

## **Appendix 1. Relationships between population density and past climate**

### **Methods**

#### *Bird data.*

SPAs in the UK are currently designated for a total of 122 species or sub-species, some of which may have separate designations for breeding, wintering and passage populations. These include a combination of Annex I species with sites designated on the basis of the proportion of the national population represented within a particular geographical area, and migratory species, with sites designated on the basis of a biogeographical threshold. For each species, additional sites may also be designated if they contain > 20,000 individuals of a range of species, of which a particular Annex I or migratory species is a component. Current data on the abundance of species were obtained from various sources and covered a wide-range of seabirds, waterbirds and terrestrial species with designated breeding, wintering and/or passage populations that were investigated separately. Given the aim of the study to make projections of the likely future impacts of climate change, we used not only data from the UK, but additionally included data from Ireland, the Netherlands and France where possible, in order to capture a wider-range of current climatic variation and therefore ensure that future projections for the UK were not made outside of the current range of observed climatic data.

Data were obtained for seabirds from Seabird 2000 and the Seabird Colony Register (Mitchell *et al.* 2004), for wintering freshwater, coastal and marine species from WeBS counts (Calbrade *et al.* 2010), for rare breeding species from SCARABBS, and 14 breeding wader species from both BTO WeBS and BBS schemes. For wintering species, we also included relevant passage species also covered by SPA designation– these passage periods covered either spring or autumn and three species were assessed in both phases of passage. In addition, we also used existing bioclimatic models to identify an additional 18 species listed on Annex I of the Birds Directive that are projected to occur in the UK by 2080 under a medium-emissions scenario (Huntley *et al.* 2007, Barbet-Massin *et al.* 2010). The total number of species\*season combinations investigated was 125, with some duplication of the same species between breeding and non-breeding periods. However, of this total, sufficient data were only available to produce 118 models; 47 for wintering waterbirds, 17 for breeding seabirds, 10 for rare breeding species, 13 for breeding waders, 13 for passage waders (three species included for both autumn and spring passage), 12 for wintering colonisers, and 6 for breeding season colonisers. For the remainder, either there was insufficient monitoring data, or the range of the species covered was too low for adequate climatic variation to be described. Note also that species were able to be modelled more than once if falling in different respective groupings (e.g. all breeding wader species were covered also as wintering wader species).

Different datasets were therefore required to model the abundance of these different species and seasons. These collated data were at one of a range of different spatial scales from 1km<sup>2</sup> for BBS to total counts for wetlands sites up to two orders of magnitude larger. The unit of analysis for each species is therefore the site, which may vary from a 1km<sup>2</sup> BBS square to an estuary 1000km<sup>2</sup> or more in extent. To standardise the results

from these, the natural log of the survey area was incorporated into the models as an offset. Seabird data were from sites of unknown area whilst the data for France was only available at the scale of French departments (Cadiou *et al.* 2004). Therefore in order to standardise analyses across the UK and France, data for the UK were aggregated into the abundance of species into 25km x 25km squares, matching the spatial resolution of the climate data. For cliff-nesting seabirds we included the natural log of the estimated length of cliff within each square / department as an offset. Cliff length within each spatial unit was defined from a 10m resolution DEM as land with a slope of  $>18^\circ$  within 50m of the high water mark, excluding areas with a height  $< 10\text{m}$ .

Given the varied range of data sources from a number of different countries, no standard habitat data could be applied across all species and groups. Indeed, for the many waterbirds and seabirds covered, no useful large-scale data were readily available that might describe relevant non-climatic habitat variation (e.g. water quality, water depth) for such a wide-range of species. Therefore in order to maintain a standard approach, species abundance was modelled purely as a function of climate variables, described below. In order to maximise the appropriateness of the bird data for such models and minimise the potentially confounding role of unmeasured habitat differences between sites influencing the climate-abundance relationships, only sites from which a particular species had been recorded were used in the analysis of that species. This means that models are based upon the role of climate in affecting species abundance within the existing species' range. As a result, models may tend to be conservative in nature with the potential for significant climatic effects to remain undetected.

#### *Climate data*

Previous studies have highlighted the importance of winter cold, summer warmth and moisture availability as important predictors of bird occurrence (e.g. Huntley *et al.* 2007, Hole *et al.* 2009). We therefore incorporated measures of both winter and summer climate, as well as for breeding birds, measures of climate relevant to the breeding season of that species. Given our need to use variables for that were both available as past climatic data and projected by UKCP09 data (for projections into the future) across the countries from which bird data were obtained, we were restricted to measures of temperature and rainfall only. We therefore selected mean minimum temperature of the coldest month as a measure of winter cold, mean maximum temperature of the warmest month as a measure of summer warmth and mean maximum temperature of the bird breeding season, which was defined separately for each species (Joys & Crick 2004), in addition to total winter (Dec-Feb), summer (Jun-Aug) and maximum breeding season precipitation. In order to better describe moisture availability from these variables we also examined the interaction between temperature and precipitation in each season. To reduce collinearity in predictor variables between bird breeding season and summer temperature and precipitation, we only included additional breeding season variables for birds which breed in the UK, and if they were strongly ( $r>0.7$ ) correlated with summer variables, the summer variables were removed. Given the potential for indirect effects of climate to affect birds (e.g. Mustin *et al.* 2007), such as mediated through prey availability (e.g. Pearce-Higgins *et al.* 2010), we included measures of summer and winter climate in models for all species, even if they were not present during that season.

Historical climate data for the UK were derived from a 25km gridded dataset (Perry & Hollis 2005). Climate data for the remaining areas in Europe were derived from a 0.25 degree gridded dataset (Haylock *et al.* 2008). In order to ensure that the two datasets were equivalent, we examined the strength of the spatial and temporal correlation between the UK and European climate data for the UK, where the two overlap. For each of the predictor variables, the correlations were very strong ( $r > 0.91$ ;  $r^2 > 0.84$ , in all cases). To ensure the two gave equivalent predictions, we used the slope of the relationship between UK and European climate data to calibrate the European values to match those from Perry & Hollis (2005). To account for potential differences in the climate between each site and the mean for each 25km square as a result of topography, we also incorporated the mean difference in altitude between the sites and the squares within which each site was located, as an additional covariate.

### *Analyses*

Species abundance was modelled as a function of climate and site size. In order to maximise the appropriateness of the bird data for such models and minimise the potentially confounding role of unmeasured habitat differences between sites influencing the climate-abundance relationships, only sites where a particular species had been recorded were used in the analysis of that species. Therefore models were based upon the role of climate in affecting species abundance within the existing species' range, which may mean that the models tend to be conservative in nature and may underestimate the significance of any climatic effects.

The unit of analyses varied according to the data source (main report; Table 3.1). For species whose abundance was assessed from periodic surveys (seabirds and SCARABBS species), count in each survey was modelled as a function of climate data over the preceding five years, in order to reduce the effects of weather variation in a single year. For species whose abundance was assessed annually (waterbirds and species covered by BBS surveys), mean abundance over a five-year window was modelled in relation to mean climate variables over the same five-year period. Models therefore predicted mean abundance within five-year time-slices, thus matching the period of surveys used for some SPA designations. Results were robust to the length and position of the temporal 'window' used for the analyses, for a sample of species tested. Hereafter, site refers to discrete geographical areas treated as independent samples in the analysis, and may refer to areas covered by WeBs surveys, grid-squares surveyed by sample surveys, or larger-scale aggregations across climatic grid-squares or French departments.

Two modelling approaches were used for each species in order to examine the extent to reduce the likely influence of modelling approach on our results. Firstly, Generalised Linear Models (GLM) were used to model abundance  $N$  for each site ( $s$ ) and five-year period ( $y$ ) as a function of temperature ( $T$ ) and precipitation ( $P$ ) during winter ( $W$ ), summer ( $S$ ) and breeding ( $B$ ) seasons. Difference in altitude ( $A$ ) was included as an additional covariate, and total site area (or cliff-length for 7 species of cliff-nesting seabirds), was included as an offset ( $Area$ ). The difference in mean altitude between the larger grid and the sites could change over time, as some sites were not recorded in all

time frames. GLMs enabled relatively simple linear relationships between abundance and climate variables to be fitted. The form of the models was as follows (where \* refers to the individual effects and the interactions between the variables and f{ } refers to a function describing the inverse link function):

$$N_{sy} = \text{Area} \times f\{(TW_{sy} * PW_{sy}) + (TS_{sy} * PS_{sy}) + (TB_{sy} * PB_{sy}) + A_{sy}\} \quad [\text{eq 1}]$$

Secondly, given the potential non-linear relationship between climate variables and abundance, we also used Generalised Additive Models (GAM) to model abundance as a function of the same variables. These models enable more complex relationships between climate and abundance to be fitted, allowing for non-parametric effects. Individual smooths were initially given four degrees of freedom, and two-dimensional smooths (i.e. interactions) eight degrees of freedom.

The bird data were extremely variable in nature, ranging from counts of dispersed wider-countryside species within 1km squares to counts of highly aggregated seabird populations from specific colonies. Given these differences, and inherent species-specific aggregation tendencies, we could not *a priori* determine an error structure appropriate to all species. Therefore for each species we tested the fit of five potential error structures; poisson, over-dispersed poisson, negative-binomial, zero-inflated poisson and zero-inflated negative-binomial. In addition for seabirds, given the extremely aggregated nature of the data and the fact we were modelling count without area information (see above) we also examined the fit of a set of distributions known as the tweedie distribution (Tweedie 1984; Dunn & Smyth 2008). For each species and for each model type (GLM or GAM) the most appropriate error distribution was determined by examination of residuals and model fit diagnostics. Backwards stepwise selection was then conducted on the model with the best fitting error distribution, with diagnostic criteria relevant for the error distribution. These diagnostic criteria included t-tests, F-tests, AIC and Generalized Cross Validation (GCV) scores.

#### *Model fit*

It is important to assess the predictive ability of each of the models. For model validation the sites in the model were randomly divided into 10 equal subsets. For each subset in turn, the final model was run using the other nine subsets, and predictions made for the removed subset. The strength of the correlation (R) between the observed and predicted densities for these removed data was used to assess the predictive ability of the models. Model validation scores (R) were used to compare the absolute and relative predictive ability of the GLM and GAM models. As seabirds did not have site area as an offset (as there are limited data on site area available), model validation for these species was based on the strength of correlation between the observed and predicted counts at sites.

Only models for which  $R > 0.1$  were used for predictions. Where the R scores for the GLM and GAM were similar ( $\Delta R < 0.125$ ), an average of predictions from the two final models were used, and where they differed, the model with the better predictive ability was used to produce final predictions. All analyses and most of the data manipulation

was conducted using the statistical software R (R Development Core Team), with some additional data manipulation in SAS 9.2.

We use the assessment of model fit to summarise the level of confidence associated with each model (Table 1). For each model we also calculated the "probability of being correct" using IPCC guidelines (IPCC 2005). These were developed for risk-based assessments and when applied to our results, generally give a high degree of confidence (Table 2). However, our models give predicted outcomes in terms of the estimated magnitude of change, rather than likelihood of change, and therefore attempt to give more precise predictions each of which accordingly has a lower degree of confidence, based upon the assessment of model fit described above (Table 3).

#### *Climatic relationships*

In order to assess the relative importance of different climate variables in driving spatial variation in the abundance of different species, we used the GLM beta model coefficients, as the structure of the GLM models was easier to interpret than the output from the GAMs. Note, however, that the final model used for predicting future changes in population (see below) were not necessarily based solely on GLMs – for some species, GAMs were used due to superior model fit, or alternatively predictions from both GAMs and GLMs were combined. Additionally, we therefore assessed the relationship between GAM and GLM model validations (see above), and the terms included in GLM and GAMs to check for consistency between the two approaches. These comparisons were made between the different species groups, many of which were based upon different data sources or combinations of data sources, as follows: breeding species (B); breeding colonisers (BC); breeding rare species (BR); passage (P); seabirds (S); wintering waterbirds (W); wintering colonisers (WC).

#### *Future projections*

Models predicted densities of birds as a function of climate at each site and were used to predict future densities of birds at each site using future climate projections from UKCP09. These give probabilistic changes in temperature and precipitation variables for a range of time-slices and scenarios of climate change (UKCP09 2010). We used projections for low, medium and high emissions scenarios for 2020, 2050 and 2080 and present predictions for the 50th percentile (we also calculate predictions for 33% and 66% percentiles and make these available on the CHAINSPAN website) of the probability distribution (i.e. the median predictions of climate) using two complementary approaches. Given the fact that UKCP09 data does not cover a number of remote seabird colonies, we were unable to make projections for 22 seabird SPA's.

Firstly (absolute method), models were used to simply estimate densities within each SPA, which were then multiplied by site area (apart from for some seabirds where area was not incorporated into the models) in order to calculate the likely population size at that site ( $P_1$ ). These projected densities are therefore equivalent to likely mean densities for a given climate, irrespective of site quality. Predicted densities which were greater than the current maximum observed density for a species, were reduced to the current maximum observed density.

Secondly (proportional method), in order to account for potential variation in site quality between sites, the proportional change in climate suitability at each site was indexed from the ratio of the projected future abundance ( $P_{1f}$ ) of birds from the modelled current abundance ( $P_{1c}$ ). This estimate of proportional change was then applied to existing observed densities ( $O_c$ ) to calculate a revised predicted abundance  $P_2$  [eq 3.1].

$$P_2 = O_c * (P_{1f} / P_{1c}) \quad [\text{eq 3.1}]$$

The two projected outputs provide different information. The first estimates mean projected densities for a given site, all other things being equal, and therefore indicates the likely range of birds projected to be supported at that site if it is of average quality relative to the sites incorporated in the analyses for that species. Using this approach it is possible to project future densities of potential colonising species to sites on the basis of climatic suitability. There are assumptions associated with doing this, that potential colonisers are able to reach those sites, and will not be limited by other processes, such as dispersal rate, habitat availability or competition. The proportional approach estimates likely projected densities given the current quality of a site relative to other sites, and therefore is more likely to produce realistic estimates of projected abundance for any given site, by taking account of existing habitat variation. However, given the lack of information about site quality for currently unoccupied sites, this approach cannot predict future colonisations and therefore is limited by not allowing range expansion and the colonisation of sites where this species has not been recorded. For wintering and passage waterbirds this is not much of a restriction, as many individuals have been recorded widely. However for breeding species, this restriction is limiting as apart from seabirds, there do not exist extensive datasets of species distributions from which to derive  $O_c$ . Therefore for breeding species (excluding seabirds) the second method can only be applied to existing SPAs, based upon the most recent count data contained within the SPA database (JNCC 2011), and furthermore, it is not possible using this proportional method for such breeding species to gain qualifying threshold status on SPAs. This twin approach of producing projections assuming either no restrictions to colonisation or completely restricted colonisation is common in bioclimatic modelling of species ranges (e.g. Huntley *et al.* 2007) and therefore encapsulates the range of possible futures. As a further control, predictions for a particular species were not made if an SPA did not contain suitable habitat for that species (e.g. marine species were not projected to inland waterbodies), based upon SPA specific habitat information provided by JNCC.

For each site and scenario combination, we assess the coverage of species by the existing SPA network, in relation to the population thresholds used for classification. In order to relate these changes to the present situation, we base them on the existing 1% national or biogeographical thresholds applied to Annex I and migratory species respectively, taking the population estimates in Stroud (2001), and updated for waterbirds from Calbrade *et al.* (2010), in order to provide a fixed measure against which we can assess the rate, direction and magnitude of projected future change. These thresholds are also likely to change as a result of the SPA review process which is currently being undertaken. Note that this approach means that estimates of current SPA coverage may differ from the

number of sites for which a particular species is designated / listed as a qualifying feature for a number of reasons

## **Results & Discussion**

### *Model Fit*

Model fit was generally similar between GAM and GLM models ( $R = 0.72$ ,  $n = 119$ ,  $P < 0.001$ ), but with considerable variation between species (Fig. 1). In relation to predictive ability, only six models achieved a good model fit (Table 3), whilst a further 79 were classed as moderate or low quality. The predictive ability for 33 models was very poor ( $R < 0.1$ ,  $R^2 < 0.01$ ), and therefore these were not used to make quantitative predictions of likely future species' abundance. However, in terms of the projected direction of change, 92 models were associated with a high or very high degree of confidence (Table 2). Models of rare breeding species from SCARABBS data, and of wintering waterbird species from WeBS, iWeBS and IWC data, achieved the greatest overall performance, whilst models of wintering and breeding colonisers had the weakest predictive ability. Overall, we were able to make quantitative predictions for 85 species x season combinations (Section 3). Poor model fit may arise for a number of reasons, for example: poor quality or biased data, no clear climate limitations, other factors which limit the population (for example, habitat change or hunting). In the results files, species which had very poor model fit were assumed to have the same numbers in the future as they do in the most recent data.

Overall, of the 125 species\*season designations initially considered, 7 could not be modelled, due to a lack of data, whilst the predictive ability of the models for a further 33 species was regarded as sufficiently low ( $R < 0.1$ ) that there was no confidence in the model projections, based upon model validation of predicted spatial variation in density. Accordingly, we did not attempt to model changes in the abundance of these species, but instead assumed that climate was such a weak driver of variation in abundance that populations would remain constant, irrespective of climate change. This left a remaining 85 species combinations for which quantitative projections of changes in abundance were produced using the models in combination with UKCP09 climate projections (Table 4).

As part of the model validation procedure, we also quantified the ability of models to predict changes in populations (comparing observed vs predicted model outputs). Most models had relatively low predictive ability in this way, offering less than 0.1% correlation between model predicted and observed data (Table 5). Rare breeding species were ranked as the species group with the greatest model fit, with the models for the two groups of colonising species and wintering waterbird generally having being models with no confidence associated in them.

### *Climate variables*

An investigation into the terms included in minimum adequate GAMs compared to GLMs revealed similar models; with between 42% and 62% coefficients common to both GAMs and GLMs, depending on species groups (Table 6). These differences typically occurred because GLMs tended to be simpler, as would be expected from a parametric-non parametric comparison. In particular, GLMs often lacked the interactions that GAMs

often included, despite the same linear terms being retained. For ease of interpretation, we then examine the terms in the GLM models (Table 7), and crudely assess potential contrasts within species groups using Chi-square.

Many more significant relationships were recorded than expected by chance (Table 7). On the basis of the number of tests (6 tests across 119 species), 36 (5%) would be expected to be statistically significant by chance. Instead, 384 were significant. Across all species, the most important variables were maximum temperature (combining breeding season or summer maximum) which occurred in 96 models, winter minimum temperature (in 80 models) and breeding season or summer rainfall (in 75 models). There were strong contrasts between species. Approximately 2/3 of relationships with breeding season / summer temperature were negative, whilst 3/4 of relationships with winter temperature were positive. Of the relationships with summer rainfall, 71% were negative.

Between the species groups, there were generally consistent positive effects of winter temperature upon both passage and wintering waterbirds, with therefore the greatest densities occurring in the warmer climates. These are species whose distribution is known to be sensitive to winter temperature (Austin & Rehfish 2005). The reverse pattern was apparent in relation to summer temperature though, whilst the abundance of wintering waterbirds tended to be negatively related to rainfall in about half of the species covered. In relation to breeding species 3/4 showed significant relationships with breeding season temperature, although generally the direction of these was mixed, with the possible exception of breeding seabirds. Further, there was a general tendency amongst breeding birds for abundance to be negatively correlated with rainfall (21 significant negative relationships as opposed to 2 significant positive relationships). We examine these tendencies in more detail below.

For breeding seabirds, data were pooled over squares, and some individual breeding colonies were not always counted equally between the two surveys, adding further noise to the data. Nonetheless, most seabird species modelled (9/14) showed negative relationship with increasing temperatures (Table 7). This was shown across a range of taxa that are known to be differently sensitive to changes in feeding conditions (e.g. from sea surface temperatures, Furness & Tasker 2000); such as the deep diving common guillemot ( $\beta = -0.652 \pm 0.007$ ,  $t = -9.197$ ,  $P < 0.001$ ) and surface feeding kittiwake ( $\beta = -0.355 \pm 0.054$ ,  $t = -6.596$ ,  $P < 0.001$ ). These effects are likely to be mediated through spatial variation in key prey abundance, such as sandeels, which is known to be negatively affected by increasing temperature (Frederikson *et al.* 2006). For three out of four gulls modelled (black-headed gull, lesser black-backed gull, and herring gull), a positive breeding season temperature coefficient was recorded, also shown for little tern ( $\beta = 0.232 \pm 0.042$ ,  $t = -5.481$ ,  $P < 0.001$ ), but not for common tern ( $\beta = -0.086 \pm 0.035$ ,  $t = -2.467$ ,  $P = 0.014$ ). Likewise, for seabirds, wetter summers suggested reduced overall population sizes (Table 7), for instance for puffin ( $\beta = -0.016 \pm 0.006$ ,  $t = -2.573$ ,  $P = 0.010$ ), as one would expect with water-logging of nest sites, whereas shag may suffer increased water-logging of feathers hampering foraging ability showed counterintuitive positive trends ( $\beta = 0.069 \pm 0.0334$ ,  $t = 2.004$ ,  $P = 0.046$ ). However, these results must all



be borne in mind with the caveats of the data, and in particular the quality of the models used.

For wintering waterbirds, in general, lower population sizes were seen with rising summer temperatures and wetter winters. However, models suggested if winter temperatures increased, there was a general trend of increasing wintering populations, as shown by generally positive effects of winter temperature on mortality (e.g. Yalden & Pearce-Higgins 1997, Insley *et al.* 1997). Of the 15 wader species included, 14 included a positive term for winter temperature (e.g. dunlin, negbin:  $\beta = 0.833 \pm 0.122$ ,  $t = 6.851$ ,  $P < 0.001$ ; curlew: negbin,  $\beta = 0.603 \pm 0.096$ ,  $t = 6.258$ ,  $P < 0.001$ , Table 5). All but one species (snipe) showed negative coefficients for summer maximum temperature (e.g. dunlin, negbin:  $\beta = -0.332 \pm 0.024$ ,  $t = -13.834$ ,  $P < 0.001$ ; curlew: negbin,  $\beta = -0.577 \pm 0.045$ ,  $t = -12.824$ ,  $P < 0.001$ ). Mixed relationships with maximum summer rainfall were seen for waders (10 species where coefficient retained, equal proportion of + and – trends), and winter mean rainfall. Six waders included a max summer temperature\*mean summer rainfall term with mixed coefficient directions, however all three waders that retained a significant winter mean rainfall\*winter minimum temperature interaction, were negative (Table 7). Similar patterns were also shown for the 29 species of waterfowl, geese, and grebes; of these species, 14/19 species that retained a significant term for winter minimum temperature showed positive coefficients, and for summer maximum temperatures 14/21 species showed negative relationships (Table 7). For mean summer rainfall, like waders, there was more of a mixed picture, however for winter mean rainfall, 12/15 species showed negative coefficients (Table 7). Fewer waterfowl, geese, and grebes had models that included interactions for winter temperature\*rainfall (5 species), and summer temperature\*rainfall (11 species), with no clear pattern across species in coefficient direction. Winter temperature was also a significant correlate for 11/13 passage models, with positive correlations for 9 of these, whilst 9 of the models also highlighted negative correlations with maximum summer temperature and summer rainfall (Table 7).

A high proportion of breeding season colonisers and rarer breeding species showed population increases with increasing maximum summer or mean breeding season temperatures. However surprisingly, not all showed such patterns. For instance Dartford warbler showed a decreasing trend (GLM:  $\beta = -1.251 \pm 0.307$ ,  $t = -4.074$ ,  $P < 0.001$ , GLM used for final model predictions) that wasn't apparently attributable to poorer model fit ( $r = 0.321$ ). The distribution of this species is closely tied to winter temperature (Bradbury *et al.* 2011). This may have been caused by site specific factors not being fully accounted. However, other heathland species, such as nightjar (GLM:  $\beta = +0.104 \pm 0.043$ ,  $t = 2.426$ ,  $P = 0.015$ ) and woodlark (GLM:  $\beta = +0.244 \pm 0.126$ ,  $t = 1.941$ ,  $P = 0.05$ , both GAM and GLM used), showed intuitive positive trends.

For breeding colonising species, some species such as little bustard showed increasing populations with increasing breeding season temperatures (negbin,  $\beta = +0.282 \pm 0.088$ ,  $t = 3.171$ ,  $P = 0.002$ ), although the model quality for this species was poor. Black woodpecker ( $r = 0.25-0.50$ ) showed the opposite pattern (negbin,  $\beta = -0.079 \pm 0.026$ ,  $t = -2.996$ ,  $P = 0.003$ ). Mixed patterns were also seen for the other coefficients included in

these models. Finally, for winter colonising species, four (Night Heron, Whimbrel, Ferruginous Duck, and Whimbrel) retained no significant GLM coefficients for climate. However, five of the six species retaining a significant coefficient for breeding season maximum temperature showed positive coefficients four out of six positive for summer mean rainfall, four out of seven had positive coefficients with winter minimum temperature, and three out of five species showed negative coefficients for winter mean rain, thus for all but summer temperature, less clear patterns were evident. Only three species included any interaction terms from GLMs (Table 7).

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**Table 1.** Summary of confidence levels applied to model validation of bird models.

<b>Model fit equivalent (R)</b>	<b>Classification</b>
>0.50	Good
0.25 – 0.50	Moderate
0.10 – 0.25	Poor
< 0.10	Very Poor

**Table 2.** Number of models meeting confidence levels using IPCC guidelines on uncertainty

IPCC Guidelines		Bird Group				Total
<b>Terminology</b>	<b>Degree of confidence</b>	Breeding	Seabirds	Wintering	Passage	
Very high confidence	At least 9/10 chance of being correct	19	15	40	9	83
High confidence	About 8/10 chance	3	0	4	1	8
Medium confidence	About 5/10 chance	4	2	10	3	19
Low confidence	About 2/10 chance	4	0	5	0	9
Very low confidence	Less than 1/10 chance	0	0	0	0	0

**Table 3.** Summary of model quality assessed through Pearson's r between predicted and observed densities from model validation

<b>Species Grouping</b>	<b>Model Quality (r) for density</b>				<b>Total</b>
	<b>&lt;0.1</b>	<b>0.1-0.25</b>	<b>0.25-0.5</b>	<b>&gt;0.5</b>	
Breeding	4	5	4	1	<b>14</b>
Breeding colonisers	2	3	1		<b>6</b>
Breeding rare	2	3	4	1	<b>10</b>
Passage	4	5	4		<b>13(10)</b>
Seabirds	5	6	6		<b>17</b>
WeBS Wintering	10	14	19	4	<b>47</b>
Wintering colonisers	7	3	2		<b>12</b>
<b>Total</b>	<b>34</b>	<b>39</b>	<b>40</b>	<b>6</b>	<b>119</b>

**Table 4.** Summary of final models used for predictions; “Bad” models were those  $r < 0.1$ , and were thus not suitable for further model predictions; “no data” were species where lack of suitable data prevented modelling; “GLM”, “GAM”, “Both” = respective final models selected for predictions.

<b>Group</b>	<b>Bad</b>	<b>No data</b>	<b>GLM</b>	<b>GAM</b>	<b>Both</b>	<b>Total</b>
Breeding	3		2	1	7	13
Breeding colonisers	2		1		3	6
Breeding rare	2	2	5		3	12
Passage	4		3	2	4	13
Seabirds	5		1	4	7	17
WeBS Wintering	10	5	11	7	19	52
Wintering colonisers	7		4	1		12
<i>Total</i>	<i>33</i>	<i>7</i>	<i>27</i>	<i>15</i>	<i>43</i>	<i>125</i>

**Table 5.** Summary of ability of models to predict change in populations, assessed through Pearson's r between predicted and observed densities from model validation

<b>Group</b>	<b>Model Quality (r) for % Change</b>				<b>Grand Total</b>
	<b>&lt;0.1</b>	<b>0.1-0.25</b>	<b>0.25-0.5</b>	<b>&gt;0.5</b>	
Breeding	10	2		1	13
Breeding colonisers	5	1			6
Breeding rare	3	1	4	2	10
Passage	8	3	2		13(10)*
Seabirds	9	6	2		17
WeBS Wintering	40	5	1	1	47
Wintering colonisers	10	2			12
<b>Grand Total</b>	85	20	9	4	119

\* three species were modelled for both autumn and spring passages



**Table 6.** Match up between GLM and GAM coefficients for all groups assessed. Match values are calculated as the proportion of coefficients (included in the model) from minimum adequate GAMs and GLMs for each species that are common between the two models.

<b>Group</b>	<b>Match</b>
Breeding	0.55±0.41
Breeding colonisers	0.44±0.50
Breeding rare	0.42±0.44
Passage	0.62±0.29
Seabirds	0.59±0.33
WeBS Wintering	0.53±0.30
Wintering colonisers	0.44±0.29
Grand Total	0.53±0.34

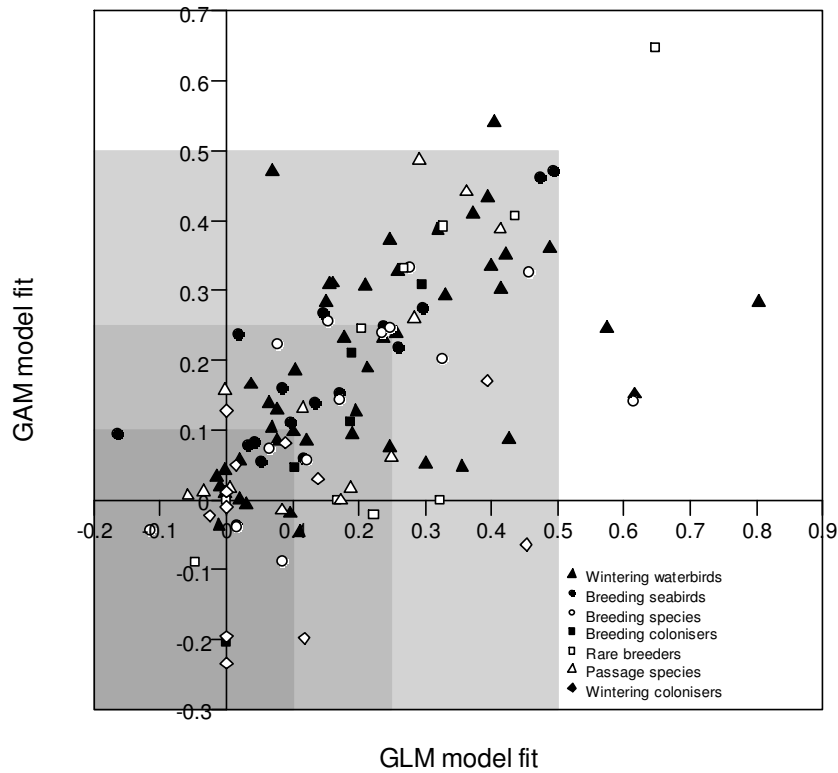
**Table 7.** Significant relationships with modelled climatic variables in GLMs, and the direction of the trend; numbers in brackets indicate the number of species in the respective grouping reaching the stated level of correlation coefficient (GAM-GLM Pearson's r). The three tables separate species with poor – good model fit (top), moderate to good model fit (middle) and all species (bottom).

<b>Q1: r&gt;0.1</b> <b>Variable</b>	<b>B[10]</b>		<b>BC[4]</b>		<b>BR[8]</b>		<b>P[9]</b>		<b>S[12]</b>		<b>W[37]</b>		<b>WC[5]</b>	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+
breed.max.max	4	5	1	1	2	3			7	3				
breed.max.rain	5	1	1		5				9	1				
breed.max.max:breed.max.rain		4				1			1	1				
sum.max.max					1		7	2			31	3		3
sum.mean.rain					1		7	2			17	12	1	2
sum.mean.rain:sum.max.max							1	4			6	12		
win.mean.rain	3	2	1			1	2	5	1		21	5	2	1
win.min.min	2	7	2	1	3	2	1	7	2	4	4	25	2	2
win.mean.rain:win.min.min	1					1	2	1			9	4		

<b>Q2: r&gt;0.25</b> <b>Variable</b>	<b>B[5]</b>		<b>BC[1]</b>		<b>BR[5]</b>		<b>P[4]</b>		<b>S[6]</b>		<b>W[23]</b>		<b>WC[2]</b>	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+
breed.max.max		4	1		2	1			4	1				
breed.max.rain	1	1			3				5	1				
breed.max.max:breed.max.rain						1			1					
sum.max.max					1		2	2			19	2		2
sum.mean.rain					1		2	2			12	7		1
sum.mean.rain:sum.max.max							1	1			3	9		
win.mean.rain	2	2	1			1	1	2			14	4		1
win.min.min	1	3	1		3	1	1	2	1	3	3	15		1
win.mean.rain:win.min.min	1					1		1			5	3		

<b>All</b> <b>Variable</b>	<b>B[14]</b>		<b>BC[6]</b>		<b>BR[10]</b>		<b>P[13]</b>		<b>S[17]</b>		<b>W[47]</b>		<b>WC[12]</b>	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+
breed.max.max	7	6	1	1	3	3			9	5				
breed.max.rain	6	1	1		5				10	1				
breed.max.max:breed.max.rain		5				1			1	2				
sum.max.max					1		9	3			34	8	1	5
sum.mean.rain					1		9	2			20	13	2	4
sum.mean.rain:sum.max.max							1	6			7	13	1	1
win.mean.rain	4	2	1			1	4	7	1		23	7	3	2
win.min.min	2	7	2	1	3	2	2	9	3	5	6	31	3	4
win.mean.rain:win.min.min	1	1				1	4	2			10	4		1
Na			2		3		2				5		4	

All: all models regardless of fit; Q1: model fit  $r > 0.1$ , Q2: model fit  $r > 0.25$ ; B breeding species; BC breeding colonisers; BR breeding rare; P passage; S seabirds; W wintering waterbirds; WC wintering colonisers; numbers in brackets [], denotes number of species reaching the level



**Figure 1.** Correlation between model fit using GLM and GAM outputs to assess the strength of support for each model. The dark grey square indicates very poor models ( $r < 0.1$ ), the medium grey square indicates poor models ( $r < 0.25$ ), the light grey square indicates moderate models ( $r < 0.5$ ) and white indicates good models ( $r > 0.5$ ).