

Trait correlates of distribution trends in the Odonata of Britain and Ireland: Southern species benefit from climate warming

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A major challenge in ecology is understanding what enables certain species to persist, while others decline, in response to environmental change. Trait-based comparative analyses are useful in this regard as they can help identify the key drivers of decline, and highlight traits that promote resistance to change. Despite their popularity trait-based comparative analyses tend to focus on explaining variation in range shift and extinction risk, seldom being applied to actual measures of species decline. Furthermore they have tended to be taxonomically restricted to birds, mammals, plants and butterflies. Here we utilise a novel approach to estimate trends for the Odonata in Britain and Ireland, and examine trait correlates of these trends using a recently available trait dataset. We found the dragonfly fauna in Britain and Ireland has undergone considerable change between 1980 and 2012, with 33 and 39% of species showing significant declines and increases respectively. **Distribution type was the key trait associated with these trends**, where southern species showed significantly **higher trends** than widespread and northern species. We believe this reflects the impact of climate change as the increased ambient temperature in Britain and Ireland better suits species that are adapted to warmer conditions. We conclude that northern species are particularly vulnerable to climate change due to the combined pressures of a decline in climate suitability, and competition from species that were previously limited by lower thermal tolerance.

1 **Trait correlates of distribution trends in the Odonata of Britain and Ireland:**
2 **Southern species benefit from climate warming**

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12 **Abstract**

13 A major challenge in ecology is understanding what enables certain species to
14 persist, while others decline, in response to environmental change. Trait-based
15 comparative analyses are useful in this regard as they can help identify the key
16 drivers of decline, and highlight traits that promote resistance to change. Despite
17 their popularity trait-based comparative analyses tend to focus on explaining
18 variation in range shift and extinction risk, seldom being applied to actual measures
19 of species decline. Furthermore they have tended to be taxonomically restricted to
20 birds, mammals, plants and butterflies. Here we utilise a novel approach to
21 estimate trends for the Odonata in Britain and Ireland, and examine trait correlates
22 of these trends using a recently available trait dataset. We found the dragonfly
23 fauna in Britain and Ireland has undergone considerable change between 1980 and

24 2012, with 33 and 39% of species showing significant declines and increases
25 respectively. Distribution type was the key trait associated with these trends, where
26 southern species showed significantly higher trends than widespread and northern
27 species. We believe this reflects the impact of climate change as the increased
28 ambient temperature in Britain and Ireland better suits species that are adapted to
29 warmer conditions. We conclude that northern species are particularly vulnerable to
30 climate change due to the combined pressures of a decline in climate suitability, and
31 competition from species that were previously limited by lower thermal tolerance.

32 **Introduction**

33 Defaunation, the loss of species and populations (Dirzo *et al.*, 2014), is occurring at
34 an alarming rate with recent estimates suggesting that the current extinction rate is
35 1000 times that of the historical natural background rate (De Vos *et al.*, 2014).
36 These declines are driven by environmental change, particularly habitat loss and
37 climate change, and can be measured in a number of ways, e.g. changes in
38 distribution and abundance (Thomas *et al.*, 2004; Biesmeijer *et al.*, 2006; Butchart
39 *et al.*, 2010; Chen *et al.*, 2011). Variation in species responses to environmental
40 change has been found across broad taxonomic groups (Hickling *et al.*, 2006; Angert
41 *et al.*, 2011) but also within taxonomic groups, i.e. between species within an order
42 (Hickling *et al.*, 2005). A major challenge in conservation ecology is to gain a better
43 understanding of this interspecific variation in response to environmental change,
44 i.e. what enables certain species to persist while others decline?

45 Species traits play an important role in determining species' ability to resist
46 environmental change. For example, several studies have shown that ecological

47 generalists out-perform specialists (Walker & Preston, 2006; Ozinga *et al.*, 2012;
48 Newbold *et al.*, 2013). Such comparative trait-based analyses are popular, as the
49 models help to identify the main drivers of change and allow the prediction of future
50 biodiversity changes based on environmental forecasts (Fisher & Owens, 2004;
51 Cardillo *et al.*, 2006). Previous comparative trait analyses have tended to focus on
52 explaining variation in range shift (Angert *et al.*, 2011; Mattila *et al.*, 2011; Grewe *et al.*,
53 *et al.*, 2012) and extinction risk (Purvis *et al.*, 2000; Koh *et al.*, 2004; Cardillo *et al.*,
54 2008; Cooper *et al.*, 2008; Fritz *et al.*, 2009). Despite its popularity, the comparative
55 trait-based approach has seldom been applied to direct measures of species'
56 changing status (i.e. rates of decline or increase). Currently data on such measures
57 of decline are rare, particularly at large (e.g. national) scales and across multiple
58 species. With the increase in public participation in biological recording, the
59 availability of large-scale distribution datasets has increased (Silvertown, 2009).
60 Such data tend to be collected without systematic protocols and thus contain many
61 forms of sampling bias and noise, making it hard to detect genuine signals of
62 change (Tingley & Beissinger, 2009; Hassall & Thompson, 2010; Isaac *et al.*, 2014b).
63 However, recent advances in analytical approaches have improved our ability to
64 estimate reliable trends from these unstructured biological records (Isaac *et al.*,
65 2014b). In this study we utilise these novel approaches to estimate trends for the
66 Odonata in Britain and Ireland, and use species traits to test hypotheses for the
67 interspecific variation in trends.

68 We chose to examine Odonata for a number of reasons. Firstly, previous trait-based
69 comparative analyses have tended to focus on birds, mammals, plants and
70 butterflies. Despite being highly species rich and their crucial role across
71 ecosystems, the non-butterfly invertebrate fauna are comparatively poorly studied

72 (IUCN, 2001; Dirzo *et al.*, 2014). Secondly, Odonata are thought to be excellent
73 bioindicators as they are sensitive to degradation of water ecosystems (Samways &
74 Steytler, 1996; Sahlén & Ekestubbe, 2001; Lee Foote & Rice Hornung, 2005).
75 Thirdly, they provide a valuable ecosystem service as they feed on many insect
76 pests (Brooks & Lewington, 2007). Finally, the publication of a new atlas (Cham *et*
77 *al.*, 2014) and trait datasets (Powney *et al.*, 2014) for British Odonata together
78 constitute some of the best quality data of any non-butterfly invertebrate group.

79 Previous research based on Odonata occurrence data has focussed on the impact of
80 climate change on phenology and distribution. For example Hassall *et al.*, (2007)
81 discovered that emergence from overwintering had significantly advanced over the
82 past 50 years, while Hickling *et al.*, (2005) showed that the upper latitudinal margin
83 shifted north between 1960 and 1995. Outside Britain, Bush *et al.*, (2014) used
84 species distribution models (SDMs) to predict which Australian odonates were under
85 threat from climate change.

86 Several studies have utilised traits to explain variation in several aspects of Odonata
87 ecology, but typically focus on explaining variation in species response to climate
88 change. In terms of phenological advancement, Hassall *et al.*, (2007) noted that
89 spring species and those without egg diapause exhibited increased phenological
90 shifts. Angert *et al.* (2011) examined trait correlates of range shift across multiple
91 taxonomic groups, finding that exophytic Odonata species in Britain shifted further
92 north, on average, than endophytic species. These insights, combined with
93 extensive knowledge about their natural history (Brooks & Lewington, 2007), form

94 the basis of seven competing hypotheses (outlined below) that aim at explain the
95 interspecific variation in the distribution trends among British Odonata.

96 All traits included in the analysis have been shown to affect species' ability to
97 respond to environmental change. Habitat breadth is frequently related to species
98 trends, where habitat generalists outperform specialists due to their greater ability
99 to adapt to novel environmental conditions (Fisher & Owens, 2004; Menéndez *et al.*,
100 2006; Botts *et al.*, 2012). Ball-Damerow *et al.*, (2014) found evidence of the
101 widespread expansion of habitat generalists which has led to biotic homogenization
102 in the dragonfly fauna of California and Nevada over the last century. We test the
103 hypothesis that Odonata in Britain and Ireland follow the patterns outlined above,
104 with generalists out-performing specialists. Dispersal ability affects species' ability
105 to respond to environmental pressures, with higher dispersal ability linked to an
106 enhanced ability to respond (Thomas *et al.*, 2001; Pöyry *et al.*, 2011; Grewe *et al.*,
107 2012). Using SDMs, Hof *et al.*, (2012) found lentic (i.e. pond and lake dwelling)
108 species had a greater ability to track changes in their climatic niche. This was linked
109 to greater dispersal ability, which is essential given the ephemeral nature of their
110 breeding sites (Hof *et al.*, 2006). We predict lentic species will have higher (more
111 positive) trend estimates than lotic species as their increased dispersal ability
112 enables them to persist during times of environmental change through the efficient
113 relocation to newly suitable areas. Geographic range size and body size are both
114 frequently used as surrogates for a whole host of traits associated with ecological
115 specialism and competitive ability (Gittleman, 1985; Gaston, 2003; Angert *et al.*,
116 2011). We predict that widespread species and the larger, therefore more
117 competitive species, are likely to show positive trends. Climate warming has
118 increased the suitability of the landscape to those species that were previously

119 limited by their lower thermal tolerance threshold (Devictor *et al.*, 2008;
120 Dingemanse & Kalkman, 2008; Bellard *et al.*, 2012), therefore we predict that
121 southerly distributed species will show the highest trend estimates. An additional
122 aspect of climate change that has been linked with trends in Odonata is the increase
123 in flood events in Britain. Species which overwinter as larvae are particularly
124 vulnerable to flooding as they can be swept away from ideal habitat areas to
125 unsuitable regions in which they cannot persist (Cham *et al.*, 2014). Alternatively,
126 floods may aid the dispersal of such species that overwinter as larvae and therefore
127 we may expect to see positive trends for such species. Finally we test the
128 hypothesis that flight period will be positively related with species' trend. Grewe *et*
129 *al.*, (2012) argued that species with longer flight periods have increased dispersal
130 ability, and therefore have a greater capacity to adapt in response to environmental
131 change.

132 **Materials & Methods**

133 *Occurrence trends*

134 Trends were estimated from Odonata distribution records in Britain and Ireland
135 collected by the Dragonfly Recording Network and coordinated by the British
136 Dragonfly Society. Our analyses are based on 895,022 records of 38 native species
137 collected between 1980 and 2012 where the recording date is known and the
138 location was recorded to 1 km² precision or better. As these occurrence records
139 were collected without a specific sampling design they contain a variety of bias
140 which inhibit their use in estimating reliable trends. For example, the number of
141 records collected each year has increased dramatically over time (Cham *et al.*,

142 2014), such that simply counting the number of occupied sites would produce
143 biased trend estimates (Prendergast *et al.*, 1993; Isaac *et al.*, 2014b). To account for
144 these biases we estimated species trends using a method known elsewhere as the
145 ‘well-sampled sites’ (Isaac *et al.*, 2014a), which aims to remove the noise and bases
146 the statistical inference on a ‘well-sampled’ subset of the data. We first arranged
147 the records into 239,392 visits, which are defined as unique combinations of date
148 and 1 km² grid cell (site). For each visit, each of the 38 species was coded as either
149 recorded (1) or not-recorded (0). We then removed all visits where less than three
150 species were recorded, since these short lists probably represent incomplete
151 sampling (van Strien *et al.*, 2010). We then selected sites with at least three years
152 of data, ensuring we retained only the ‘well-sampled’ sites (Figure 1). Our final
153 dataset contains 357,654 records from 67,382 visits to 5,352 sites (30,481 site-year
154 combinations). Different thresholds for defining the well-sampled set (two species
155 recorded and two years of data) produced qualitatively identical results (not shown).
156 For each species, we estimated a linear trend in the probability of being recorded on
157 an average site visit. This was achieved using binomial generalised linear mixed-
158 effects models (GLMMs), implemented by the R package *lme4* (Bates *et al.*, 2011),
159 with the log odds of being recorded modelled as a linear function of a fixed effect for
160 year, and a random intercept for site. We used the slope estimate for the fixed
161 effect of year as our trend measure.

162 *Traits*

163 We included data on seven traits extracted from Powney *et al.* (2014) (Table 1). Two
164 traits were based on characteristics of a species’ distribution pattern, the first,
165 species status, was measured as an ordinal variable based on distribution size,

166 moving from very rare through to very widespread. Secondly, distribution type was
167 a categorical variable that defined a species broad climatic restriction. Species were
168 classified into one of four levels, northern, southern, **oceanic** or widespread based on
169 their distribution pattern. We included a single morphological trait, thorax length
170 (mm), which was taken as the mean of multiple measurements from museum
171 specimens. Flight period duration was measured as the number of months during
172 which adults are typically recorded in flight. We included two habitat based traits,
173 habitat breadth measured the number of broad habitats a species can utilise, while
174 breeding habitat classified species based on breeding habitat preference, lentic, lotic
175 or both. Finally, we classified species based on their overwintering stage, either
176 eggs, larvae or both. Overwintering stage, breeding habitat and distribution type
177 were coded as continuous variables: Overwintering stage (eggs = -1, both = 0,
178 larvae = 1), breeding habitat (lentic = -1, both = 0, lotic = 1), distribution type (very
179 rare = -1.5, rare = -1, scarce = -0.5, local = 0.5, widespread = 1, very widespread =
180 1.5). All continuous traits were centred on zero prior to the analysis and ordinal
181 variables were treated as continuous. **Following the various exclusion criteria and**
182 **the coverage of trait data, the final dataset used in this study covered 36 species.**

183 *Trait analysis*

184 We used the *pgls* function from the R package *caper* (Orme, 2012) to run
185 phylogenetically informed linear models to examine trait-trend relationships while
186 accounting for phylogenetic non-independence (Freckleton *et al.*, 2002). In all
187 phylogenetically informed models, the level of phylogenetic correction (Pagel's λ)
188 was estimated via maximum likelihood (Pagel, 1999; Freckleton *et al.*, 2002). Due to
189 data limitations we used a phylogeny based on taxonomy for the analyses. The

190 phylogeny was built using the *as.phylo* function from the R package *ape* (Paradis *et*
191 *al.*, 2005) with nodes based on Suborder, Family, Genus and Species, and all branch
192 lengths were set to one.

193 The trend measures extracted from each species model formed the response
194 variable for the trait-trend analysis. While this year slope estimate is a useful
195 measure of the direction and intensity of the temporal trend in occupancy in an
196 average site, it does not account for uncertainty in its estimation. We therefore
197 repeated all trait analyses using the year slope estimate weighted by the inverse of
198 its standard error and also the z-score of the fixed effect of year as the response
199 variables. These additional analyses enabled us to examine how robust our results
200 were in relation to uncertainty in our trend estimates.

201 To determine the main trait correlates of our species trends we utilised a multi-
202 model inference approach. We applied the *dredge* function of the R package *MuMIn*
203 (Barton, 2013) to fit models for all possible combinations of explanatory trait
204 variables and then ranked them based on AICc. We then extracted the model
205 averaged coefficient for each trait that was present in at least one candidate model
206 from the subset of top models. In addition, we identified the importance of each
207 trait based on its frequency in the subset of top models. The importance scores and
208 the model averaged coefficients were used to determine the main traits for
209 explaining species trends. The set of candidate models was defined as models with
210 $\Delta AIC \leq 2$. Burnham *et al.* (2010) suggest there is often support for models where
211 ΔAIC is < 7 , however, we chose to use $\Delta AIC < 2$ as the null model was the 3rd best

212 model with a ΔAIC of 1.12 and therefore increasing the ΔAIC threshold was simply
213 adding noise (models with little evidence to support them) to the key result.

214 A multi-model inference approach while accounting for phylogeny is not straight-
215 forward. In our PGLS models, λ was estimated independently for each model and
216 can therefore be different between the candidate models. Using AIC to compare
217 between these models could be misleading as we could not disentangle the
218 influence of a difference in the evolutionary model (λ) from the influence caused by
219 changing which traits were included in the model on AIC scores. However, all of the
220 models in the top subset had an estimated λ value of 0, implying that species trend
221 in the UK is not phylogenetically-patterned. Therefore ΔAIC was measuring the
222 effect of the trait differences rather than any potential difference in the evolutionary
223 model in this case. All analyses were carried out using R 3.0.2 (R Core Team, 2013).

224 **Results**

225 We found significant trends for 72% of the species in this study: of these, 12 were
226 decreasing and 14 species were increasing. Species included that showed the
227 greatest declines included: *Ischnura pumilio*, *Leucorrhinia dubia* and *Sympetrum*
228 *danae*, while *Libellula fulva*, *Erythromma najas* and *Brachytron pratense* showed the
229 greatest increases. Using the fitted values from the species trend models we
230 estimated the change in probability of observation over a ten year period for each
231 species. Each species was then categorised using these ten year changes (Figure
232 2). This figure illustrates the substantial variation in the trend estimates between
233 species, and again highlights the large proportion declining species which is a cause
234 for concern.

235 Six models containing various combinations of three traits (distribution type, flight
236 period and thorax length) formed the top subset of models for explaining Odonata
237 distribution trends (Table 2). Of these three traits, distribution type was the most
238 important (importance score = 0.6), and was present in three of the top models.
239 The model averaged coefficients for distribution type reveal that southern species
240 tend to have increased relative to the other categories and northern species have
241 declined on average, with the other two categories (oceanic and widespread)
242 intermediate (Figure 3). Notable exceptions to this trend include the strong declines
243 in *Ischnura pumilio* and *Gomphus vulgatissimus* both of which were classified as
244 southern species. Flight period was present in two of the top models and had an
245 importance score of 0.34. The coefficient was negative, suggesting that species
246 with longer flight periods had a lower trend estimates (i.e. they declined relative to
247 species with short flight periods). Thorax length was also present in two of the top
248 models but had the lowest importance score (0.24) of all traits present in the top
249 model subset. The model averaged slope for the relationship between thorax length
250 and trend estimate was marginally positive, which suggests that larger species were
251 faring better than smaller species. We note that the 95% confidence intervals of
252 both flight period and thorax length spanned zero, and that the null model was the
253 third best model based on AICc. The top two models explained a modest 13 and
254 16% of the variation in species trend.

255 In general, the key trait-trend relationships and importance scores were robust
256 across the different response variables and modelling approaches (Appendix 1 & 2).
257 Distribution type was the most important trait for four of the five response/modelling

258 approach combinations, while flight period and thorax length were consistently
259 important (Appendix 3). The model averaged coefficients for these three traits were
260 similar across approaches. Other traits including habitat breadth, overwintering
261 stage, breeding habitat and status, were retained in the top model subset for some
262 of the other approaches. However, the model averaged 95% confidence intervals
263 spanned zero in the vast majority of cases for these additional traits (Appendix 2).

264 Discussion

265 We found that the dragonfly fauna in Britain and Ireland has undergone considerable
266 change during recent decades, with high levels of inter-specific variation in
267 occurrence trends (Figure 2). We found twelve species (33%) had significant
268 negative trends, while 14 species (39%) showed significant increases. Although
269 more species increasing than decreasing is good news for conservation, this could
270 be interpreted as a signal of biotic homogenization, i.e. the fauna becomes
271 dominated by a small number of species, and local and regional difference between
272 communities are eroded (Keith *et al.*, 2009).

273 We found distribution type was the key correlate of Odonata trends, with southern
274 species tending to have higher trend estimates than the all other distribution types
275 (Figure 3). This result is in line with our hypothesis that increased temperatures has
276 increased the climate suitability of Britain and Ireland for southerly distributed
277 species. A variety of studies have provided evidence of this relationship, i.e.
278 Devictor *et al.* (2008) found bird communities in France between 1989 and 2006
279 were increasingly dominated by species that prefer warmer conditions, while Lima
280 *et al.* (2007) found evidence of northward range expansions in warm-water adapted

281 Portuguese algae. Hickling *et al.* (2005) used distribution type to explain variation in
282 range shift and expansion in British Odonata, finding that southern species showed
283 greater poleward shifts and expansions compared to northern species. By contrast,
284 Angert *et al.* (2011) found no correlation between range shift and position of the
285 northern range limit (which is related to our measure of distribution type). Despite
286 the wealth of evidence that points to climate change as the likely driver of increases
287 in southern species, we cannot ignore the role of improved water quality and
288 standing water availability in southern Britain (Hickling *et al.*, 2005; Cham *et al.*,
289 2014). Not all southern species showed positive trend (notably *Ischnura pumilio* and
290 *Gomphus vulgatissimus*), this limited expansion in response to climate warming is
291 likely due to availability of suitable habitat.

292 The lower trend estimates for northern species is likely to be the result of the
293 combined pressures of a decline in climate suitability and competition from species
294 that were previously limited by lower thermal tolerance (Myers *et al.*, 2009; Thomas,
295 2010). Evidence of the loss of northern species has been seen in a variety of
296 taxonomic groups across a variety of geographic regions (Hill *et al.*, 2002; Devictor
297 *et al.*, 2008; Myers *et al.*, 2009; Foufopoulos *et al.*, 2011), and with the persistent
298 and increasing threat of anthropogenically induced climate change, northern species
299 and those reliant upon them are likely to become increasingly threatened.

300 We found no evidence for six other hypotheses about the drivers of species trends.
301 Flight period and thorax length appeared marginally important but evidence for this
302 was weak as the 95% CI of these traits spanned zero. Additionally when these two
303 traits were modelled against species trend individually they performed no better

304 than the null model. Body size and flight period were used as surrogates for
305 competitive ability and dispersal ability: it is plausible that more direct measures of
306 these traits do predict the species in decline. The reliability of the trait-trend results
307 depend on the accuracy of the underlying trait data. We note that within a given
308 species, traits can vary spatially (i.e. habitat specificity can vary across a species
309 range - Oliver *et al.*, 2009), however here we use a single value per trait per
310 species. This is a common approach within the comparative analysis literature but
311 is a potential source of noise in the results. One problem with “well-sampled sites”
312 approach is that it amplifies the spatial gradient in recording intensity, such that
313 trends for northern species are estimated from a relatively small number of sites.
314 This has implications for the precision of trend estimates for northern vs southern
315 species, which is accounted-for in the weighted trait models (Appendix 1b). Basing
316 the trend on a small number of sites is unlikely, on its own, to bias the estimate
317 (Isaac *et al.*, 2014b), although we don’t know the degree to which trends on these
318 sites (and others considered well-sampled) reflect changes in the wider countryside.
319 We found no evidence of phylogenetic signal in our models, although our phylogeny
320 was based on taxonomy. Using a phylogeny constructed from sequence data would
321 be more rigorous, but such genetic data are currently limited.

322 In conclusion, we found variation in species distribution trends was best explained
323 by distribution type, with southern species showing significantly higher trends than
324 widespread and northern species. We believe this reflects the impact of climate
325 change as the increased ambient temperature in Britain and Ireland better suits
326 species that are adapted to warmer conditions. The lower trend estimates for
327 northern species is a cause of conservation concern as this result combined with
328 evidence in previous studies shows that northern species are shifting to higher

329 latitudes and altitudes, are declining in range size and abundance, and are therefore
330 particularly vulnerable to the ever increasing threat of climate change.

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Table 1 (on next page)

Table 1. An overview of the Odonata traits included in the comparative analysis.

Trait	Description
Species status	Species categorised on distribution size: very widespread, widespread, local, scarce, rare, very rare.
Distribution type	Broad climatic categorisation of species: widespread, southern, northern or oceanic.
Thorax length	Mean thorax length based on 10 museum specimens (mm).
Flight period	The duration of the flight period in months.
Habitat breadth	A count of the number of habitat types utilised by the species.
Breeding habitat	Species were classified on their preferred breeding habitat, either lentic, lotic or both.
Overwint. stage	Species categorised as overwintering as larvae, eggs, or both.

Table 2 (on next page)

Table 2 Parameter estimates for the subset of best models.

For the categorical variable (distribution type) ● denotes that it was present in the selected model, while the slope is displayed for the continuous traits present in the selected model. The final column expresses the importance value for each trait included in the subset of best models.

	Model rank						Importance
	1	2	3	4	5	6	
Distribution	●	●			●		0.60
Flight period		-0.022		-0.023			0.34
Thorax length					0.002	0.002	0.24
AICc	-154.3	-153.7	-153.2	-153.1	153.0	152.5	
Δ AIC	0	0.58	1.12	1.17	1.29	1.85	
weight	0.263	0.197	0.150	0.147	0.138	0.104	
Adjusted R^2	0.131	0.155	-	0.032	0.138	0.013	

Figure 1 (on next page)

Figure 1 The distribution and density of monads from which the trend estimates were derived.

The shading represents the number of unique monads within the hectad that were included in the analysis, the “well-sampled sites”.

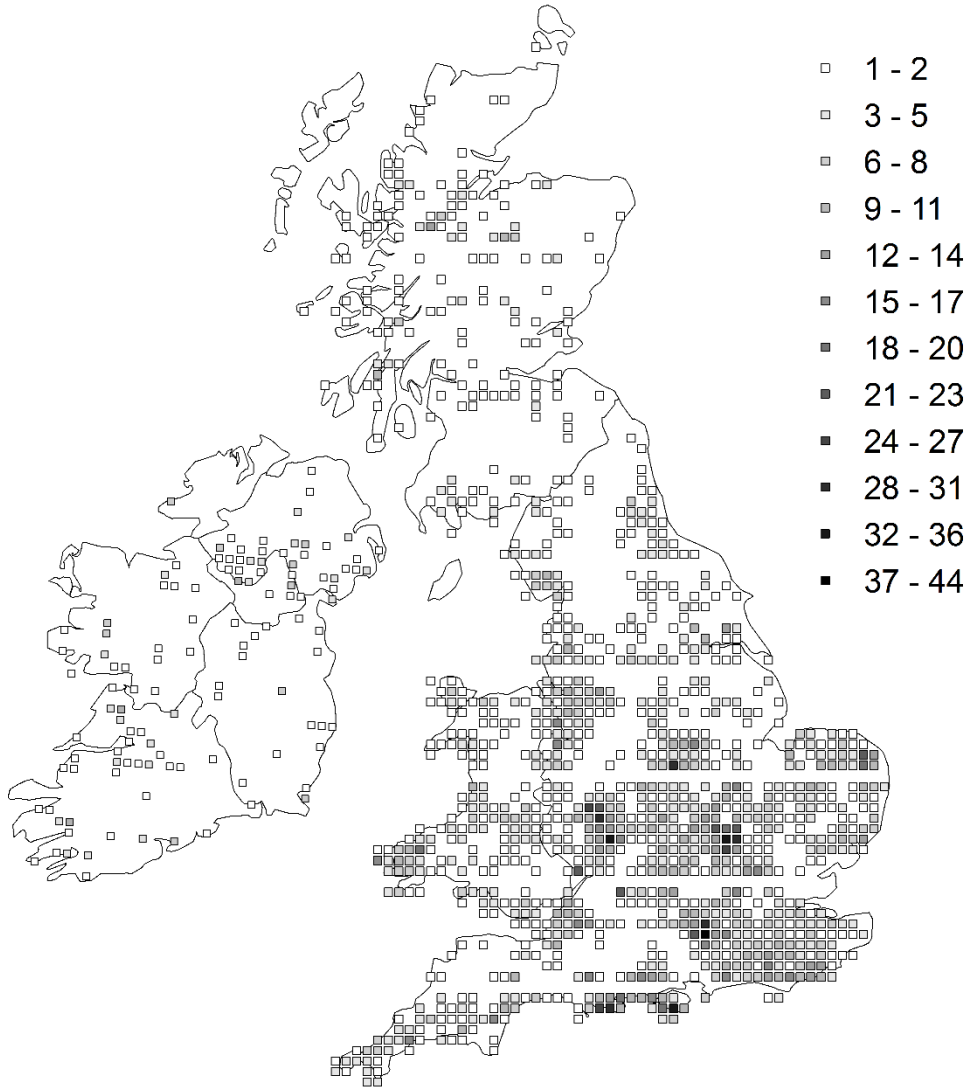


Figure 2 (on next page)

Figure 2 The proportion of species in each trend category.

Using the fitted values from the species models, trends were estimated as the percentage change in probability of observation over a ten year period. Shades of red symbolises declines while shades of green are used for increases, the intensity of colour reflects the strength of the trend.

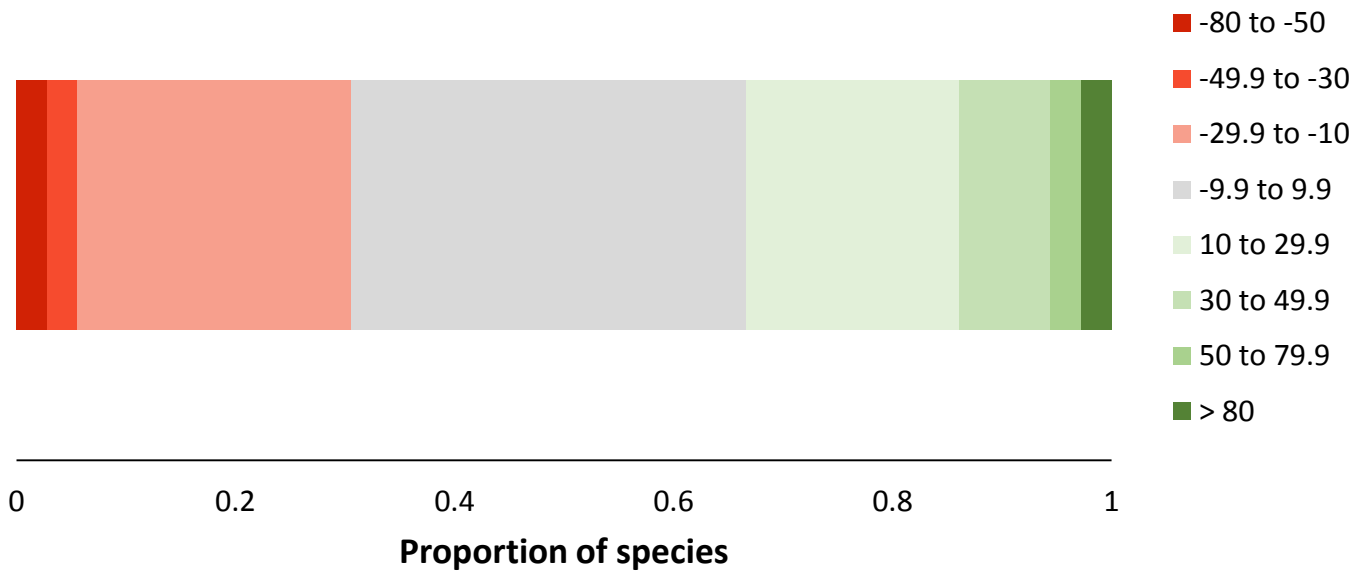
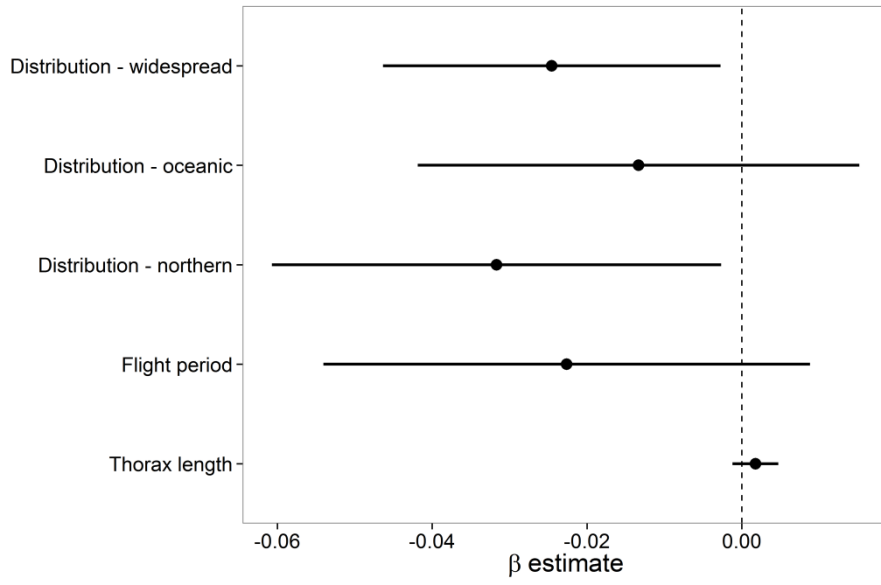


Figure 3 (on next page)

Figure 3 The model averaged coefficients for traits that were retained in the subset of best models.

The reference distribution type was “southern”, which has a parameter estimate set to 0.



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