Z > -1.96).

#### 3 Results

After filtering out species for which data were insufficient, or which had known taxonomic issues, 1344 species remained of the initial 3013. These species were analysed and the number of species falling into each category is shown in Table 1. Comparison across taxonomic groups becomes clearer when the data are plotted as the proportion of species in each category (Figure 1).

Trend	Declining	Stable-declining	Stable increasing	Increasing
Bryophytes	66	89	57	41
Hymenoptera: Ants	5	8	7	9
Hymenoptera: Bees	42	52	45	39
Hymenoptera: Wasps	47	61	39	28
Ladybirds	20	9	4	9
Moths	319	67	78	203

Table 2 – A summary of results from the consensus approach indicating the number of species for each group that fell into each of the categories.

Overall, a larger proportion of species show significant declines (37%) than increases (24%). Groups with the highest proportion of declining species are moths and ladybirds, both with nearly half the species assessed showing significant declines. Only ants contain a higher proportion of increasing versus decreasing species.

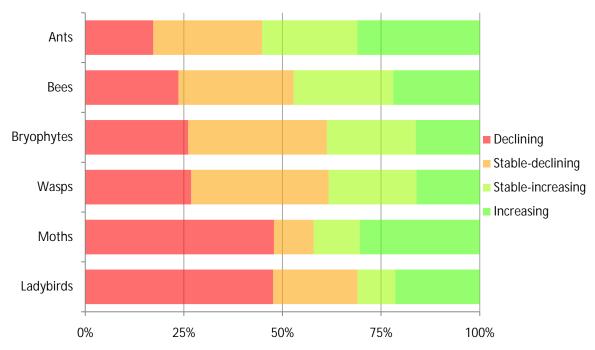


Figure 1 – For each group examined a summary of the proportion of species that fall into each of the four categories, sorted in order of increasing proportion of declining species

#### 4 Conclusions

Our preliminary trend estimates provide a broad overview of changes in the status of UK biodiversity over four decades. The results demonstrate the great potential for estimating quantitative trends from biological records data: previously this had been possible only for taxonomic groups with repeat atlases (Thomas *et al* 2004). The predominance of declining over increasing species is perhaps not surprising, but a cause for concern nonetheless. More refined models for individual species could be used to inform conservation priorities and assess species against IUCN categories of extinction risk.

### 5 References

Hickling, R, Roy, D., Hill, J.K., Fox, R. & Thomas, C. (2006) The distribution of a wide range of taxonomic groups are expanding polewards. *Global Change Biology*, 12, 450-455

Hill, M.H., 2011. Local frequency as a key to interpreting species occurrence data when recording effort is not known. *Methods in Ecology & Evolution*, 3 (1), 195-205.

Isaac, N. J., B. 2012 Extracting trends from biological recording data. National Biodiversity Network Conference. London. *doi:10.6084/m9.figshare.428369* 

Roy, H.E., Adriaens, T., Isaac, N.J.B. *et al.* 2012 Invasive alien predator causes rapid declines of native European ladybirds. *Diversity & Distributions*, 18, 717-725.

Szabo, J.K., Vesk, P.A., Baxter, P.W.J., & Possingham, H.P2010 Regional avian species declines estimated from volunteer-collected long-term data using List Length Analysis. *Ecological Applications*, 20, 2157–2169.

Trends in the Distribution of UK native species 1970-2010 - Preliminary report to JNCC

Thomas, J. A., Telfer, M. G., Roy, D. B., Preston, C. D., Greenwood, J. J. D., Asher, J., Fox, R., et al. 2004. Comparative losses of British butterflies, birds, and plants and the global extinction crisis. *Science*, 303(5665), 1879–81.

Whitlock, M. C. 2005. Combining probability from independent tests: the weighted Z-method is superior to Fisher's approach. *Journal of Evolutionary Biology*, 18(5), 136