PNAS

Supporting Information for

Ecological barriers mediate spatiotemporal shifts of bird communities at a continental scale

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S1. Additional Methods

Equation S1   **Jaccard dissimilarity coefficient (1)** $= 1 - a/(a + b + c)$ **, where**
$a =$ number of species shared by focal and comparison grid cells,
$b =$ number of species unique to the EBBA1 focal grid cell,
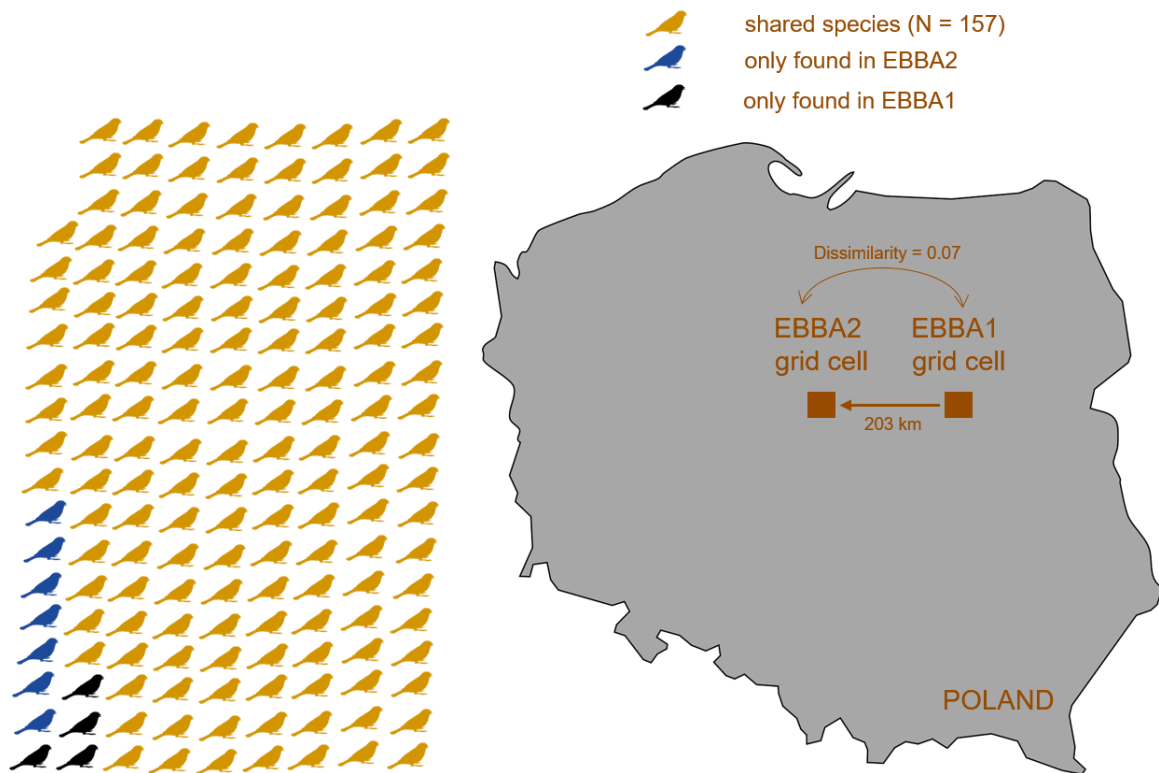$c =$ number of species unique to the EBBA2 comparison grid cell.

Figure S1. Exemplified representation of how spatiotemporal community composition dissimilarity between focal EBBA1 grid cells and their best matching EBBA2 grid cells were calculated. This specific example from Poland illustrates the pair of EBBA1–EBBA2 grid cells with lowest dissimilarity value between them and highlights the gradients of dissimilarity. That is, even the grid cell with the lowest dissimilarity with its best match does not have a one-to-one correspondence in the lists of species. Here, in addition to the 157 shared species, four unique species were only observed during EBBA1 period and seven unique species were only observed during EBBA2 period.

S1.1 Response variables: community composition shift distance and direction

To confirm the robustness of our approach, we tested for the difference in spatial and spatiotemporal dissimilarity in community composition shift distances. For this, we calculated the distance from each EBBA1 grid cell to another EBBA1 grid cell with the most similar community composition. Then, we quantified the difference between the distance to the most similar EBBA1 and most similar EBBA2 grid cells and found that most EBBA1 communities shifted further than expected based on the distance to the most similar EBBA1 grid cell ('residual shift distance'; Fig. S8).

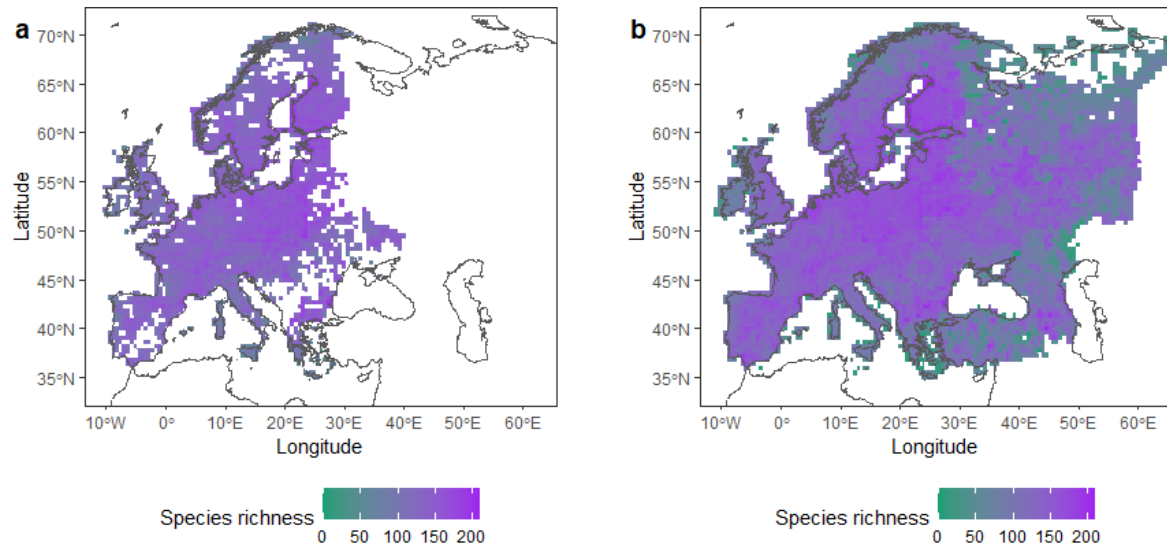**Figure S2.** Breeding bird species richness and the data coverage of the European Breeding Bird Atlas surveys. Panel a shows the species richness during the first atlas (EBBA1: 1985-1988; 2) and panel b the species richness during the second atlas (EBBA2: 2013-2017; 3). Color gradient represents the number of species in one 50 x 50 kilometer grid cell in which all breeding birds were recorded during the study period years.

Figure S3. Variation in Jaccard dissimilarity index values among pairs of grid cells. In panel a, the dissimilarity between focal EBBA1 grid cell and the best matching EBBA2 grid cell is included. In panel b, the variation in initial EBBA1 dissimilarity (i.e., initial uniqueness) among EBBA1 grid cells is illustrated. Initial EBBA1 dissimilarity is calculated as Jaccard dissimilarity between each focal EBBA1 grid cell and its best matching EBBA1 grid cell. The higher the dissimilarity value, the less similar the community compositions between the two grid cells. The black vertical lines indicate means of the dissimilarities across EBBA1 grid cells with their best matching EBBA2 and EBBA1 grid cells, respectively.

Figure S4. Percent increase in Jaccard's dissimilarity calculated for the best matching EBBA2 grid cell disregarding geographic distance (i.e., lowest dissimilarity value) and the closest of the five best matching EBBA2 grid cells. That is, we compared two Jaccard's dissimilarity values: 1) the dissimilarity between each focal EBBA1 grid cell and the EBBA2 grid cell with lowest dissimilarity value and 2) the dissimilarity between each focal EBBA1 grid cell and the geographically closest EBBA2 grid cell among the five EBBA2 grid cells that had the lowest dissimilarity values. In the panel on the left, the orange line indicates the 0.5 quantile across the % increase values for all focal EBBA1 grid cells (3.53% increase). In the zoomed-in panel on the right, the orange line indicates the same 0.5 quantile, while the black lines indicate the % increase values used in the sensitivity analyses (see section S3).

Figure S5. Variation in community shift distance (panel a) and direction (panels b and c). In panel a), the black vertical line indicates the mean distance among those grid cells that had non-zero shifts. In panels b) and c), compass directions are indicated on the circular plots. Panel b) illustrates the shift directions of all EBBA1 grid cells that shifted, while panel c) illustrates the shift directions of those EBBA1 grid cells that shifted more than one grid cell (~70 km).

Figure S6. Locations of the EBBA1 grid cells that had only poor compositional matches (Jaccard dissimilarity > 0.3) in EBBA2, suggesting 'community composition extinctions' (N = 140) (top panel) and that did not shift from EBBA1 to EBBA2, meaning that the best matching community composition was found in their original grid cell (bottom panel). The Jaccard's dissimilarity index values quantified as the dissimilarity between each focal EBBA1 grid cell and its best matching EBBA2 grid cell is shown for those communities in the bottom panel (N = 681).

Figure S7. Distance (panel a) and direction (panel b) of breeding bird community shift between 1980's and 2010's. Color gradient in panel a shows the distance of community shift in numbers of grid cells shifted, such that the darker the color the further the best matching community is in 2010's. The shift distances are assigned in ordinal groups similarly as in the shift distance models. Arrows in panel b indicate the direction of community shift, such that the starting point of the arrow is at the focal EBBA1 grid cell centroid and the ending point of the arrow is at the best matching EBBA2 grid cell centroid. For clarity, only directions of shifts further than one grid cell (i.e., shift distance classes 2-7) are plotted on the maps. For illustrative purposes, shift directions have been grouped into 25% compass direction quantiles and colored accordingly.

Figure S8. Residual shift distance calculated as the difference in spatial and spatiotemporal distances to the most similar EBBA1 and EBBA2 grid cells, respectively.

S1.2 Predictor variables

Figure S9. Correlation matrices of predictor variables relating to the community shift distance (upper panel) and direction (lower panel).

S1.2.1 Terrestrial biome boundaries

Our study area covered six different biomes (Fig. S10). The distance and direction to the nearest terrestrial biome boundary varied across the study area (Fig. S11).

i) The Mediterranean forests, woodlands, and scrublands are located around the Mediterranean Sea. The area has hot and dry summers, but cool and moist winters. The area has a long history of intensive agricultural use and is mainly characterized by semi-natural landscapes. Urbanization is ongoing and threatens the coastal woodland remnants. Human-induced forest fires and degradation due to agricultural intensification are typical.
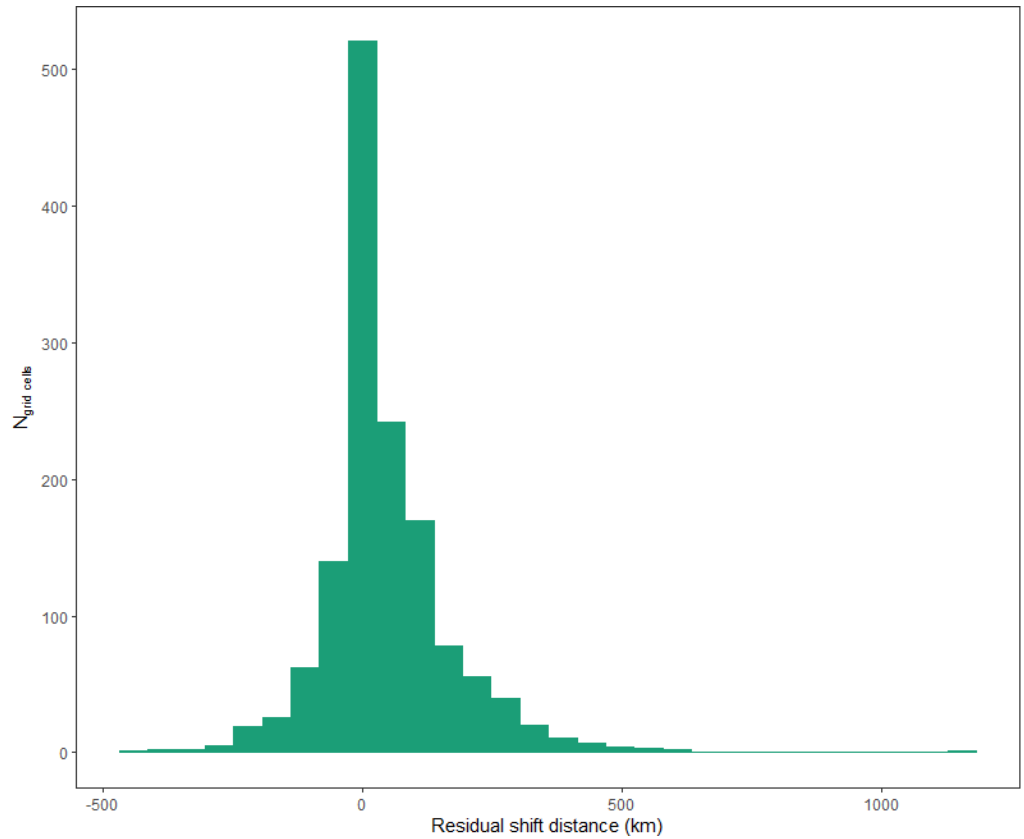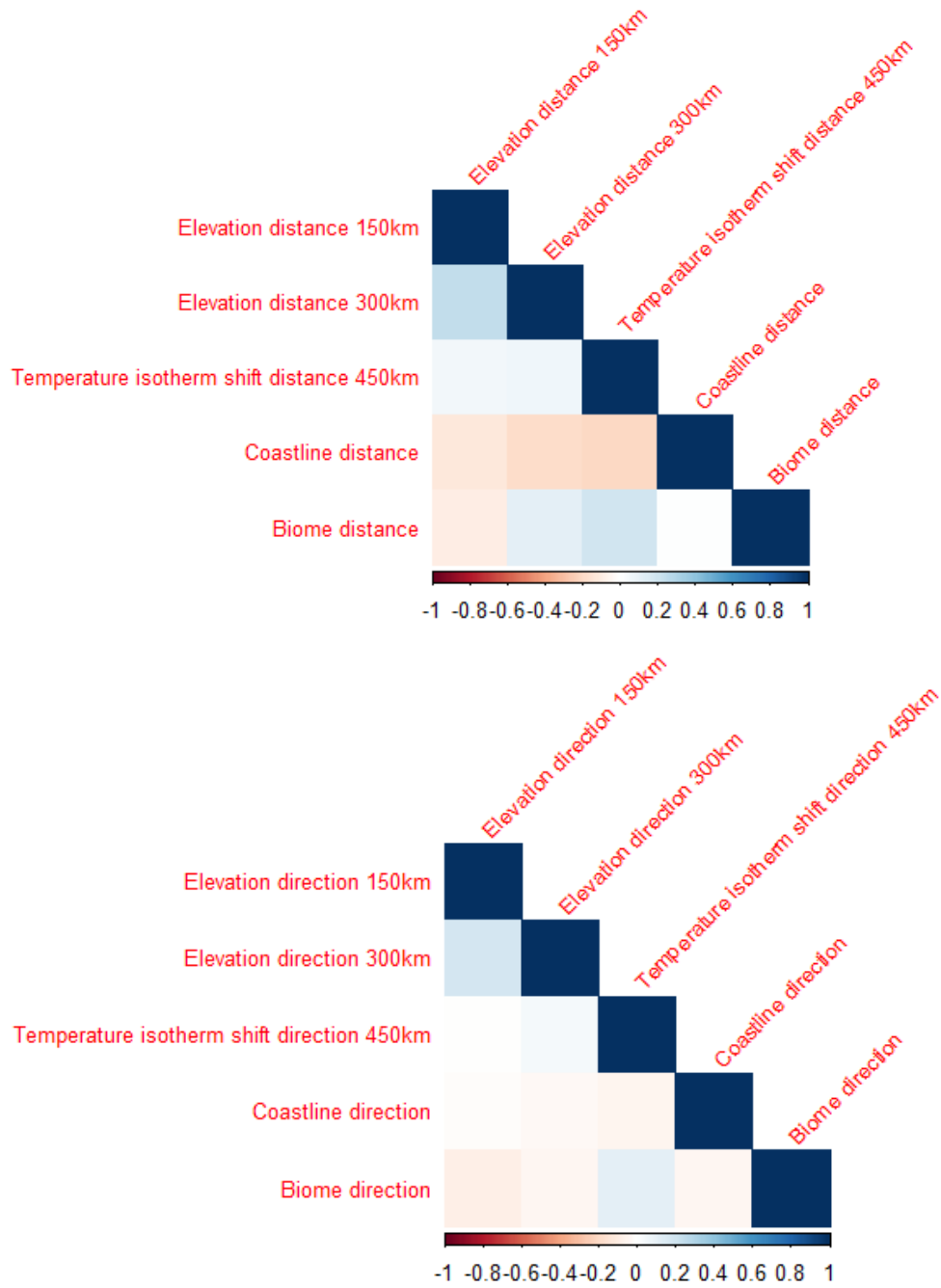
ii) The temperate coniferous forests are located at the Alps and the Carpathian Mountains. They have high faunal diversity and altitudinal specialization. Areas include pristine habitats, but they have been fragmented by increasing human pressure. The native mixed forests have been replaced by spruce monocultures due to logging.

iii) The temperate broadleaf and mixed forests cover the majority of mainland Europe and the British islands. The biome is highly fragmented due to intensive agricultural land use that stretches a very long time period. Biodiversity patterns are rather robust, and many dominant species have widespread distributions. However, for example due to unusual soils, local endemics also occur. The biome includes several Important Bird Areas (IBAs), which are under the pressure of agricultural expansion and intensification. Anthropogenic effects increase with urbanization and lead to pollution of air, water and soil.

iv) The boreal forest or taiga covers most of Fennoscandia. The biome typically has low temperatures and possible snow cover during the winter. Pristine areas prevail. Species richness and endemism are typically low, and many species are widespread (i.e., low alpha and beta diversity).

v) The temperate grasslands, savannas and shrublands within our study area cover a small area in northern Africa. They have relatively low alpha, beta, and gamma diversities.

vi) The tundra is located in the Scandinavian mountains and in the high Scandinavian arctic. The treeless tundra had long dark winters and short summers. This leads to extremely seasonal occurrences of birds. Species have typically widespread distributions, resulting in low alpha and beta diversities. Human pressure has increased also in remote areas and the biome is particularly sensitive and strongly influenced by climate change.

Figure S10. The full spatial distribution of the terrestrial biomes that overlapped the EBBA data used in our study. For the spatial extents of EBBA1 and EBBA2, see Fig. S1.

Figure S11. Panel a illustrates the spatial distribution of the shortest distance in kilometers from all 2092 EBBA1 grid cells to the nearest terrestrial biome boundary. Panel b shows the distribution of the distance values. Panel c illustrates the direction towards the nearest terrestrial biome boundary such that the gray arrows point from the focal EBBA1 grid cells to the nearest terrestrial biome boundary. Panel d shows the distribution of the direction values, weighted by distance.

S1.2.2 Coastlines

We quantified the shortest distance from each focal EBBA1 grid cell to the coastline. The distance and direction to the shortest distance to coastline varied across the study area (Fig. S12).

Figure S12. Panel a shows the spatial variation in coastline distance and panel b the variation in the coastline distance values. Panel c depicts the direction to the shortest distance from all 2092 EBBA1 grid cells to the coastline (green arrows). Panel d shows the direction values, weighted by distance.

S1.2.3 Elevation

We used the average elevation in each EBBA1 and EBBA2 grid cell to quantify elevation distance and direction (Fig. S13). We quantified the distance to the most different elevation within 150 km and 300 km buffers as well as the direction along most similar average elevation within 150 km and 300 km buffers (Fig. S14).

Figure S13. Map showing the average elevation (m a.s.l.) for all EBBA1 and EBBA2 grid cells across the study area.

Figure S14. Panels a and b show the variation in elevation distance within 150 km and 300 km buffers, respectively. Panels c and d show the variation in the elevation direction (weighted by distance) within 150 km and 300 km buffers, respectively.

S1.2.4 Temperature isotherm shift

We used mean temperature data for each EBBA1 and EBBA2 grid cell to quantify temperature isotherm shift distance and direction. There were missing values in the original temperature data (Fig. S15) that were imputed (see Online Methods for details). We quantified the distance to most similar temperatures between EBBA1 and EBBA2 within a 450 km buffer. We quantified the direction to most similar temperatures between EBBA1 and EBBA2 within a 450 km buffer (Fig. S16).

Figure S15. EBBA1 and EBBA2 grid cells with missing temperature data.

Figure S16. Panel a shows the spatial variation in temperature isotherm shift distance values within the 450 km buffer. Panel b shows the spatial variation in temperature isotherm shift directions within the 450 km buffer.

S2. Additional results

S2.1 Model results

Table S1. Community composition shift distance model estimates ± standard error (SE), t- and p-values, confidence intervals (CI) as well as variable importance (indicated as the relative contribution [%] in the drop in R^2) for community shift distance. The last column indicates whether the effect sign follows our hypotheses in Fig. 1, independent of the strength of the correlation (which is given by p-value and CI). Effects with $p < 0.05$ are shown in bold.

Predictor	Estimate ± SE	t	p	2.5% CI	97.5% CI	VarImp (%)	Follows hypothesis
Intercept	**0.621 ± 0.074**	**8.390**	**<0.001**	**0.476**	**0.767**		
Elevation distance 300 km	-0.006 ± 0.027	-0.244	0.807	-0.058	0.046	0.06	yes
Coastline distance	**0.109 ± 0.037**	**2.934**	**0.003**	**0.036**	**0.183**	**77.44**	**yes**
Biome distance	-0.025 ± 0.039	-0.642	0.521	-0.101	0.051	2.02	no
Temperature isotherm shift distance 450 km	**0.047 ± 0.023**	**2.071**	**0.038**	**0.003**	**0.092**	**11.18**	
Initial EBBA1 dissimilarity	-0.656 ± 0.429	-1.532	0.126	-1.496	0.183	9.30	

Community shift distance

Figure S17. Transformed (exp) effect sizes given as incidence rate ratios ± confidence intervals (error bars) for the predictors in the full distance model. Significance levels are given by asterisks, positive effects shown in blue, negative in red. BG dissimilarity = Initial EBBA1 dissimilarity.

Table S2. Community composition shift direction model estimates ± standard error (SE), t- and p-values, confidence intervals (CI) as well as variable importance (indicated as the relative contribution [%] in the drop in AIC) for community shift direction (eastness and northness separately). The last column indicates whether the effect sign follows our hypotheses in Fig. 1, independent of the strength of the correlation (which is given by p-value and CI). Effects with $p < 0.05$ are shown in bold.

Predictor	Estimate ± SE	t	p	2.5% CI	97.5% CI	VarImp (%)	Follows hypothesis
Eastness: $R^2 = 0.023$							
Intercept	**0.136 ± 0.064**	**2.122**	**0.034**	**0.010**	**0.262**		
Elevation direction 150 km	**0.066** ± 0.025	**2.622**	**0.009**	**0.017**	**0.115**	37.81	**yes**
Coastline direction	-0.058 ± 0.035	-1.681	0.093	-0.126	0.010	5.94	yes
Biome direction	**-0.089** ± 0.039	**-2.278**	**0.023**	**-0.166**	**-0.012**	24.75	**yes**
Temperature isotherm shift direction 450 km	0.038 ± 0.030	1.288	0.198	-0.020	0.097	2.65	
Initial EBBA1 dissimilarity	**-0.850 ± 0.354**	**-2.402**	**0.016**	**-1.543**	**-0.156**	28.85	
Northness: $R^2 = 0.024$							
Intercept	**0.195** ± 0.060	**3.257**	**0.001**	**0.078**	**0.312**		
Elevation direction 150 km	**0.088** ± 0.024	**3.693**	**<0.001**	**0.041**	**0.134**	72.60	**yes**
Coastline direction	-0.037 ± 0.030	-1.237	0.216	-0.095	0.021	3.24	yes
Biome direction	-0.023 ± 0.028	-0.838	0.402	-0.078	0.031	8.15	yes
Temperature isotherm shift direction 450 km	0.019 ± 0.029	0.672	0.501	-0.037	0.075	9.76	
Initial EBBA1 dissimilarity	-0.564 ± 0.325	-1.734	0.083	-1.202	0.074	6.34	

a

Eastness community shift

Figure S18. Effect sizes given as estimates ± confidence intervals (error bars) for the predictors in the full eastness (a) and northness (b) direction models. Significance levels are illustrated with asterisks, positive effects shown in blue, negative in red. BG dissimilarity = Initial EBBA1 dissimilarity.

S2.1.1 Accounting for spatial autocorrelation in model fitting

Shift distance. To account for spatial autocorrelation in the data, we included a spatial correlation structure in the models. To confirm that we correctly corrected for a spatial structure in the data, we visually inspected variograms (R package 'nlme', 5) of the residuals to check for remaining spatial autocorrelation of the final glmmPQL model. We found no strong residual spatial autocorrelation (Fig. S19).

Shift direction. To account for spatial autocorrelation in the data before fitting the models, we implemented Moran's I test for distance-based autocorrelation (R package 'DHARMa', 6). Subsequently, we included a spatial correlation structure in the models (R package 'nlme'). We visually inspected variograms (R package 'nlme') of the residuals to check for remaining spatial autocorrelation of the final gls models, finding no strong residual spatial autocorrelation (Fig. S20 and S21).

Full model distance

Figure S19. Residual spatial autocorrelation from the full model of the distance of community composition shifts. The semivariogram was plotted against distance. We found no apparent strong change over distance. Plot call was based on the variogram function of the R package 'nmle' (5) with X and Y coordinates specified as 'form' and normalized residuals.

Full model direction eastness

Figure S20. Residual spatial autocorrelation from the full model of community composition shift eastness. Plotted as a semivariogram against distance, with no apparent change over distance, except for a slight decrease towards larger distances. Plot call was based on the variogram function of the package 'nmle' (5) with X and Y coordinates specified as 'form' and normalized residuals.

Full model direction northness

Figure S21. Residual spatial autocorrelation from the full model of community shift northness. Plotted as a semivariogram against distance, with a slight increase towards larger distances. Plot call was based on the variogram function of the package 'nmle' (5) with X and Y coordinates specified as 'form' and normalized residuals.

S3. Sensitivity analyses

We conducted several sensitivity analyses to test the robustness of the results to the i) data selection and ii) matching criteria to select the best match from EBBA1 to EBBA2 community compositions. First, we tested how different cut-off values to select the best match influenced the resulting shift distances and direction (see section S1, Fig. S4) and the observed relationships with the ecological barriers. In the main manuscript we used the following procedure: We first identified the five most similar EBBA2 grid cells for each focal EBBA1 grid cell. Out of these five EBBA2 grid cells, we selected as the best match the grid cell that either had the lowest dissimilarity value (N = 1798) or a maximum of 3.5% increase in dissimilarity value compared to the lowest dissimilarity value and was located closest to the focal EBBA1 grid cell (N = 294). In the sensitivity analysis here, we combined a set of alternative values for i) the number of EBBA2 grid cells with most similar community compositions, and ii) the percentage threshold in dissimilarity increase compared to the grid cell with the lowest dissimilarity:

- 2_1: 2 best matching grid cells and a max 1% increase in the dissimilarity value
- 4_2: 4 best matching grid cells and a max 2% increase in the dissimilarity value
- 10_4: 10 best matching grid cells and a max 4% increase in the dissimilarity value
- 20_5: 20 best matching grid cells and a max 5% increase in the dissimilarity value
- 1_0: 1 best matching grid cell and no additional criteria (single best match)

In a next sensitivity analysis we tested how the selection of species influenced the observed community composition shift ~ ecological barrier -relationships (using the matching criteria used in the main manuscript). We did this to disentangle how particular groups of species influenced the overall shifts of communities in relation to ecological barriers. For example, the coastal and marine species may shift along coastlines instead of moving away from them unlike other, more terrestrial species.

Third, we tested whether coastal communities shift differently than communities located inland. This is expected, since coastal communities likely consist of species adapted to coastal or marine ecosystems and would thus not shift away but shift along coastlines in order to remain in the same or similar habitat type.

Finally, we tested whether the weights (community similarity value) affected the full model results, by running the same models for shift distance and direction (eastness and northness) without weights.

S3.1 Effects of different matching criteria

Table S3. Model outputs from sensitivity analyses based on **shift directions** resulting from different combinations of selection criteria to choose the best match between EBBA1 and EBBA2. Presented are the estimates (±SE), t- and p-values. T = Temperature. * indicate relationship significance different from those shown in the main results (5 grid cells and 3.5% increase).

Predictor	Beta	SE	t-value	p-value
2_1: 2 best matching grid cells and a max 1% increase in the dissimilarity value				
Eastness				
Intercept	**0.136**	**0.063**	**2.170**	**0.030**
* Elevation direction 300 km	0.043	0.024	1.761	0.079
Coastline direction	-0.061	0.033	-1.830	0.067
Biome direction	**-0.080**	**0.038**	**-2.090**	**0.037**
T isotherm shift direction 450 km	0.027	0.029	0.935	0.350
* Initial EBBA1 dissimilarity	-0.626	0.342	-1.830	0.068
Northness				
Intercept	**0.196**	**0.056**	**3.498**	**0.000**
Elevation direction 300 km	**0.072**	**0.023**	**3.191**	**0.001**
Coastline direction	-0.047	0.028	-1.691	0.091
Biome direction	-0.027	0.027	-1.005	0.315
T isotherm shift direction 450 km	0.028	0.027	1.038	0.299
Initial EBBA1 dissimilarity	-0.557	0.306	-1.821	0.069
4_2: 4 best matching grid cells and a max 2% increase in the dissimilarity value				
Eastness				
Intercept	**0.137**	**0.063**	**2.165**	**0.031**
* Elevation direction 300 km	0.044	0.025	1.804	0.072
*** Coastline direction**	**-0.071**	**0.034**	**-2.089**	**0.037**
Biome direction	**-0.076**	**0.039**	**-1.959**	**0.050**
T isotherm shift direction 450 km	0.017	0.029	0.601	0.548
Initial EBBA1 dissimilarity	**-0.788**	**0.348**	**-2.261**	**0.024**
Northness				
Intercept	**0.186**	**0.058**	**3.210**	**0.001**

Elevation direction 300 km	**0.087**	**0.023**	**3.755**	**0.000**
Coastline direction	-0.045	0.029	-1.568	0.117
Biome direction	-0.030	0.027	-1.101	0.271
T isotherm shift direction 450 km	0.028	0.028	1.000	0.317
Initial EBBA1 dissimilarity	-0.495	0.318	-1.557	0.120

10_4: 10 best matching grid cells and a max 4% increase in the dissimilarity value

Eastness

Intercept	0.124	0.067	1.862	0.063
Elevation direction 300 km	**0.079**	**0.025**	**3.129**	**0.002**
Coastline direction	-0.035	0.035	-0.990	0.322
Biome direction	**-0.093**	**0.040**	**-2.347**	**0.019**
T isotherm shift direction 450 km	0.049	0.030	1.636	0.102
* Initial EBBA1 dissimilarity	-0.668	0.361	-1.849	0.065

Northness

Intercept	**0.203**	**0.059**	**3.449**	**0.001**
Elevation direction 300 km	**0.068**	**0.024**	**2.839**	**0.005**
Coastline direction	-0.055	0.030	-1.848	0.065
Biome direction	-0.019	0.028	-0.682	0.496
T isotherm shift direction 450 km	0.017	0.029	0.592	0.554
Initial EBBA1 dissimilarity	-0.588	0.324	-1.818	0.069

20_5: 20 best matching grid cells and a max 5% increase in the dissimilarity value

Eastness

* Intercept	0.119	0.067	1.778	0.076
Elevation direction 300 km	**0.070**	**0.025**	**2.732**	**0.006**
Coastline direction	-0.064	0.035	-1.805	0.071
Biome direction	**-0.102**	**0.040**	**-2.525**	**0.012**
T isotherm shift direction 450 km	0.057	0.031	1.865	0.062
* Initial EBBA1 dissimilarity	-0.561	0.364	-1.541	0.124

Northness

Intercept	**0.201**	**0.058**	**3.470**	**0.001**
Elevation direction 300 km	**0.086**	**0.024**	**3.580**	**0.000**

Coastline direction	-0.049	0.030	-1.657	0.098
Biome direction	-0.028	0.028	-1.016	0.310
T isotherm shift direction 450 km	0.027	0.029	0.929	0.353
Initial EBBA1 dissimilarity	-0.583	0.320	-1.821	0.069

1_0: 1 best matching grid cell and no additional criteria (single best match)

Eastness

* Intercept	0.112	0.064	1.762	0.078
* Elevation direction 300 km	0.038	0.024	1.564	0.118
*** Coastline direction**	**-0.066**	**0.033**	**-1.967**	**0.049**
* Biome direction	-0.071	0.038	-1.854	0.064
T isotherm shift direction 450 km	0.047	0.029	1.664	0.096
* Initial EBBA1 dissimilarity	-0.515	0.343	-1.503	0.133

Northness

Intercept	**0.199**	**0.055**	**3.651**	**0.000**
Elevation direction 300 km	**0.082**	**0.022**	**3.717**	**0.000**
*** Coastline direction**	**-0.058**	**0.027**	**-2.131**	**0.033**
Biome direction	-0.028	0.026	-1.067	0.286
T isotherm shift direction 450 km	0.026	0.027	0.971	0.332
Initial EBBA1 dissimilarity	-0.556	0.298	-1.869	0.062

Figure S22. Forest plots for the original model (5 best matches, 3.5% increase in dissimilarity), and the five additional models ran in the sensitivity analyses for the **community shift directions** (1_0 = 1 best match with no additional criteria, 2_1 = 2 best matches with 1% increase in dissimilarity, 4_2 = 4 best matches with 2% increase in dissimilarity, 10_4 = 10 best matches with 4% increase in dissimilarity, 20_5 = 20 best matches with 5% increase in dissimilarity). The different predictors included in all the models are shown on the x-axis, the mean model estimates are shown as symbols (depending on the p-value) and the error bar is the 95% confidence interval. See Table S3 for detailed model outputs.

Table S4. Model outputs from sensitivity analyses based on **shift distances** resulting from different combinations of selection criteria to choose the best match between EBBA1 and EBBA2. Presented are the estimates (±SE), t- and p-values. T = Temperature. * indicate relationship significance different from those shown in the main results (5 grid cells and 3.5% increase).

Predictor	Beta	SE	t-value	p-value
2_1: 2 best matching grid cells and a max 1% increase in the dissimilarity value				
Intercept	**0.621**	**0.074**	**8.390**	**0.000**
Elevation distance 300 km	-0.006	0.027	-0.244	0.807
Coastline distance	**0.109**	**0.037**	**2.934**	**0.003**
Biome distance	-0.025	0.039	-0.642	0.521
T isotherm shift distance 450 km	**0.047**	**0.023**	**2.071**	**0.038**
Initial EBBA1 dissimilarity	-0.656	0.429	-1.532	0.126
4_2: 4 best matching grid cells and a max 2% increase in the dissimilarity value				
Intercept	**0.669**	**0.072**	**9.357**	**0.000**
Elevation distance 300 km	-0.004	0.026	-0.173	0.862
Coastline distance	**0.104**	**0.036**	**2.857**	**0.004**
Biome distance	-0.030	0.038	-0.788	0.431
* T isotherm shift distance 450 km	0.037	0.022	1.700	0.089
Initial EBBA1 dissimilarity	-0.552	0.411	-1.345	0.179
10_4: 10 best matching grid cells and a max 4% increase in the dissimilarity value				
Intercept	**0.643**	**0.077**	**8.314**	**0.000**
Elevation distance 300 km	0.001	0.027	0.034	0.973
Coastline distance	**0.109**	**0.040**	**2.760**	**0.006**
Biome distance	-0.033	0.041	-0.806	0.420
T isotherm shift distance 450 km	**0.046**	**0.023**	**1.999**	**0.046**
Initial EBBA1 dissimilarity	-0.651	0.442	-1.473	0.141
20_5: 20 best matching grid cells and a max 5% increase in the dissimilarity value				
Intercept	**0.664**	**0.082**	**8.072**	**0.000**
Elevation distance 300 km	-0.004	0.028	-0.161	0.872
Coastline distance	**0.118**	**0.043**	**2.729**	**0.006**
Biome distance	-0.032	0.045	-0.707	0.479
* T isotherm shift distance 450 km	0.035	0.023	1.481	0.139

Initial EBBA1 dissimilarity	-0.740	0.461	-1.605	0.109

1_0: 1 best matching grid cell and no additional criteria (single best match)

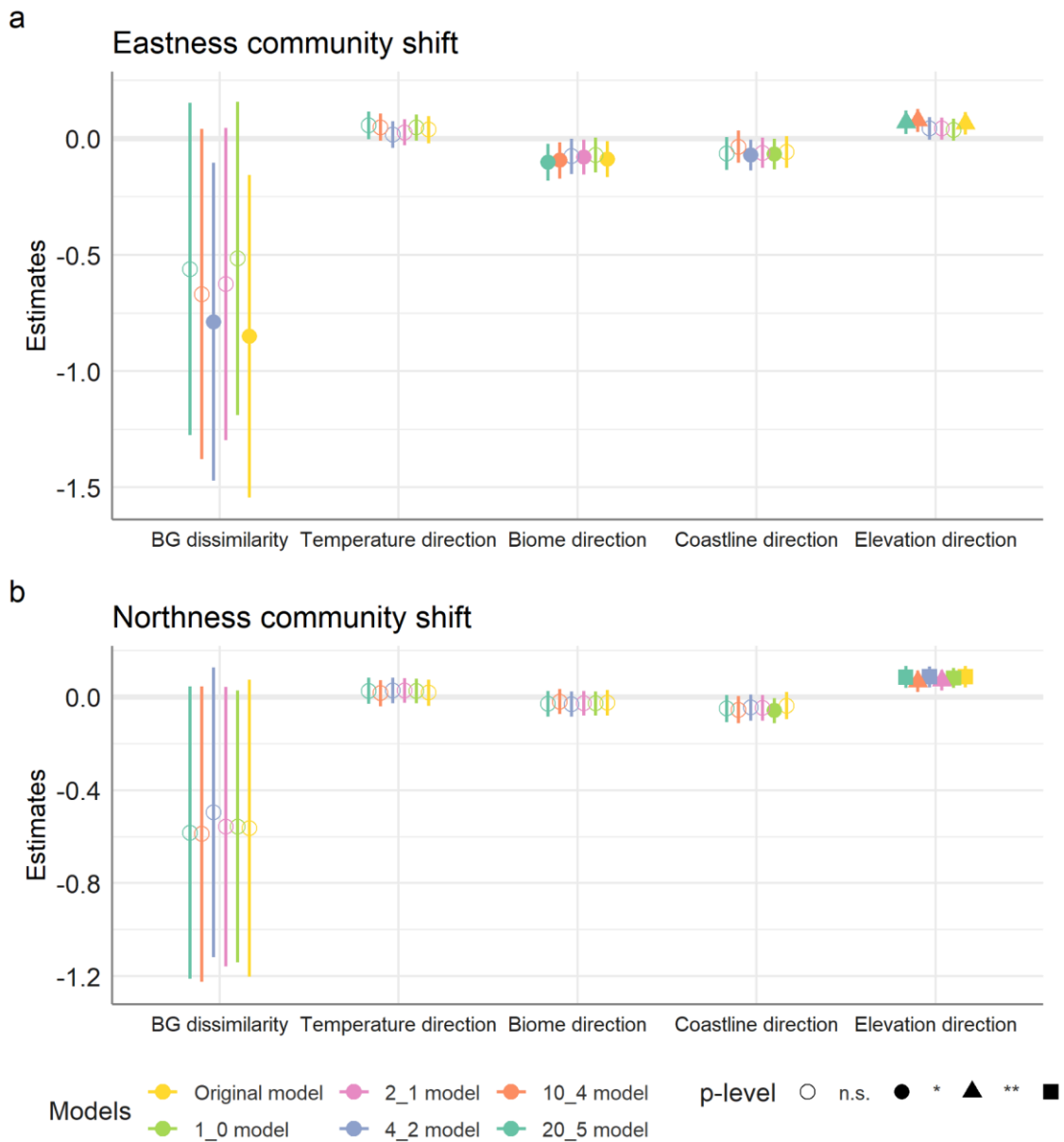|				
Intercept	**0.729**	**0.073**	**9.963**	**0.000**
Elevation distance 300 km	0.007	0.024	0.294	0.769
Coastline distance	**0.111**	**0.039**	**2.829**	**0.005**
Biome distance	-0.064	0.041	-1.557	0.120
T isotherm shift distance 450 km	**0.042**	**0.020**	**2.103**	**0.036**
Initial EBBA1 dissimilarity	-0.136	0.390	-0.348	0.728

Figure S23. Forest plots for the original model (5 best matches, 3.5% increase in dissimilarity), and the five additional models ran in the sensitivity analyses for the **community shift distances** (1_0 = 1 best match with no additional criteria, 2_1 = 2 best matches with 1% increase in dissimilarity, 4_2 = 4 best matches with 2% increase in dissimilarity, 10_4 = 10 best matches with 4% increase in dissimilarity, 20_5 = 20 best matches with 5% increase in dissimilarity). The different predictors included in all the models are shown on the x-axis, the mean model estimates are shown as symbols (depending on the p-value) and the error bar is the 95% confidence interval. See Table S4 for detailed model outputs.

S3.2 Effect of species selection

We repeated the analyses on community shift for a subset of species data such that we excluded 1) coastal and marine species, 2) rare species, and 3) rare and non-native species. Below we compare the results of the full analyses and the analyses conducted with a subset of species. For the lists of marine, rare, and non-native species, see Appendix S2.

Community shift distance. Community composition shift distances varied depending on the species inclusion criteria (Figure S24), such that the shift distances tended to be longer when excluding marine, rare or rare and non-native species. When marine species were excluded (subset), we found that the modeling results did not change compared with the full model (full data) except for the temperature isotherm shift which was no longer significant in the reduced analysis. In the case of excluding rare species, and both rare and nonnative species, model outcomes showed beside distance to coastline, a near-significant (rare) and strong (rare and nonnative) effect of biome. For both models the effect of biome distance was negative, indicating that communities closer to the biome border shifted larger distances (Table S3).

Community shift direction. In the case of marine species, biome direction was no longer significantly related to community shift eastness, while the other effects remained the same. For northness there were no major changes.
For rare species, effects of elevation direction on shift eastness were the same in the reduced dataset with no detectable effect of biome direction at all, while for shift northness they were the same with highly significant relations to elevation direction.
In the case of rare and non-native species, there was no effect of elevation direction while biome direction remained significant in the reduced dataset. There was again no difference between the two datasets for shift northness (Table S4).

Figure S24. Comparison of community composition shift distances between different scenarios of species inclusion. All = all species included, results shown in the main text. Exclusion of marine species increased the average shift distance by ~10 km in comparison to the average shift distance across all species (p = 0.04). Exclusion of rare and nonnative species increased the average shift distance by ~25 km in comparison to the average shift distance across all species (p < 0.001). Exclusion of rare species alone increased the average shift distance by ~27 km in comparison to the average shift distance across all species (p < 0.001). Community composition shift distances of subset communities different significantly from the shift distances of the full community (p-values in parentheses earlier in the caption).

Table S5. Model outputs from sensitivity analyses with 1) marine species, 2) rare species, and 3) rare and non-native species excluded from the original dataset. Presented are the estimates (±SE), t- and p-values. T = Temperature.

Predictor	Beta	SE	t-value	p-value
1) Marine species excluded				
Intercept	**0.720**	**0.069**	**10.471**	**0.000**
Elevation distance 300 km	-0.006	0.023	-0.250	0.803
Coastline distance	**0.110**	**0.037**	**2.989**	**0.003**
Biome distance	-0.022	0.038	-0.584	0.559
T isotherm shift distance 450 km	0.029	0.020	1.448	0.148
Initial EBBA1 dissimilarity	-0.053	0.378	-0.140	0.889
2) Rare species excluded				
Intercept	**0.765**	**0.071**	**10.826**	**0.000**
Elevation distance 300 km	-0.010	0.024	-0.444	0.657
Coastline distance	**0.081**	**0.038**	**2.146**	**0.032**
Biome distance	-0.075	0.039	-1.922	0.055
T isotherm shift distance 450 km	**0.055**	**0.020**	**2.700**	**0.007**
Initial EBBA1 dissimilarity	-0.183	0.387	-0.473	0.636
3) Rare and nonnative species excluded				
Intercept	**0.751**	**0.071**	**10.606**	**0.000**
Elevation distance 300 km	-0.014	0.024	**-0.580**	0.562
Coastline distance	**0.083**	**0.038**	**2.176**	**0.030**
Biome distance	**-0.084**	**0.039**	**-2.129**	**0.033**
T isotherm shift distance 450 km	0.039	0.020	1.900	0.058
Initial EBBA1 dissimilarity	-0.181	0.390	-0.465	0.642

Table S6. Model outputs from sensitivity analyses where (1) marine species, (2) rare species, and (3) rare and nonnative species were excluded from the original dataset. Presented are beta estimates and standard errors (SE), t- and p-values of full models, separately for eastness and northness of community shift directions. T = Temperature.

Term	Beta	SE	t-value	p-value
(1) Direction Eastness: marine species excluded				
Intercept	0.089	0.063	1.418	0.156
Elevation direction 150km	**0.054**	**0.025**	**2.204**	**0.028**
Coastline direction	-0.061	0.033	-1.827	0.068
Biome direction	-0.073	0.038	-1.901	0.057
T isotherm shift direction 450 km	0.042	0.029	1.451	0.147
Initial EBBA1 dissimilarity	-0.379	0.339	-1.117	0.264
(1) Direction Northness: marine species excluded				
Intercept	**0.170**	**0.057**	**2.977**	**0.003**
Elevation direction 150km	**0.071**	**0.023**	**3.141**	**0.002**
Coastline direction	-0.043	0.028	-1.517	0.129
Biome direction	-0.011	0.027	-0.416	0.677
T isotherm shift direction 450 km	0.018	0.028	0.634	0.526
Initial EBBA1 dissimilarity	-0.328	0.307	-1.069	0.285
(2) Direction Eastness: rare species excluded				
Intercept	**0.138**	**0.061**	**2.263**	**0.024**
Elevation direction 150km	0.047	0.024	1.924	0.054
Coastline direction	-0.019	0.033	-0.579	0.563
Biome direction	-0.058	0.038	-1.530	0.126
T isotherm shift direction 450 km	0.029	0.029	1.015	0.310
Initial EBBA1 dissimilarity	-0.616	0.335	-1.840	0.066
(2) Direction Northness: rare species excluded				
Intercept	**0.262**	**0.055**	**4.724**	**p<0.001**
Elevation direction 150km	**0.074**	**0.022**	**3.414**	**0.001**
Coastline direction	-0.039	0.027	-1.411	0.159
Biome direction	-0.016	0.026	-0.630	0.529
T isotherm shift direction 450 km	0.018	0.026	0.690	0.490
Initial EBBA1 dissimilarity	**-0.866**	**0.298**	**-2.910**	**0.004**

(3)   Direction Eastness: rare and nonnative species excluded

Intercept	0.113	0.061	1.843	0.066
Elevation direction 150km	0.030	0.024	1.248	0.212
Coastline direction	-0.025	0.033	-0.738	0.460
Biome direction	**-0.077**	**0.038**	**-2.039**	**0.042**
T isotherm shift direction 450 km	0.029	0.029	1.021	0.307
Initial EBBA1 dissimilarity	-0.483	0.339	-1.426	0.154

(3) Direction Northness: rare and nonnative species excluded

Intercept	**0.249**	**0.055**	**4.529**	**p<0.001**
Elevation direction 150km	**0.083**	**0.022**	**3.764**	**p<0.001**
Coastline direction	-0.022	0.028	-0.800	0.424
Biome direction	-0.003	0.026	-0.132	0.895
T isotherm shift direction 450 km	0.007	0.027	0.250	0.802
Initial EBBA1 dissimilarity	**-0.775**	**0.299**	**-2.590**	**0.010**

S3.3 Effect of bird community location: coastal vs inland communities

We did a sensitivity analysis to explore whether coastal communities were more likely to stay in the coastal areas rather than to move inland, i.e., away from coastlines. For this, we conducted a bootstrapping analysis where each coastal community was allowed to move randomly to available grid cells within 1.05 and 1.55 degrees (or ~105 km and 155 km radius respectively: equivalent of 2 and 3 grid cells to cardinal directions respectively). We used these buffers as larger shifts would substantially increase the proportion of inland grid cells compared to coastal grid cells. As on average these shifts in communities have been 93 km, the used buffers should capture the average shifts of the communities. Next, we checked whether the simulated shift happened to a coastal or inland grid cell and calculated the frequency distribution of coastal communities that shifted along coastal grid cells *vs* moved inland. These distributions were compared to observed spatiotemporal shifts between EBBA1 and EBBA2. This was conducted for all 429 and 491 communities which were situated in coastal areas during the first atlas period and had moved a maximum of 105 and 155 kilometers, respectively. The simulation was repeated 10 000 times, using only grid cells where the communities had moved at least one grid cell (165 and 227 grids with 105 and 155 km radius).

The bootstrapping analysis showed that coastal communities were significantly more likely to shift to coastal grid cells compared to simulated random shifts. When using 155 km radius, among all coastal communities during EBBA1, 442 communities stayed in coastal grid cells in EBBA2, whereas in the simulated shifts on average only 341 did the same (99.9% confidence intervals: 310–370). Correspondingly, among all coastal communities, only 49 communities moved inland, whereas in the simulated shifts 150 communities moved inland (99.9% confidence intervals: 121– 180). When using 105 km radius 396 communities stayed in coastal grid cells, whereas from the simulated communities on average only 322 stayed on the coast (99.9 % CI: 297–347). Correspondingly, only 33 communities moved inland, whereas in the simulated shifts on average 42.5 communities moved inland (95% CI: 82–131).

Among the communities that moved at least one grid cell when using 155 km radius, 178 communities stayed in coastal grid cells whereas in the simulated shifts on average only 154 did the same (99.9% CI: 132–172; Fig. S25a). Among the communities that moved at least one grid cell, only 49 communities moved inland, whereas in the simulated shifts 74 communities moved inland (99.9% CI: 55–94; Fig. S25b). Among the communities that moved at least one grid cell when using 105 km radius, 132 communities stayed in coastal grid cells whereas in the simulated shifts on average only 122.5 did the same (95% CI: 113–132). Among the communities that moved at least one grid cell, only 33 communities moved inland, whereas in the simulated shifts on average 42.5 communities moved inland (95% CI: 33–52).

Figure S25. Distribution of the number of communities where the simulated random shift of coastal communities would have ended to: a) another coastal grid cell and b) an inland grid cell. The red line shows the observed pattern between EBBA1 and EBBA2 among all communities. N = 10 000 simulations using 155 km radius.

S3.4 Effect of model weights

Community composition shift distance. Inclusion of model weights did not substantially influence the strength nor direction of predictor effects on community shift distances (Table S5).

Community composition shift direction. Inclusion of model weights did not substantially influence the predictor effect, neither in their effect size nor the direction (positive or negative) of the relationship (Table S6). Effects were slightly less pronounced when including model weights.

Table S7. Model estimates ± standard error (SE), t- and p-values from full models for community shift direction (eastness and northness separately) with model weights excluded. Effects with p < 0.05 are shown in bold.

Predictor	Beta	SE	t-value	p-value
Model weights excluded				
Intercept	**0.621**	**0.074**	**8.390**	**p<0.001**
Elevation distance 300 km	-0.006	0.027	-0.244	0.807
Coastline distance	**0.109**	**0.037**	**2.934**	**0.003**
Biome distance	-0.025	0.039	-0.642	0.521
Temperature isotherm shift distance 450 km	**0.047**	**0.023**	**2.071**	**0.038**
Initial EBBA1 dissimilarity	-0.656	0.429	-1.532	0.126

Table S8. Model estimates ± standard error (SE), t- and p-values from full models for community composition shift direction (eastness and northness) with model weights excluded. Effects with p < 0.05 are bolded.

Term	Beta	SE	t-value	p-value
Direction Eastness: model weights excluded				
Intercept	0.123	0.065	1.900	0.058
Elevation direction 150 km	**0.068**	**0.025**	**2.732**	**0.006**
Coastline direction	-0.063	0.035	-1.814	0.070
Biome direction	**-0.094**	**0.039**	**-2.371**	**0.018**
Temperature isotherm shift direction 450 km	0.035	0.030	1.166	0.244
Initial EBBA1 dissimilarity	**-0.757**	**0.372**	**-2.035**	**0.042**
Direction Northness: model weights excluded				
Intercept	**0.196**	**0.060**	**3.250**	**0.001**
Elevation direction 150 km	**0.087**	**0.024**	**3.660**	**p<0.001**
Coastline direction	-0.044	0.030	-1.502	0.133
Biome direction	-0.026	0.028	-0.911	0.362
Temperature isotherm shift direction 450 km	0.020	0.029	0.684	0.494
Initial EBBA1 dissimilarity	-0.579	0.342	-1.691	0.091

S4. Species list

Table S9. Species list with occurrences in EBBA1, EBBA2, and whether they were listed as rare, non-native or marine species.

Species	EBBA1	EBBA2	Rare	Non-native	Marine
Acanthis flammea	1	1	0	0	0
Accipiter badius	1	1	0	0	0
Accipiter brevipes	1	1	0	0	0
Accipiter gentilis	1	1	0	0	0
Accipiter nisus	0	1	0	0	0
Acridotheres cristatellus	1	1	0	1	0
Acridotheres tristis	1	1	0	1	0
Acrocephalus agricola	1	1	0	0	0
Acrocephalus arundinaceus	1	1	0	0	0
Acrocephalus dumetorum	1	1	0	0	0
Acrocephalus melanopogon	1	1	0	0	0
Acrocephalus paludicola	1	1	0	0	0
Acrocephalus palustris	1	1	0	0	0
Acrocephalus schoenobaenus	1	1	0	0	0
Acrocephalus scirpaceus	0	1	0	0	0
Actitis hypoleucos	1	1	0	0	0
Actitis macularius	1	1	0	0	0
Aegithalos caudatus	1	1	0	0	0
Aegolius funereus	0	1	0	0	0
Aegypius monachus	0	1	0	0	0
Agapornis fischeri	1	1	0	1	0
Agapornis personatus	1	1	0	1	0
Aix galericulata	1	1	0	1	0
Aix sponsa	0	1	0	1	0
Alauda arvensis	1	1	0	0	0
Alauda leucoptera	1	1	0	0	0
Alaudala rufescens	1	1	0	0	0
Alca torda	1	1	0	0	1
Alcedo atthis	1	1	0	0	0
Alectoris barbara	1	1	0	0	0
Alectoris chukar	1	1	0	0	0
Alectoris graeca	0	1	0	0	0
Alectoris rufa	1	1	0	0	0
Alle alle	1	1	0	0	1
Alopochen aegyptiaca	0	1	0	1	0
Amandava amandava	0	1	0	1	0
Amazona aestiva	0	1	0	0	0
Amazona oratrix	0	1	0	1	0

Ammomanes deserti	1	1	0	0	0
Ammoperdix griseogularis	0	1	0	0	0
Anas acuta	1	1	0	0	0
Anas bahamensis	1	1	0	1	0
Anas crecca	0	1	0	0	0
Anas platyrhynchos	0	1	0	0	0
Anas rubripes	1	1	0	0	0
Anser albifrons	1	1	0	0	0
Anser anser	0	1	0	0	0
Anser brachyrhynchus	0	1	0	0	0
Anser caerulescens	0	1	0	1	0
Anser canagicus	1	1	0	1	0
Anser cygnoid	1	1	0	1	0
Anser erythropus	0	1	0	0	0
Anser fabalis	1	1	0	0	0
Anser indicus	1	1	0	1	0
Anthropoides virgo	1	1	0	0	0
Anthus campestris	0	1	0	0	0
Anthus cervinus	1	1	0	0	0
Anthus hodgsoni	1	1	0	0	0
Anthus petrosus	1	1	0	0	1
Anthus pratensis	1	1	0	0	0
Anthus spinoletta	0	1	0	0	0
Anthus trivialis	1	1	0	0	0
Apus affinis	1	1	0	0	0
Apus apus	1	1	0	0	0
Apus caffer	1	1	0	0	0
Apus pallidus	1	1	0	0	0
Aquila adalberti	1	1	0	0	0
Aquila chrysaetos	1	1	0	0	0
Aquila fasciata	0	1	0	0	0
Aquila heliaca	0	1	0	0	0
Aquila nipalensis	1	1	0	0	0
Aratinga nenday	1	1	0	1	0
Ardea alba	1	1	0	0	0
Ardea cinerea	1	1	0	0	0
Ardea purpurea	1	1	0	0	0
Ardeola ralloides	0	1	0	0	0
Arenaria interpres	1	1	0	0	0
Argya altirostris	1	1	0	0	0
Asio flammeus	1	1	0	0	0
Asio otus	0	1	0	0	0
Athene noctua	0	1	0	0	0

Aythya affinis	1	1	0	0	0
Aythya collaris	1	1	0	0	0
Aythya ferina	1	1	0	0	0
Aythya fuligula	1	1	0	0	0
Aythya marila	1	1	0	0	0
Aythya nyroca	1	1	0	0	0
Bombycilla garrulus	1	1	0	0	0
Bonasa bonasia	1	0	0	0	0
Botaurus stellaris	1	1	0	0	0
Branta bernicla	0	1	0	0	0
Branta canadensis	1	1	0	1	0
Branta hutchinsii	1	1	0	1	0
Branta leucopsis	1	1	0	0	0
Bubo bubo	1	1	0	0	0
Bubo scandiacus	1	1	0	0	0
Bubulcus ibis	0	1	0	0	0
Bucanetes githagineus	1	1	0	0	0
Bucanetes mongolicus	1	1	0	0	0
Bucephala clangula	1	1	0	0	0
Bulweria bulwerii	0	0	0	0	1
Burhinus oedicnemus	1	1	0	0	0
Buteo buteo	1	1	0	0	0
Buteo lagopus	0	1	0	0	0
Buteo rufinus	1	1	0	0	0
Cairina moschata	1	1	0	1	0
Calandrella brachydactyla	1	1	0	0	0
Calcarius lapponicus	1	1	0	0	0
Calidris alpina	1	1	0	0	0
Calidris falcinellus	0	1	0	0	0
Calidris maritima	1	1	0	0	0
Calidris melanotos	1	1	0	0	0
Calidris minuta	1	1	0	0	0
Calidris pugnax	0	1	0	0	0
Calidris temminckii	1	1	0	0	0
Calliope calliope	0	1	0	0	0
Callipepla californica	1	1	0	1	0
Callonetta leucophrys	1	1	0	1	0
Calonectris borealis	1	1	0	0	1
Calonectris diomedea	1	1	0	0	1
Caprimulgus europaeus	1	1	0	0	0
Caprimulgus ruficollis	1	1	0	0	0
Carduelis carduelis	1	1	0	0	0
Carduelis citrinella	1	1	0	0	0

Carduelis corsicana	0	1	0	0	0
Carpodacus erythrinus	0	1	0	0	0
Carpodacus rubicilla	0	1	0	0	0
Carpodacus sibiricus	1	1	0	0	0
Carpospiza brachydactyla	1	1	0	0	0
Catharacta skua	1	1	0	0	1
Cecropis daurica	1	1	0	0	0
Cepphus grylle	1	1	0	0	1
Cercotrichas galactotes	1	1	0	0	0
Certhia brachydactyla	0	1	0	0	0
Certhia familiaris	1	1	0	0	0
Ceryle rudis	1	1	0	0	0
Cettia cetti	0	1	0	0	0
Charadrius alexandrinus	1	1	0	0	1
Charadrius asiaticus	1	1	0	0	0
Charadrius dubius	0	1	0	0	0
Charadrius hiaticula	1	1	0	0	0
Charadrius leschenaultii	1	1	0	0	0
Chersophilus duponti	1	1	0	0	0
Chlidonias hybrida	1	1	0	0	0
Chlidonias leucopterus	0	1	0	0	0
Chlidonias niger	1	1	0	0	0
Chloephaga picta	1	1	0	1	0
Chloris chloris	1	1	0	0	0
Chrysolophus amherstiae	1	1	0	1	0
Chrysolophus pictus	1	1	0	1	0
Ciconia ciconia	1	1	0	0	0
Ciconia nigra	1	1	0	0	0
Cinclus cinclus	1	1	0	0	0
Circaetus gallicus	1	1	0	0	0
Circus aeruginosus	1	1	0	0	0
Circus cyaneus	1	1	0	0	0
Circus macrourus	1	1	0	0	0
Circus pygargus	1	1	0	0	0
Cisticola juncidis	1	1	0	0	0
Clamator glandarius	1	1	0	0	0
Clanga clanga	1	1	0	0	0
Clanga pomarina	1	1	0	0	0
Clangula hyemalis	1	1	0	0	0
Coccothraustes coccothraustes	1	1	0	0	0
Colinus virginianus	1	1	0	1	0
Columba livia	1	1	0	0	0
Columba oenas	1	1	0	0	0

Columba palumbus	1	1	0	0	0
Coracias garrulus	1	1	0	0	0
Corvus corax	1	1	0	0	0
Corvus corone	1	1	0	0	0
Corvus frugilegus	0	1	0	0	0
Corvus monedula	1	1	0	0	0
Corvus splendens	1	1	0	1	0
Coturnix coturnix	1	1	0	0	0
Coturnix japonica	0	0	0	1	0
Crex crex	0	1	0	0	0
Cuculus canorus	0	1	0	0	0
Cuculus saturatus	1	1	0	0	0
Cursorius cursor	1	1	0	0	0
Cyanecula svecica	1	1	0	0	0
Cyanistes caeruleus	0	1	0	0	0
Cyanistes cyanus	1	1	0	0	0
Cyanistes teneriffae	0	1	0	0	0
Cyanopica cooki	0	1	0	0	0
Cygnus atratus	1	1	0	1	0
Cygnus columbianus	1	1	0	0	0
Cygnus cygnus	1	1	0	0	0
Cygnus olor	1	1	0	0	0
Delichon urbicum	1	1	0	0	0
Dendrocopos leucotos	1	1	0	0	0
Dendrocopos major	1	1	0	0	0
Dendrocopos syriacus	1	1	0	0	0
Dryobates minor	1	1	0	0	0
Dryocopus martius	0	1	0	0	0
Egretta garzetta	1	1	0	0	0
Egretta gularis	1	1	0	0	1
Elanus caeruleus	0	1	0	0	0
Emberiza aureola	0	1	0	0	0
Emberiza bruniceps	1	1	0	0	0
Emberiza buchanani	1	1	0	0	0
Emberiza caesia	1	1	0	0	0
Emberiza calandra	1	1	0	0	0
Emberiza cia	1	1	0	0	0
Emberiza cineracea	1	1	0	0	0
Emberiza cirlus	1	1	0	0	0
Emberiza citrinella	1	1	0	0	0
Emberiza hortulana	0	1	0	0	0
Emberiza melanocephala	1	1	0	0	0
Emberiza pallasi	1	1	0	0	0

Emberiza pusilla	1	1	0	0	0
Emberiza rustica	1	1	0	0	0
Emberiza schoeniclus	1	1	0	0	0
Eremophila alpestris	1	1	0	0	0
Erithacus rubecula	1	1	0	0	0
Estrilda astrild	0	1	0	1	0
Estrilda melpoda	1	1	0	1	0
Estrilda troglodytes	0	1	0	1	0
Eudromias morinellus	0	1	0	0	0
Euodice malabarica	1	1	0	1	0
Euplectes afer	1	1	0	1	0
Falco biarmicus	1	1	0	0	0
Falco cherrug	1	1	0	0	0
Falco columbarius	1	1	0	0	0
Falco eleonorae	1	1	0	0	0
Falco naumanni	1	1	0	0	0
Falco peregrinus	1	1	0	0	0
Falco rusticolus	1	1	0	0	0
Falco subbuteo	1	1	0	0	0
Falco tinnunculus	1	1	0	0	0
Falco vespertinus	1	1	0	0	0
Ficedula albicollis	1	1	0	0	0
Ficedula hypoleuca	1	1	0	0	0
Ficedula parva	0	1	0	0	0
Ficedula semitorquata	1	1	0	0	0
Francolinus francolinus	1	1	0	0	0
Fratercula arctica	1	1	0	0	1
Fringilla coelebs	1	1	0	0	0
Fringilla montifringilla	1	1	0	0	0
Fulica atra	1	1	0	0	0
Fulica cristata	1	1	0	0	0
Fulmarus glacialis	1	1	0	0	1
Galerida cristata	1	1	0	0	0
Galerida theklae	1	1	0	0	0
Gallinago gallinago	0	1	0	0	0
Gallinago media	0	1	0	0	0
Gallinago megala	1	1	0	0	0
Gallinago stenura	0	1	0	0	0
Gallinula chloropus	1	1	0	0	0
Gallus gallus	1	1	0	1	0
Garrulus glandarius	1	0	0	0	0
Gavia arctica	1	1	0	0	0
Gavia immer	1	1	0	0	0

Gavia stellata	0	1	0	0	0
Gelochelidon nilotica	1	1	0	0	1
Geronticus eremita	1	1	0	1	0
Glareola nordmanni	1	1	0	0	0
Glareola pratincola	1	1	0	0	0
Glaucidium passerinum	0	1	0	0	0
Grus grus	1	1	0	0	0
Gymnoris xanthocollis	1	1	0	0	0
Gypaetus barbatus	1	1	0	0	0
Gyps fulvus	0	1	0	0	0
Haematopus ostralegus	1	1	0	0	1
Halcyon smyrnensis	1	1	0	0	0
Haliaeetus albicilla	1	1	0	0	0
Hieraaetus pennatus	1	1	0	0	0
Himantopus himantopus	0	1	0	0	0
Hippolais icterina	1	1	0	0	0
Hippolais languida	1	1	0	0	0
Hippolais olivetorum	1	1	0	0	0
Hippolais polyglotta	1	1	0	0	0
Hirundo rustica	1	1	0	0	0
Hydrobates castro	0	1	0	0	1
Hydrobates leucorhous	1	1	0	0	1
Hydrobates monorhis	1	1	0	0	0
Hydrobates monteiroi	0	0	0	0	1
Hydrobates pelagicus	1	1	0	0	1
Hydrocoloeus minutus	0	1	0	0	0
Hydroprogne caspia	1	1	0	0	1
Iduna caligata	1	1	0	0	0
Iduna opaca	0	1	0	0	0
Iduna pallida	0	1	0	0	0
Iduna rama	1	1	0	0	0
Irania gutturalis	1	1	0	0	0
Ixobrychus minutus	0	1	0	0	0
Jynx torquilla	1	1	0	0	0
Ketupa zeylonensis	1	1	0	0	0
Lagopus lagopus	1	1	0	0	0
Lagopus muta	1	1	0	0	0
Lanius collurio	1	1	0	0	0
Lanius excubitor	1	1	0	0	0
Lanius minor	0	1	0	0	0
Lanius nubicus	0	1	0	0	0
Lanius phoenicuroides	1	1	0	0	0
Lanius schach	1	1	0	0	0

Lanius senator	0	1	0	0	0
Larus argentatus	1	1	0	0	0
Larus armenicus	1	1	0	0	0
Larus audouinii	1	1	0	0	1
Larus cachinnans	0	1	0	0	0
Larus canus	1	1	0	0	0
Larus delawarensis	1	1	0	0	0
Larus fuscus	0	1	0	0	0
Larus genei	1	1	0	0	1
Larus hyperboreus	1	1	0	0	1
Larus ichthyaetus	1	1	0	0	1
Larus marinus	1	1	0	0	1
Larus melanocephalus	1	1	0	0	0
Larus michahellis	1	1	0	0	0
Larus ridibundus	0	1	0	0	0
Leiopicus medius	1	1	0	0	0
Leiothrix lutea	1	1	0	1	0
Limosa lapponica	1	1	0	0	0
Limosa limosa	1	1	0	0	0
Linaria cannabina	1	1	0	0	0
Linaria flavirostris	0	1	0	0	0
Locustella fluviatilis	1	1	0	0	0
Locustella lanceolata	1	1	0	0	0
Locustella luscinioides	0	1	0	0	0
Locustella naevia	1	1	0	0	0
Lonchura malacca	0	0	0	1	0
Lonchura punctulata	1	1	0	1	0
Lophodytes cucullatus	0	0	0	1	0
Lophophanes cristatus	1	1	0	0	0
Loxia curvirostra	1	1	0	0	0
Loxia leucoptera	1	1	0	0	0
Loxia pytyopsittacus	1	1	0	0	0
Loxia scotica	1	1	0	0	0
Lullula arborea	1	1	0	0	0
Luscinia luscinia	1	1	0	0	0
Luscinia megarhynchos	0	1	0	0	0
Lymnocryptes minimus	1	1	0	0	0
Lyrurus mlokosiewiczi	1	1	0	0	0
Lyrurus tetrix	1	1	0	0	0
Mareca penelope	1	1	0	0	0
Mareca strepera	1	1	0	0	0
Marmaronetta angustirostris	1	1	0	0	0
Melanitta fusca	0	1	0	0	0

Melanitta nigra	1	1	0	0	0
Melanocorypha bimaculata	0	1	0	0	0
Melanocorypha calandra	1	1	0	0	0
Melanocorypha yeltoniensis	1	1	0	0	0
Meleagris gallopavo	1	1	0	1	0
Mergellus albellus	1	1	0	0	0
Mergus merganser	1	1	0	0	0
Mergus serrator	1	1	0	0	0
Merops apiaster	1	1	0	0	0
Merops persicus	1	1	0	0	0
Microcarbo pygmaeus	1	1	0	0	0
Milvus migrans	1	1	0	0	0
Milvus milvus	1	1	0	0	0
Monticola saxatilis	1	1	0	0	0
Monticola solitarius	1	1	0	0	0
Montifringilla nivalis	1	1	0	0	0
Morus bassanus	1	1	0	0	1
Motacilla alba	1	1	0	0	0
Motacilla cinerea	1	1	0	0	0
Motacilla citreola	1	1	0	0	0
Motacilla flava	1	1	0	0	0
Muscicapa striata	1	1	0	0	0
Myiopsitta monachus	1	1	0	1	0
Neophron percnopterus	1	1	0	0	0
Netta rufina	1	1	0	0	0
Nucifraga caryocatactes	1	1	0	0	0
Numenius arquata	0	1	0	0	0
Numenius phaeopus	1	1	0	0	0
Numida meleagris	0	1	0	1	0
Nycticorax nycticorax	0	1	0	0	0
Oenanthe chrysopygia	0	1	0	0	0
Oenanthe cypriaca	0	1	0	0	0
Oenanthe deserti	1	1	0	0	0
Oenanthe finschii	1	1	0	0	0
Oenanthe hispanica	1	1	0	0	0
Oenanthe isabellina	1	1	0	0	0
Oenanthe leucura	1	1	0	0	0
Oenanthe oenanthe	0	1	0	0	0
Oenanthe pleschanka	1	1	0	0	0
Oenanthe xanthoprymna	1	1	0	0	0
Oriolus oriolus	0	1	0	0	0
Otis tarda	0	1	0	0	0
Otus brucei	1	1	0	0	0

Otus cyprius	1	1	0	0	0
Otus scops	1	1	0	0	0
Oxyura jamaicensis	1	1	0	1	0
Oxyura leucocephala	1	1	0	0	0
Pandion haliaetus	0	1	0	0	0
Panurus biarmicus	1	1	0	0	0
Parabuteo unicinctus	1	1	0	1	0
Parus major	1	1	0	0	0
Passer domesticus	1	1	0	0	0
Passer hispaniolensis	0	1	0	0	0
Passer italiae	1	1	0	0	0
Passer moabiticus	1	1	0	0	0
Passer montanus	0	1	0	0	0
Pastor roseus	1	1	0	0	0
Pavo cristatus	1	1	0	1	0
Pelecanus crispus	1	1	0	0	0
Pelecanus onocrotalus	1	1	0	0	0
Perdix perdix	1	1	0	0	0
Periparus ater	1	1	0	0	0
Perisoreus infaustus	1	1	0	0	0
Pernis apivorus	1	1	0	0	0
Petronia petronia	1	1	0	0	0
Phalacrocorax aristotelis	0	1	0	0	1
Phalacrocorax carbo	1	1	0	0	0
Phalaropus fulicarius	1	1	0	0	0
Phalaropus lobatus	0	1	0	0	0
Phasianus colchicus	0	1	0	0	0
Phoeniconaias minor	1	1	0	0	0
Phoenicopterus chilensis	0	1	0	1	0
Phoenicopterus roseus	0	1	0	0	0
Phoenicopterus ruber	1	1	0	1	0
Phoenicurus erythrogastrus	1	1	0	0	0
Phoenicurus ochruros	1	1	0	0	0
Phoenicurus phoenicurus	1	1	0	0	0
Phylloscopus bonelli	1	1	0	0	0
Phylloscopus borealis	0	1	0	0	0
Phylloscopus collybita	0	1	0	0	0
Phylloscopus inornatus	1	1	0	0	0
Phylloscopus nitidus	1	1	0	0	0
Phylloscopus orientalis	0	1	0	0	0
Phylloscopus sibilatrix	0	1	0	0	0
Phylloscopus sindianus	1	1	0	0	0
Phylloscopus tristis	1	1	0	0	0

Phylloscopus trochiloides	1	1	0	0	0
Phylloscopus trochilus	1	1	0	0	0
Pica pica	1	1	0	0	0
Picoides tridactylus	1	1	0	0	0
Picus canus	1	1	0	0	0
Picus viridis	0	1	0	0	0
Pinicola enucleator	1	1	0	0	0
Pionus maximiliani	1	1	0	1	0
Platalea leucorodia	1	1	0	0	0
Plectrophenax nivalis	0	1	0	0	0
Plegadis falcinellus	1	1	0	0	0
Ploceus melanocephalus	0	1	0	1	0
Pluvialis apricaria	0	1	0	0	0
Pluvialis fulva	1	1	0	0	0
Pluvialis squatarola	1	1	0	0	0
Podiceps auritus	1	1	0	0	0
Podiceps cristatus	1	1	0	0	0
Podiceps grisegena	0	1	0	0	0
Podiceps nigricollis	1	1	0	0	0
Podilymbus podiceps	0	1	0	0	0
Poecile cinctus	1	1	0	0	0
Poecile hyrcanus	1	1	0	0	0
Poecile lugubris	1	1	0	0	0
Poecile montanus	0	1	0	0	0
Poecile palustris	0	1	0	0	0
Poicephalus senegalus	1	1	0	1	0
Porphyrio alleni	1	1	0	0	0
Porphyrio porphyrio	0	1	0	0	0
Porzana porzana	0	1	0	0	0
Prinia gracilis	1	1	0	0	0
Prunella atrogularis	1	1	0	0	0
Prunella collaris	0	1	0	0	0
Prunella modularis	0	1	0	0	0
Prunella montanella	0	1	0	0	0
Prunella ocularis	0	1	0	0	0
Psittacara acuticaudatus	0	1	0	1	0
Psittacara erythrogenys	0	1	0	1	0
Psittacara mitratus	1	1	0	1	0
Psittacula eupatria	0	1	0	1	0
Psittacula krameri	1	1	0	1	0
Pternistis erckelii	1	1	0	1	0
Pterocles alchata	1	1	0	0	0
Pterocles orientalis	1	1	0	0	0

Pterodroma deserta	0	0	0	0	1
Ptyonoprogne rupestris	1	1	0	0	0
Puffinus lherminieri	0	0	0	0	1
Puffinus mauretanicus	1	1	0	0	1
Puffinus puffinus	0	1	0	0	1
Puffinus yelkouan	0	1	0	0	1
Pycnonotus barbatus	0	1	0	0	0
Pycnonotus cafer	0	0	0	1	0
Pycnonotus jocosus	0	1	0	1	0
Pycnonotus leucotis	1	1	0	0	0
Pycnonotus xanthopygos	1	1	0	0	0
Pyrrhocorax graculus	1	1	0	0	0
Pyrrhocorax pyrrhocorax	0	1	0	0	0
Pyrrhula pyrrhula	1	1	0	0	0
Quelea quelea	1	1	0	1	0
Rallus aquaticus	1	1	0	0	0
Recurvirostra avosetta	1	1	0	0	0
Regulus ignicapilla	1	1	0	0	0
Regulus regulus	0	1	0	0	0
Remiz pendulinus	0	1	0	0	0
Rhea americana	0	1	0	1	0
Rhodopechys sanguineus	1	1	0	0	0
Rhodospiza obsoleta	1	1	0	0	0
Riparia riparia	1	1	0	0	0
Rissa tridactyla	1	1	0	0	0
Saxicola rubetra	1	1	0	0	0
Saxicola torquatus	0	1	0	0	0
Scolopax rusticola	1	1	0	0	0
Serinus pusillus	0	1	0	0	0
Serinus serinus	0	1	0	0	0
Sinosuthora alphonsiana	1	1	0	0	0
Sinosuthora webbiana	1	1	0	1	0
Sitta europaea	1	1	0	0	0
Sitta krueperi	0	1	0	0	0
Sitta neumayer	1	1	0	0	0
Sitta tephronota	1	1	0	0	0
Sitta whiteheadi	1	1	0	0	0
Somateria mollissima	1	1	0	0	1
Somateria spectabilis	0	1	0	0	1
Spatula clypeata	0	1	0	0	0
Spatula cyanoptera	1	1	0	0	0
Spatula discors	0	1	0	0	0
Spatula querquedula	1	1	0	0	0

Spilopelia senegalensis	1	1	0	0	0
Spinus spinus	1	1	0	0	0
Stercorarius longicaudus	0	1	0	0	0
Stercorarius parasiticus	1	1	0	0	1
Stercorarius pomarinus	1	1	0	0	0
Sterna dougallii	1	1	0	0	1
Sterna hirundo	1	1	0	0	0
Sterna paradisaea	1	1	0	0	0
Sternula albifrons	0	1	0	0	0
Streptopelia decaocto	0	1	0	0	0
Streptopelia orientalis	1	1	0	0	0
Streptopelia roseogrisea	1	1	0	1	0
Streptopelia turtur	1	1	0	0	0
Strix aluco	1	1	0	0	0
Strix nebulosa	1	1	0	0	0
Strix uralensis	1	1	0	0	0
Sturnus unicolor	1	1	0	0	0
Sturnus vulgaris	1	1	0	0	0
Surnia ulula	1	1	0	0	0
Sylvia atricapilla	1	1	0	0	0
Sylvia balearica	1	1	0	0	0
Sylvia borin	1	1	0	0	0
Sylvia cantillans	1	1	0	0	0
Sylvia communis	1	1	0	0	0
Sylvia conspicillata	1	1	0	0	0
Sylvia crassirostris	1	1	0	0	0
Sylvia curruca	1	1	0	0	0
Sylvia hortensis	0	1	0	0	0
Sylvia melanocephala	0	1	0	0	0
Sylvia melanothorax	0	1	0	0	0
Sylvia mystacea	1	1	0	0	0
Sylvia nana	1	1	0	0	0
Sylvia nisoria	1	1	0	0	0
Sylvia ruppeli	1	1	0	0	0
Sylvia sarda	1	1	0	0	0
Sylvia undata	1	1	0	0	0
Syrmaticus reevesii	1	1	1	1	0
Tachybaptus ruficollis	1	1	1	0	0
Tachymarptis melba	1	1	1	0	0
Tadorna ferruginea	0	1	0	0	0
Tadorna tadorna	1	1	1	0	0
Taeniopygia castanotis	1	1	1	0	0
Taeniopygia guttata	0	0	0	1	0

Tarsiger cyanurus	0	1	1	0	0
Tetrao urogallus	0	1	1	0	0
Tetraogallus caspius	1	1	1	0	0
Tetraogallus caucasicus	1	0	0	0	0
Tetrax tetrax	0	1	1	0	0
Thalasseus bengalensis	1	1	1	0	1
Thalasseus elegans	0	1	1	0	1
Thalasseus sandvicensis	1	1	1	0	1
Threskiornis aethiopicus	1	1	1	1	0
Tichodroma muraria	1	1	1	0	0
Tringa erythropus	1	1	1	0	0
Tringa glareola	1	1	1	0	0
Tringa nebularia	1	1	1	0	0
Tringa ochropus	1	1	1	0	0
Tringa stagnatilis	1	1	1	0	0
Tringa totanus	1	1	1	0	0
Troglodytes troglodytes	1	1	1	0	0
Turdus iliacus	1	1	1	0	0
Turdus merula	1	1	1	0	0
Turdus philomelos	0	1	1	0	0
Turdus pilaris	1	1	1	0	0
Turdus ruficollis	1	1	1	0	0
Turdus torquatus	1	1	1	0	0
Turdus viscivorus	1	1	1	0	0
Tyto alba	1	1	1	0	0
Upupa epops	1	1	1	0	0
Uria aalge	0	1	1	0	1
Uria lomvia	0	1	1	0	1
Vanellus gregarius	0	1	1	0	0
Vanellus indicus	1	1	1	0	0
Vanellus leucurus	1	1	1	0	0
Vanellus spinosus	0	1	1	0	0
Vanellus vanellus	1	1	1	0	0
Vidua macroura	1	1	1	1	0
Xenus cinereus	1	1	1	0	0
Zapornia parva	0	1	1	0	0
Zapornia pusilla	1	1	1	0	0
Zoothera aurea	0	1	1	0	0

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