

Supporting Information

Eco-evolutionary drivers of avian migratory connectivity

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Appendix S1. *Detailed hypotheses and predictions on the determinants of migratory connectivity*

Our hypotheses on the drivers of migratory connectivity, especially those concerning geographic effects, stem from the optimisation of migration costs, by which individuals are expected to migrate in the most energy efficient way (Somveille et al. 2021). Migration distance is a proxy for the cost of relocating between seasonal grounds, with the shortest available path between breeding and nonbreeding sites corresponding to the maximum travel cost optimisation for birds (Somveille et al. 2021). When migration distance increases, migration cost tends to be more similar between alternative strategies representing either strong or weak connectivity (Fig. S1), in turn more mixing (lower connectivity) is likely to occur in the population (see also Gilroy et al. 2016; Somveille et al. 2021, for more details). In fact, empirical data has suggested low connectivity in long-distance migrants (Finch et al. 2018; Patchett et al. 2018). Thus, we expect that migratory connectivity would decrease with migration distance. The same principle underlies the effect of nonbreeding population spread on the strength of migratory connectivity. When breeding range spread and migration distance are held constant while the nonbreeding population spread decreases, migration cost tends to be more similar between the two opposite situations of strong and weak migratory connectivity (Fig. S1, main text), therefore population mixing (lower connectivity) is promoted. In fact, Finch et al. (2018) have found that species spreading over a larger nonbreeding range showed a stronger migratory connectivity than those spreading over a smaller nonbreeding range. Consequently, we predict that migratory connectivity would increase with increasing nonbreeding population spread. Following this prediction, geographical constraints related to the landmass configuration and availability of suitable land in the European and African continents (the occurrence of peninsulas in Southern Europe and the triangular shape of the African continent) also lead us to hypothesise that migratory populations should be constrained to mix more during the nonbreeding period at southern latitudes due to decreasing land availability (Finch et al. 2018). Therefore, we may expect a decrease in migratory connectivity with decreasing nonbreeding latitude (i.e., more southwards, because we consider latitude as ranging from negative to positive values from the equator). Moreover, the relative population spreads in seasonal grounds might also shape migratory connectivity. In fact, individuals should mix more in the nonbreeding range when nonbreeding population spread is lower than the breeding one, but should also mix more in the breeding range when the breeding population spread is lower than the nonbreeding

one. Indeed, since the measure used to quantify connectivity (r_M) is symmetric, i.e. does not consider breeding and nonbreeding ranges differently, it declines whenever mixing of individuals occurs in either range. This consideration allows predicting that migratory connectivity should peak when the breeding and nonbreeding ranges have the same extent, i.e. when the relative population spread is one, and decrease for lower or larger values. Thus, we expect a quadratic effect of relative population spread on migratory connectivity. The relative population spread is similar to the concept of migratory dispersion, which was defined as the extent to which species occupy larger or smaller nonbreeding ranges relative to that occupied in the breeding period (Gilroy et al. 2016). However, this measure is strongly affected by the absolute size of the breeding and nonbreeding ranges, while the ratio between the range sizes is not, and this allows a better comparison among geographical populations that can largely differ in population size.

Amongst species-specific traits, low niche specialization is common in long-distance migrants, as it can be advantageous due to the variety of habitats and food resources met *en route* and on the nonbreeding grounds (Reif et al. 2016). If so, natural selection could have maintained a stronger migratory connectivity in specialized species in terms of habitat and dietary breadths, whereas a weaker migratory connectivity should be associated to generalists (Cresswell 2014). Body mass is a fundamental predictor of life-history traits and might affect migratory connectivity in several ways. Larger birds generally show longer migration distances due to an optimization of the aerial locomotion costs (Hein et al. 2012), which may exert an indirect effect on migratory connectivity by increasing population mixing. However, larger species also live longer and, in avian migrants, a longer lifespan promotes the social transmission of migratory routes towards nonbreeding sites and helps maintaining migratory knowledge across generations (Teitelbaum et al. 2016; Foss-Grant et al. 2018). Once the effect of migration distance is accounted for, a larger body mass could thus be expected to favour the evolution of a stronger migratory connectivity.

Finally, we tested whether migratory connectivity differed between passerine and non-passerine birds. Our expectation is based on the serial residency hypothesis (Cresswell 2014), which predicts that birds should tend to redistribute stochastically over a wider nonbreeding area if they are unable to forecast and compensate for any favourable or unfavourable events during migration, particularly juveniles at first migration, with consequences on the strength of migratory connectivity. Passerine and non-passerine birds typically show contrasting behaviour upon the first migration. Among passerines, juveniles usually migrate separately from

adults, whilst non-passerine juveniles tend to follow adults upon migration. The serial residency hypothesis indeed predicts that passerines would retain a generally lower migratory connectivity than non-passerines due to larger unpredictability of conditions during migration and in the nonbreeding grounds (Cresswell 2014).

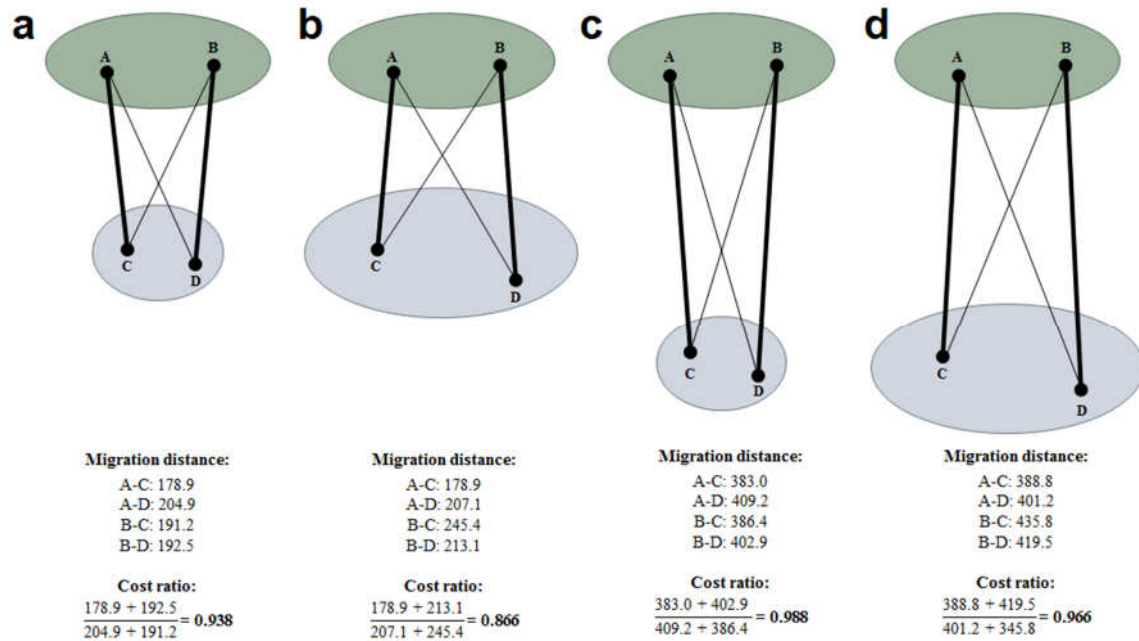


Figure S1. Schematic diagram showing how migration cost potentially underpins the effect of migration distance and nonbreeding population spread on the strength of migratory connectivity, as predicted by theory and assuming that migration cost is linearly related to migration distance (Somveille et al. 2021). Dark and light grey ellipses depict breeding and nonbreeding ranges, respectively. Dots represent two breeding and nonbreeding locations per seasonal range (each is indicated by a different letter). Population spread within a seasonal range can be considered as the linear distance between the two locations in same range (not shown). Migration distance is the line connecting a breeding to a nonbreeding site (either thick line in case of strong migratory connectivity or thin line for weak migratory connectivity). Four scenarios, with populations having the same breeding population spread, are shown: (a) short distance and small nonbreeding spread; (b) short distance and large nonbreeding spread; (c) long distance and small nonbreeding spread; (d) long distance and large nonbreeding spread. For each scenario, migration distances between two breeding and two wintering locations are calculated. Migration distances are summed for each situation (strong migratory connectivity vs weak migratory connectivity), and the ratio (cost ratio) between the two sums is derived. Both when migration distance increases (a vs c, and b vs d) and when nonbreeding population spread decreases (b vs a, and d vs c), the cost ratio increases, meaning that the cost of migration tends to be more similar between the two situations (strong vs weak migratory connectivity), and therefore population mixing (lower migratory connectivity) is more likely to occur.

Appendix S2. *Selection of ringing encounters*

Ringing data are largely heterogeneous as to individual encounter conditions and circumstances, such as those of birds in poor health status or kept in captivity or manipulated for long, or those for which the place/time of recovery was not determined accurately, therefore preliminary data filtering is necessary to reduce heterogeneity (e.g. Paradis et al. 1998). Moreover, ringing encounters collected outside species-specific breeding or nonbreeding grounds and periods, potentially resulting from occasional movements, would introduce spatial and temporal biases in migratory connectivity analysis (e.g. Somveille et al. 2021). Hence, we implemented a robust data selection procedure to discard ringing encounters potentially affecting our estimates of migratory connectivity. Our conservative approach relied on 21 condition-based selection criteria and applied a spatiotemporal masking for each species, discarding on average 97.2% of ringing encounters per species (range: 58% – 99%; see Ambrosini et al. 2016 for a similar data selection procedure).

First, we selected ringing encounter previously validated for their usage in the European-African Bird Migration Atlas (EURING level for ‘use.for.atlas’ = TRUE). Then, following previous studies on ringing encounters obtained from the EURING Data Bank (e.g. Paradis et al. 1998; Ambrosini et al. 2016), we implemented condition-based criteria in order to reduce encounter heterogeneity. In details, we removed:

- 1) birds that were not found freshly dead, or birds that were in poor condition or had an accident when ringed, or birds that were alive and probably healthy but taken into captivity (EURING levels for ‘condition’ = 3, 4, 5, 6);
- 2) birds that were kept for more than 13 hours during ringing, or birds that have been moved or held extensively during ringing, or those hand reared (EURING levels for ‘manipulated’ = C, F, T, M, H);
- 3) birds that were moved unintentionally by man or other agency, or intentionally by man, or moved by water e.g. found on shoreline (EURING levels for ‘moved’ = 2, 4, 6);
- 4) birds for which the dates of ringing and/or recovery were not recorded accurately to the nearest 1 week for both the ringing and the finding date (EURING levels for ‘date accuracy’ = 4, 5, 6, 7, 8);
- 5) birds for which the places of ringing and/or recovery were not recorded accurately to the nearest 100 km for the ringing or finding places (EURING levels for ‘coordinates accuracy’ = 6, 7, 8, 9).

Then, we applied a spatiotemporal masking using species-specific criteria in order to remove encounters in non-stationary periods or found within occasional ranges, thus retaining all individuals at their breeding and nonbreeding grounds. Following the phenology reported by Cramp (1998), we identified for each species an “extended” breeding period, corresponding to that spanning the breeding of the whole species (even though it may still include *en route* birds for some populations), a “focal” breeding stationary period from the end of spring migration for the latest population to the onset of autumn migration of the earliest population, and a nonbreeding stationary period from the end of autumn migration of the latest population until the onset of spring migration of the earliest population (Table S1). We then removed:

6) encounters found out of the focal breeding and the nonbreeding stationary periods. However, we retained encounters of chicks unable to fledge or of individuals found at nest (EURING levels for ‘catching method’ = N and for ‘age by scheme’ = 1) if they occurred during the extended breeding period of each species because we considered that they have occurred in the breeding area of the individual.

Moreover we identified breeding, resident and nonbreeding stationary ranges for each species according to the distribution maps provided by BirdLife International (2019), removing:

7) encounters outside the breeding and resident ranges during the focal or the extended breeding periods;

8) encounters outside the nonbreeding and resident ranges during the nonbreeding stationary period.

After the above step, we checked and manually discarded a few encounters of long-distance migrants remaining outside the European-African migration system, even though within their nonbreeding stationary ranges, to avoid spatial biases in migratory connectivity analysis (e.g. encounters of *Larus* spp. in North America; *Platalea leucorodia* in India; *Sterna hirundo* in Australia and South America). Eventually, we also removed:

9) repeated encounters for the same individual in either the breeding or the nonbreeding range, if any, by retaining the earliest encounter in order to minimise age-bias.

10) individuals that, after the previous steps of data selection, did not have one observation in both the breeding and the nonbreeding ranges.

Table S1. Species-specific phenology reported by Cramp (1998): the first integer represents the month, the second one represents the monthly quarter. An exception was made for *Turdus merula*, for which we considered different periods than those reported by Cramp (1998), which were referred mainly to British populations, particularly for the start of the nonbreeding period (Santos 1982; Olioso 1995; Main 2002; Andreotti et al. 2010).

Species	Extended breeding period		Focal breeding period		Nonbreeding period	
	Start	End	Start	End	Start	End
<i>Anas crecca</i>	3-4	8-2	6-1	7-3	12-3	2-2
<i>Erithacus rubecula</i>	3-1	7-3	5-2	6-4	11-3	2-3
<i>Hirundo rustica</i>	4-4	10-2	6-1	6-4	12-3	1-4
<i>Phalacrocorax carbo</i>	2-4	10-2	4-3	6-2	12-1	1-2
<i>Cygnus olor</i>	4-2	11-2	4-4	8-4	1-1	2-4
<i>Larus argentatus</i>	4-2	8-4	5-3	8-2	12-2	2-2
<i>Larus ridibundus</i>	4-1	9-1	5-2	6-2	12-1	2-2
<i>Turdus merula</i>	2-4	9-2	5-2	7-2	12-1	2-2
<i>Parus caeruleus</i>	4-1	7-3	5-1	6-1	12-1	1-4
<i>Parus major</i>	3-2	7-4	5-1	6-1	12-1	1-4
<i>Anas platyrhynchos</i>	2-1	11-4	5-3	7-4	12-1	1-4
<i>Anser albifrons</i>	6-2	9-1	6-3	8-3	1-1	2-3
<i>Anser anser</i>	3-4	8-1	4-3	7-3	12-3	1-3
<i>Accipiter gentilis</i>	4-1	8-2	6-1	7-3	12-3	2-2
<i>Calidris alpina</i>	5-4	8-4	6-2	7-1	11-3	3-1
<i>Carduelis chloris</i>	4-4	7-2	5-3	7-1	12-1	2-4
<i>Carduelis spinus</i>	4-3	8-3	5-3	7-4	12-3	2-2
<i>Haematopus ostralegus</i>	3-4	9-3	5-1	6-2	11-1	1-4
<i>Larus canus</i>	5-3	9-1	6-1	7-2	12-2	2-2
<i>Larus fuscus</i>	4-4	9-1	6-1	6-4	12-2	1-4
<i>Larus marinus</i>	4-3	8-4	5-2	8-2	12-2	2-2
<i>Ciconia ciconia</i>	4-2	8-2	5-3	7-4	12-1	1-4
<i>Cygnus cygnus</i>	5-3	9-4	6-3	9-2	1-1	2-3
<i>Falco tinnunculus</i>	3-4	8-2	6-1	7-3	12-3	2-2
<i>Haliaeetus albicilla</i>	4-2	9-2	6-1	8-4	12-3	2-1
<i>Larus melanocephalus</i>	5-2	8-3	6-1	6-4	12-1	2-4
<i>Sturnus vulgaris</i>	4-2	6-2	5-1	6-1	12-1	1-4
<i>Turdus philomelos</i>	2-4	9-1	5-3	8-2	11-2	2-3
<i>Phalacrocorax aristotelis</i>	2-3	10-1	4-3	6-4	12-1	1-1
<i>Platalea leucorodia</i>	4-1	9-2	6-1	7-3	11-4	1-4
<i>Riparia riparia</i>	4-4	8-4	6-1	6-4	12-1	2-3
<i>Sylvia atricapilla</i>	4-3	8-1	6-3	7-2	12-1	1-3
<i>Tyto alba</i>	2-4	12-1	4-1	10-4	12-2	2-3
<i>Alauda arvensis</i>	3-3	8-4	5-1	7-4	12-1	1-3
<i>Anas acuta</i>	4-1	8-3	6-1	7-4	12-3	1-4

<i>Anser brachyrhynchus</i>	5-2	8-4	5-3	8-2	12-1	3-2
<i>Anser fabalis</i>	5-3	9-1	6-1	8-3	1-1	2-4
<i>Aythya ferina</i>	4-3	8-2	5-3	7-4	12-2	1-4
<i>Aythya fuligula</i>	5-2	9-3	5-3	8-4	1-1	2-3
<i>Aythya marila</i>	5-3	9-3	5-4	8-2	12-1	2-3
<i>Branta canadensis</i>	3-3	6-4	4-1	7-2	12-1	1-4
<i>Bucephala clangula</i>	5-2	9-2	5-3	8-3	1-1	2-2
<i>Columba oenas</i>	4-3	10-4	5-1	8-2	12-1	1-4
<i>Columba palumbus</i>	2-3	12-1	5-2	8-3	12-2	2-2
<i>Corvus corone</i>	4-1	6-2	5-1	5-4	11-4	2-2
<i>Corvus frugilegus</i>	3-1	5-3	4-2	5-1	12-1	2-2
<i>Corvus monedula</i>	4-2	6-3	4-4	6-1	11-3	2-2
<i>Fulica atra</i>	2-4	10-1	5-3	8-2	12-2	2-3
<i>Gallinago gallinago</i>	3-4	9-3	5-1	7-2	12-1	1-4
<i>Gallinula chloropus</i>	4-3	8-3	5-3	7-2	12-3	2-3
<i>Garrulus glandarius</i>	3-4	7-4	6-2	6-4	11-2	3-3
<i>Limosa limosa</i>	4-1	8-3	5-2	6-3	11-1	2-1
<i>Anas penelope</i>	5-3	8-4	6-1	8-2	12-3	2-4
<i>Anas strepera</i>	4-3	8-3	5-3	7-4	12-3	2-4
<i>Mergus merganser</i>	5-2	9-3	6-2	9-1	1-1	2-4
<i>Netta rufina</i>	4-4	8-3	5-3	8-1	12-2	2-2
<i>Numenius arquata</i>	4-4	9-1	5-2	6-4	11-3	2-3
<i>Pluvialis apricaria</i>	5-2	9-3	6-3	7-4	1-1	2-2
<i>Scolopax rusticola</i>	3-2	10-3	5-2	8-3	12-1	2-3
<i>Somateria mollissima</i>	4-3	9-3	5-2	8-4	12-2	2-3
<i>Anas clypeata</i>	4-4	8-3	5-3	8-1	12-2	2-2
<i>Streptopelia decaocto</i>	5-1	10-1	6-1	7-3	12-1	2-1
<i>Tetrao urogallus</i>	4-3	9-2	5-3	8-2	9-3	4-2
<i>Tringa totanus</i>	3-4	8-3	5-1	6-2	11-1	2-2
<i>Turdus iliacus</i>	4-4	8-1	6-2	7-2	12-2	2-3
<i>Turdus pilaris</i>	4-4	8-4	5-2	8-1	12-2	2-3
<i>Turdus viscivorus</i>	3-3	7-3	4-4	6-4	11-2	2-2
<i>Vanellus vanellus</i>	3-1	9-2	4-2	6-2	12-2	1-3
<i>Carduelis flammea</i>	4-3	7-4	5-3	7-2	12-3	2-3
<i>Accipiter nisus</i>	4-4	8-2	6-1	7-4	12-1	2-3
<i>Acrocephalus melanopogon</i>	4-4	8-2	6-1	7-4	12-2	2-2
<i>Aegithalos caudatus</i>	4-2	9-1	5-2	8-1	11-2	3-3
<i>Aegolius funereus</i>	2-4	8-3	5-1	7-4	12-1	2-4
<i>Aix galericulata</i>	4-3	8-1	4-4	7-3	8-2	4-2
<i>Alca torda</i>	4-3	8-2	5-2	7-2	11-1	2-2
<i>Alcedo atthis</i>	4-3	10-1	6-1	7-2	12-2	2-4
<i>Anthus pratensis</i>	3-4	8-4	5-3	6-2	12-1	1-4
<i>Aquila chrysaetos</i>	3-1	8-2	4-2	7-4	12-2	2-4
<i>Ardea cinerea</i>	3-3	8-2	4-1	6-2	12-1	1-2
<i>Asio otus</i>	2-4	7-4	6-3	7-2	12-3	2-3
<i>Athene noctua</i>	3-3	8-3	4-2	7-4	8-4	3-2
<i>Branta leucopsis</i>	5-4	8-4	6-1	8-2	1-1	3-3

<i>Buteo buteo</i>	3-4	8-1	5-3	7-3	12-1	1-4
<i>Carduelis carduelis</i>	5-1	8-4	5-4	8-1	12-2	2-4
<i>Certhia brachydactyla</i>	3-4	7-4	4-3	7-2	8-1	3-3
<i>Certhia familiaris</i>	3-4	7-4	5-1	6-4	12-1	2-4
<i>Cettia cetti</i>	6-1	8-4	6-3	8-2	11-1	4-4
<i>Charadrius alexandrinus</i>	4-2	9-1	5-4	6-4	11-3	2-2
<i>Charadrius hiaticula</i>	3-4	9-3	5-3	7-4	12-1	1-4
<i>Cinclus cinclus</i>	2-4	9-1	6-1	8-2	11-1	1-4
<i>Coccothraustes coccothraustes</i>	4-2	8-4	4-3	8-3	12-2	1-4
<i>Corvus corax</i>	1-4	8-4	4-1	6-3	9-1	1-3
<i>Luscinia svecica</i>	4-4	8-2	6-2	7-4	12-1	1-4
<i>Dendrocopos major</i>	4-3	7-3	5-1	7-1	11-2	2-4
<i>Emberiza citrinella</i>	4-3	8-2	5-3	7-4	11-3	3-2
<i>Emberiza schoeniclus</i>	5-1	7-3	5-3	7-1	11-3	2-2
<i>Falco peregrinus</i>	5-1	8-3	5-3	7-4	11-3	2-3
<i>Fratercula arctica</i>	4-1	8-4	4-3	7-4	10-2	3-2
<i>Fringilla coelebs</i>	4-3	7-2	5-4	6-3	12-1	2-3
<i>Fringilla montifringilla</i>	5-2	7-3	6-2	7-1	11-3	2-3
<i>Glaucidium passerinum</i>	4-3	7-4	4-4	7-2	12-2	2-4
<i>Grus grus</i>	4-4	9-2	5-3	7-2	12-1	2-2
<i>Sterna caspia</i>	5-1	8-3	5-4	7-2	12-3	2-3
<i>Larus audouinii</i>	4-3	8-3	5-1	7-4	11-3	2-2
<i>Carduelis cannabina</i>	4-3	8-4	5-3	7-4	11-3	2-2
<i>Carduelis flavirostris</i>	4-1	8-3	5-3	7-4	12-3	2-3
<i>Milvus milvus</i>	3-4	7-4	5-3	7-2	12-1	1-4
<i>Sula bassana</i>	4-2	11-1	6-2	7-4	12-1	1-4
<i>Motacilla alba</i>	4-1	8-2	6-1	7-3	11-3	1-4
<i>Nucifraga caryocatactes</i>	2-4	7-4	4-1	5-4	11-1	2-3
<i>Pandion haliaetus</i>	4-3	8-1	6-1	7-4	12-1	2-3
<i>Panurus biarmicus</i>	3-3	7-1	4-3	6-3	12-1	2-3
<i>Passer hispaniolensis</i>	3-1	10-4	5-3	8-3	12-1	2-4
<i>Passer montanus</i>	4-1	9-2	4-4	8-2	11-3	3-3
<i>Parus ater</i>	4-2	7-4	4-4	6-3	10-3	2-4
<i>Phoenicurus ochruros</i>	4-3	7-4	5-1	7-1	11-3	2-3
<i>Phylloscopus collybita</i>	4-4	8-1	6-1	7-2	11-4	2-3
<i>Podiceps cristatus</i>	2-3	9-1	5-3	7-3	12-3	1-4
<i>Parus montanus</i>	4-3	8-1	5-3	6-1	12-1	3-1
<i>Prunella modularis</i>	3-1	9-2	6-1	8-2	11-3	2-3
<i>Pyrrhula pyrrhula</i>	4-3	8-3	5-2	7-3	12-1	2-3
<i>Recurvirostra avosetta</i>	4-2	9-1	5-3	7-2	11-2	2-2
<i>Regulus ignicapillus</i>	4-2	8-2	5-3	7-4	12-3	1-4
<i>Regulus regulus</i>	4-3	8-3	6-1	7-3	12-1	2-3
<i>Remiz pendulinus</i>	4-4	8-3	5-1	6-4	12-3	1-4
<i>Rissa tridactyla</i>	5-2	9-2	6-1	7-4	12-1	1-4
<i>Saxicola torquata</i>	4-2	8-2	6-1	7-4	11-4	1-3
<i>Serinus serinus</i>	4-1	8-2	5-1	7-3	11-2	2-3
<i>Sitta europaea</i>	3-4	7-3	5-1	6-2	11-1	3-3

<i>Sterna hirundo</i>	5-2	9-2	6-3	7-2	11-2	3-1
<i>Sterna albifrons</i>	5-2	9-1	6-1	7-2	11-2	3-1
<i>Strix aluco</i>	2-3	7-1	2-4	6-3	7-4	2-2
<i>Sylvia melanocephala</i>	3-3	7-2	5-1	5-4	1-1	2-2
<i>Tadorna tadorna</i>	4-3	9-1	5-1	8-3	1-1	2-2
<i>Sterna sandvicensis</i>	4-4	7-4	5-2	6-4	12-1	1-2
<i>Troglodytes troglodytes</i>	3-4	8-3	5-4	7-4	12-3	3-2
<i>Uria aalge</i>	4-4	8-1	5-1	7-2	12-1	1-4

Appendix S3. *Discrimination of strongly and weakly migratory geographical populations*

The distinction between migratory and non-migratory species or populations is particularly challenging for birds, where different types of migration are exhibited and large differences exist, even within populations of the same species (Chapman et al. 2011; Gilroy et al. 2016). In this work, we avoided to classify migratory vs resident geographical populations (i.e. clusters identified by the migratory connectivity analysis) on the basis of a cut-off migration distance, because many populations of birds are known to migrate even when migration distance is short, and migration distance is often population-specific as well as is influenced by various ecological and climatic drivers (Visser et al. 2009; Meller et al. 2016; Curley et al. 2020). Indeed, migration distance is only one amongst the many other characteristics that are used to define migration, such as periodicity or directionality of movements (Eyres et al. 2017). Consequently, we implemented a classification based on the inspection of the overall spatial pattern of individual positions observed in the nonbreeding stationary range, (i.e. after migration), relative to that found in the breeding range, i.e. prior to migration. For each geographical population, we first calculated the 95% minimum convex polygon (MCP) of individual locations in the breeding period (breeding MCP) and the 95% MCP of the same individual locations in the nonbreeding stationary period (nonbreeding MCP). We then overlapped the breeding and nonbreeding MCPs and classified those geographical populations for which the overlap was more than 75% of the area of the breeding MCP as weakly migratory. Populations were classified as strongly migratory otherwise. The distribution of the overlap values obtained from our data was clearly bimodal (Fig. S2), indicating that a dichotomous classification into strongly and weakly migratory populations is helpful to distinguish the ‘more’ from the ‘less mobile’ geographical populations. The presence of overlap between breeding and nonbreeding ranges has been already used previously as a criterion to discriminate, at the species level, full migrants, partial migrants and residents (Gilroy et al. 2016). Moreover, MCP has been used to quantify population spread of birds in the breeding and nonbreeding grounds (e.g. Blackburn et al. 2017; Burgess et al. 2020) and we should note that, in our case, the increase in MCP extent with increasing sample size (Burgess et al. 2020) would not affect the classification outcome because both the MCPs include exactly the same number of individuals.

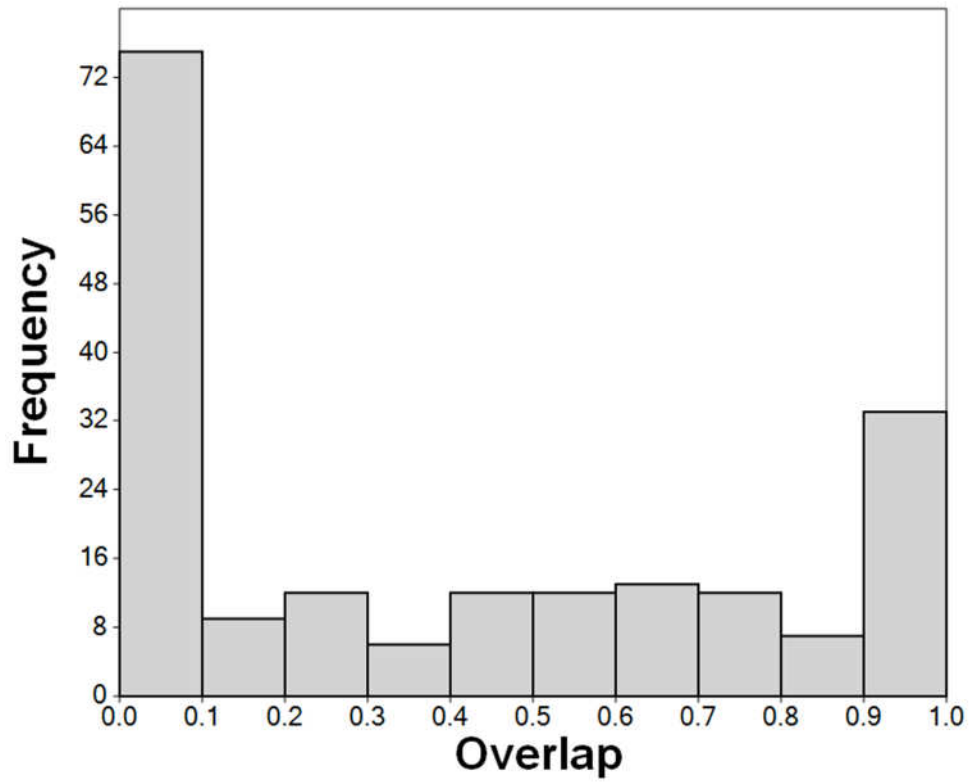


Figure S2. Frequency distribution of values reflecting the overlap between nonbreeding and breeding MCPs in our study populations.

Appendix S4. *Species investigated in phylogenetic comparative analysis*

Table S2. Number of geographical populations (i.e., clusters) and individuals for each bird species included in the phylogenetic comparative analysis of the strength of migratory connectivity.

Family	Species	N geographical populations	N individuals
Accipitridae	<i>Accipiter nisus</i>	6	3481
	<i>Aquila chrysaetos</i>	2	437
	<i>Buteo buteo</i>	1	3509
	<i>Haliaeetus albicilla</i>	2	2629
	<i>Milvus milvus</i>	2	862
Alaudidae	<i>Alauda arvensis</i>	1	53
Alcidae	<i>Alca torda</i>	2	521
	<i>Fratercula arctica</i>	2	193
Anatidae	<i>Anas acuta</i>	1	34
	<i>Anas clypeata</i>	1	278
	<i>Anas crecca</i>	1	305
	<i>Anas penelope</i>	3	147
	<i>Anas platyrhynchos</i>	1	6333
	<i>Anas strepera</i>	1	234
	<i>Anser anser</i>	3	157
	<i>Anser brachyrhynchus</i>	2	1089
	<i>Anser fabalis</i>	2	289
	<i>Aythya ferina</i>	1	552
	<i>Aythya fuligula</i>	2	1095
	<i>Branta leucopsis</i>	3	402
	<i>Bucephala clangula</i>	1	69
	<i>Cygnus cygnus</i>	2	529
	<i>Somateria mollissima</i>	3	1182
<i>Tadorna tadorna</i>	5	310	
Charadriidae	<i>Charadrius hiaticula</i>	1	42
	<i>Vanellus vanellus</i>	1	3646
Ciconiidae	<i>Ciconia ciconia</i>	2	3783
Columbidae	<i>Columba oenas</i>	2	345
	<i>Columba palumbus</i>	1	1522
Corvidae	<i>Corvus corone</i>	1	1264
	<i>Corvus frugilegus</i>	1	517
	<i>Corvus monedula</i>	9	1557
Emberizidae	<i>Emberiza schoeniclus</i>	2	937
Falconidae	<i>Falco peregrinus</i>	3	201

	<i>Falco tinnunculus</i>	5	7662
Fringillidae	<i>Carduelis cannabina</i>	1	491
	<i>Carduelis flammea</i>	2	202
	<i>Carduelis flavirostris</i>	2	66
	<i>Carduelis spinus</i>	2	1370
	<i>Coccothraustes coccothraustes</i>	7	571
	<i>Fringilla coelebs</i>	1	2682
	<i>Serinus serinus</i>	2	672
Gruidae	<i>Grus grus</i>	1	372
Haematopodidae	<i>Haematopus ostralegus</i>	1	2349
Hirundinidae	<i>Hirundo rustica</i>	2	96
Laridae	<i>Larus argentatus</i>	1	19,823
	<i>Larus canus</i>	1	3878
	<i>Larus fuscus</i>	1	5015
	<i>Larus marinus</i>	6	2380
	<i>Larus melanocephalus</i>	9	1099
	<i>Larus ridibundus</i>	1	27,479
	<i>Rissa tridactyla</i>	1	134
Motacillidae	<i>Anthus pratensis</i>	1	51
	<i>Motacilla alba</i>	2	439
Muscicapidae	<i>Erithacus rubecula</i>	2	6621
	<i>Luscinia svecica</i>	1	35
	<i>Phoenicurus ochruros</i>	2	306
	<i>Saxicola torquata</i>	2	65
Pandionidae	<i>Pandion haliaetus</i>	1	369
Paridae	<i>Panurus biarmicus</i>	2	145
Phalacrocoracidae	<i>Phalacrocorax aristotelis</i>	4	916
	<i>Phalacrocorax carbo</i>	1	2033
Phylloscopidae	<i>Phylloscopus collybita</i>	1	133
Rallidae	<i>Fulica atra</i>	9	3806
	<i>Gallinula chloropus</i>	2	528
Recurvirostridae	<i>Recurvirostra avosetta</i>	2	372
Remizidae	<i>Remiz pendulinus</i>	1	53
Scolopacidae	<i>Gallinago gallinago</i>	1	137
	<i>Limosa limosa</i>	2	165
	<i>Numenius arquata</i>	2	485
	<i>Scolopax rusticola</i>	1	518
	<i>Tringa totanus</i>	4	363
Sternidae	<i>Sterna hirundo</i>	2	1089
	<i>Sterna sandvicensis</i>	3	423

Strigidae	<i>Asio otus</i>	3	618
Sturnidae	<i>Sturnus vulgaris</i>	3	7038
Sulidae	<i>Sula bassana</i>	1	350
Sylviidae	<i>Sylvia atricapilla</i>	4	255
Threskiornithidae	<i>Platalea leucorodia</i>	7	817
Turdidae	<i>Turdus iliacus</i>	1	683
	<i>Turdus philomelos</i>	3	5137
	<i>Turdus pilaris</i>	1	1572
	<i>Turdus viscivorus</i>	1	542

Appendix S5. *Compilation of species-specific life-history traits*

Species-specific life-history traits entered as fixed effects in the meta-analysis were: diet breadth, habitat breadth, and body mass. Information on diet breadth was obtained from del Hoyo et al. (2017). We considered the following food sources: 1) terrestrial invertebrates, 2) aquatic invertebrates, 3) terrestrial vertebrates, 4) aquatic vertebrates, 5) fruits and berries, 6) sedges and seeds, 7) other plant materials (e.g. nectar, grass or aquatic plants) and counted the number of them representing a substantial contribution to a species diet to obtain an estimate of the diet breadth. Similarly, habitat breadth was estimated as the total number of primary habitat types exploited by a species, as reported in BirdLife (2020). Body mass was also compiled from BirdLife (2020).

Appendix S6. *Moderators entered in the phylogenetic model*

Table S3. Information on moderators initially considered as fixed effects for the phylogenetic mixed model concerning 191 geographical populations of 83 bird species. For relevant hypotheses, see Table 1 in the main text and Appendix S1.

Moderator (units)	Type	Transformation	Level	Notes
Mean migration distance (km)	Continuous	$\ln(\ln(x) + 1)$	Geographical population	Not collinear with nonbreeding latitude ($r = -0.31$) or nonbreeding population spread ($r = 0.54$)
Mean nonbreeding latitude ($^{\circ}$)	Continuous	–	Geographical population	Not collinear with migration distance ($r = -0.31$) or nonbreeding population spread ($r = -0.35$)
Mean nonbreeding population spread (km)	Continuous	$\ln(x)$	Geographical population	Not collinear with migration distance ($r = 0.54$) or nonbreeding latitude ($r = -0.35$)
Relative population spread (both linear and squared term)	Continuous	–	Geographical population	Not collinear with nonbreeding population spread ($r = -0.21$)
Body mass (grams)	Continuous	–	Species	–
Habitat breadth	Integer	–	Species	Not collinear with diet breadth ($r = 0.14$)
Diet breadth	Integer	–	Species	Not collinear with habitat breadth ($r = 0.14$)
Passerine or non-passerine	Binary	–	Species	–

Appendix S7. Preliminary data exploration and model performance

Visual inspection of the data showed that Z_r values varied non-linearly with mean migration distance. In contrast, the relationship was linear after double-natural logarithm transformation (Fig. S3). The variance of Z_r values also markedly differed between passerine and non-passerines (Fig. S4). Z_r values predicted from the full model showed a good agreement with observed ones indicating a proper fit of the model (Fig. S5).

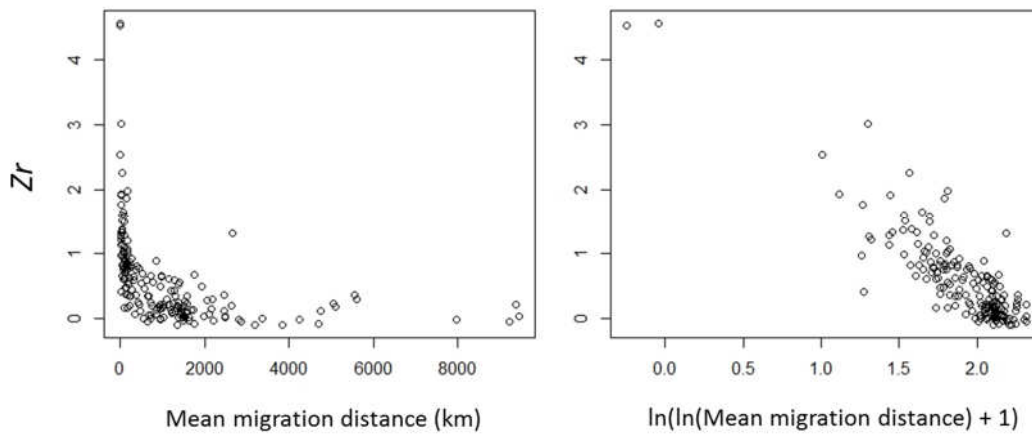


Figure S3. Z_r values according to mean migration distance before and after the double logarithmic transformation. Note that a constant term (1) was added to avoid negative values in the second logarithm.

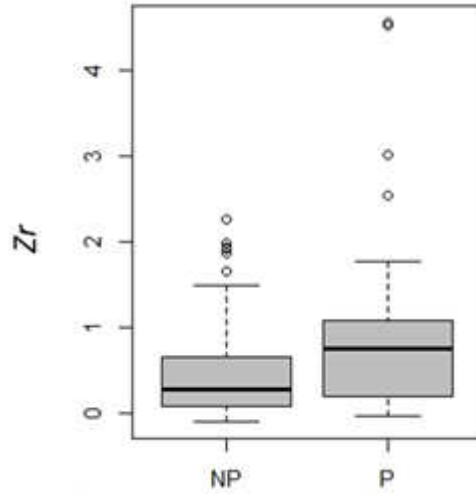


Figure S4. Z_r values of passerine (P) and non-passerine (NP) birds showing variance heterogeneity between groups.

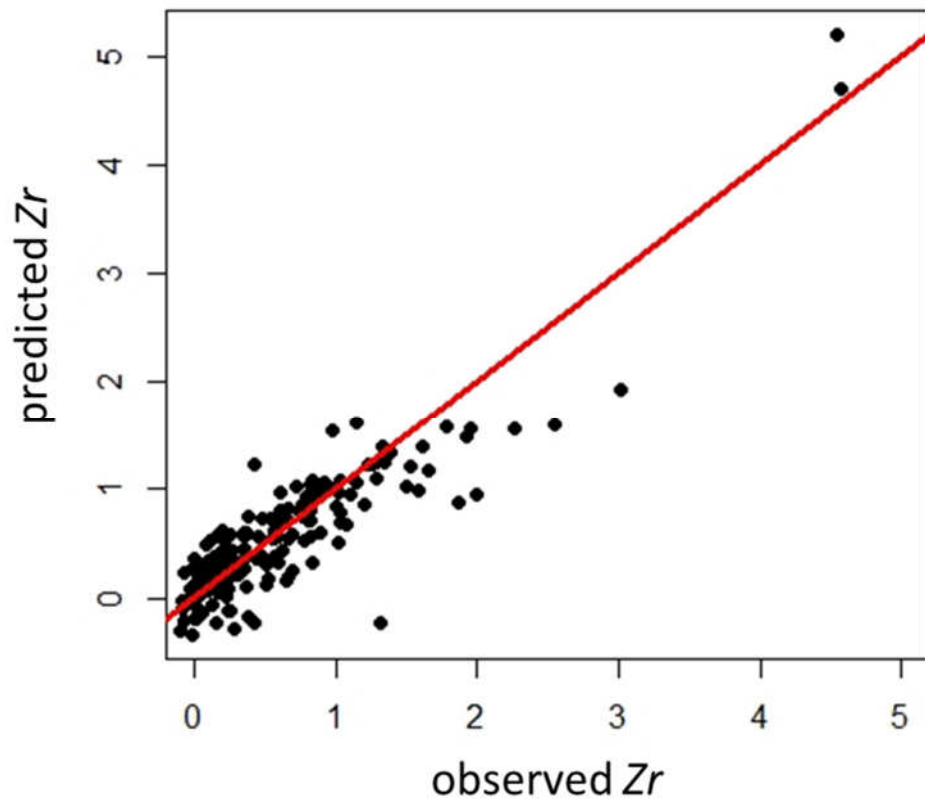


Figure S5. Model performance evaluated through inspection of predicted vs. observed Z_r values ($R^2 = 0.80$). Diagonal line is the 1 to 1 line.

Appendix S8. Modelling the annual surplus in resource availability due to migration strategy

Somveille et al. (2019) have shown that birds travelling farther distances exploit annually better access to resources due to their migration strategy. Hence, stronger connectivity may occur for populations wintering farther south, after controlling for the other geographic predictors in our model, because they can exploit larger amount of resources. To test for this hypothesis, we re-run our analysis to explicitly account for the benefit in resource availability gained annually by birds.

We followed the approach described by Somveille et al. (2019) to assess the annual surplus in resources available to birds. However, we note that these authors first calculated this measure and then took the opposite for their analyses, thus ending up calculating an index of resource scarcity, while we use this measure directly, as we aimed at considering resource availability. We used the normalized difference vegetation index (NDVI), as a general proxy of the resources available to bird species (e.g. food, roosting sites; Somveille et al. 2015; 2019). Similarly to Somveille et al. (2019), we considered only land bird species for this analysis (N = 145 populations of 66 species), because NDVI values would not be representative of resource availability at sea, where marine species spend the nonbreeding period. We obtained NDVI monthly averages, for the period 2000-2019, at a resolution of 0.05° (MOD13C2 Version 6 product; Didan 2015). Only land areas were considered for the calculation of NDVI, through a spatial masking discarding marine areas and water bodies. Previous studies assumed that the resources available to terrestrial birds are related to the surplus in NDVI, i.e. the difference between NDVI in the season when the migrant birds are present and the season when they are absent (Herrera 1978, Hurlbert and Haskell 2003, Dalby et al. 2014, Somveille et al. 2015; 2019). For each geographical population, we calculated the mean NDVI experienced in both the breeding and the nonbreeding ranges when the population is present (i.e., between May-August for breeding and between November-February for nonbreeding periods; Somveille et al. 2015; 2019) and the mean NDVI over the same ranges but when the population is absent (i.e., between November-February for breeding and between May-August for nonbreeding periods; Somveille et al. 2015; 2019). Specifically, we took the average of NDVI values across all pixels over a 'sample population area' corresponding to the range of 75% individuals' locations in each seasonal range (to avoid considering NDVI exploited by individuals located at the borders of each geographical population; mean \pm SE, breeding range: 7837 \pm 1046 pixels/population; nonbreeding range: 6701 \pm 862

pixels/population). For each population and for both seasonal grounds, we then calculated the difference between the mean NDVI value when the species is present and the mean NDVI value when the species is absent, i.e. the resource surpluses each population gained in both seasons (positive values indicate that a resource surplus is available to the population, whereas negative values imply a deficit; Somveille et al. 2019). Finally, we summed the two seasonal surpluses to obtain a measure of the annual surplus in resources available to birds (Somveille et al. 2019). Most of our study populations exploited a resource deficit in the nonbreeding grounds (85% populations) and a resource gain in the breeding grounds (97% populations), leading to an overall annual gain for most (83%) populations, strongly supporting previous findings (cf. Bonnet-Lebrun et al. 2021).

In our models fitted on both weakly and strongly migratory populations and strongly migratory populations only, we replaced the nonbreeding latitude with the annual resource surplus. While other main results were unaffected, the resource surplus gained by each population annually showed a positive effect on the strength of migratory connectivity (Table 2b, main text, and Table S4b, Appendix S9), likely explaining why populations wintering farther south showed stronger migratory connectivity (see Discussion, main text). Model performance (observed vs. predicted values: $R^2 = 0.81$ when considering weakly and strongly migratory populations; $R^2 = 0.68$ when considering strongly migratory populations only) and diagnostics (Appendix S10) were robust and consistent with those of the model including the nonbreeding latitude.

Appendix S9. *Analysis excluding weakly migratory populations*

Our phylogenetic mixed models were re-run by excluding the geographical populations classified as weakly migratory. For the model without moderators, the results confirmed that migratory connectivity was moderate and significantly larger than zero (estimated $Zr = 0.397 \pm 0.083$ SE, $t_{82} = 4.769$, $P < 0.001$, corresponding to $r_M = 0.377$, 95% CI: 0.229 – 0.510; Fig. 2 in main text). In this analysis, we found no significant phylogenetic signal in the strength of migratory connectivity ($H^2 = 0.146$, $\chi^2 = 2.543$, $df = 1$, $P = 0.111$).

For the model with moderators, results confirmed the negative effect of migration distance, the positive effect of population spread and the negative effect of the mean nonbreeding latitude on the strength of migratory connectivity (Table S4a), whereas the quadratic effect of the ratio between the breeding and nonbreeding population spread and the effect of habitat breadth were not significant (Table S4a). Also in this case, there was no phylogenetic signal on migratory connectivity ($H^2 = 0.086$, $\chi^2 = 1.006$, $df = 1$, $P = 0.316$), and there was significant residual heterogeneity ($Q_E = 2490.710$, $df = 140$, $P < 0.001$). Replacing the nonbreeding latitude with the annual resource surplus available to birds (Appendix S8) provided qualitatively identical results, showing that connectivity increased with better access to resources (Table S4b). Both the alternative models showed good performance (observed *vs.* predicted values: $R^2 = 0.66$ and $R^2 = 0.69$, respectively) and the diagnostics indicated that no relevant deviation from assumptions occurred (Appendix S10).

Table S4. (a) Parameters estimated from the phylogenetic mixed model explaining the strength of migratory connectivity (as Fisher Z-transformation of r_M value) across 150 strongly migratory populations of 83 species. Transformations were applied to ‘Migration distance’ and ‘Nonbreeding population spread’ (Appendix S6-S7), while the second order polynomial term of ‘Relative population spread’ was included to account for quadratic effects (Table 1). All moderators are mean-centered and scaled to 1 SD. An asterisk marks significant ($P < 0.05$) moderators. In (b), ‘Nonbreeding latitude’ is replaced with ‘Annual resource surplus (NDVI)’ and the model was fitted to data on land birds only (Appendix S8, for details).

	Moderator	Coefficient	SE	t	df	P
a.	Intercept	0.404	0.042	9.522	73	< 0.001 *
	Migration distance (km)	-0.377	0.014	-26.957	140	< 0.001 *
	Nonbreeding latitude (°)	-0.038	0.012	-3.184	140	0.002 *
	Nonbreeding population spread (km)	0.044	0.017	2.494	140	0.014 *
	Relative population spread	-0.006	0.023	-0.265	140	0.791
	Relative population spread ²	0.003	0.026	0.098	140	0.918
	Body mass (kg)	-0.012	0.023	-0.515	73	0.608
	Habitat diversity	0.035	0.024	1.444	73	0.153
	Diet diversity	0.027	0.021	1.282	73	0.204
	Passerine	-0.009	0.030	-0.282	73	0.779
b.	Intercept	0.438	0.036	12.229	56	< 0.001 *
	Migration distance (km)	-0.465	0.023	-20.142	101	< 0.001 *
	Annual resource surplus (NDVI)	0.051	0.015	3.403	101	0.001 *
	Nonbreeding population spread (km)	0.098	0.025	3.903	101	< 0.001 *
	Relative population spread	0.019	0.028	0.671	101	0.503
	Relative population spread ²	-0.013	0.032	-0.403	101	0.688
	Body mass (kg)	-0.012	0.029	-0.405	56	0.687
	Habitat diversity	0.042	0.027	1.520	56	0.134
	Diet diversity	0.025	0.025	1.011	56	0.316
	Passerine	-0.017	0.032	-0.542	56	0.590

Appendix S10. Model diagnostics

Although this study does not represent a meta-analysis, as information were not retrieved from the literature, we applied a set of techniques typical of meta-analyses to assess the robustness of the results. Indeed, these data are, essentially, based on ringing data, and it is well known that some species or some geographical populations may be under or overrepresented due to the large temporal and spatial variability in encounter probability. We argued that these processes may generate biases in the data similar to those deriving from publication bias in typical meta-analyses and we thus assessed the robustness of the results. Rosenthal's fail-safe number was always very large in all the analyses (all geographical populations: 1,787,814; $P < 0.001$; all geographical populations of land bird species: 1,241,064; $P < 0.001$; strongly migratory populations only: 561,658; $P < 0.001$; strongly migratory populations of land bird species only: 338,970; $P < 0.001$). In addition, funnel plots (Fig. S6) were rather symmetric (rank correlation test for funnel plot asymmetry; all geographical populations: Kendall's tau = 0.061, $P = 0.208$; all geographical populations of land bird species: Kendall's tau = 0.046, $P = 0.416$; strongly migratory populations only: Kendall's tau = 0.085, $P = 0.123$; strongly migratory populations of land bird species only: Kendall's tau = 0.030, $P = 0.641$), and the intercepts of Egger's regressions were not significant (all geographical populations: $t_{189} = -0.230$, $P = 0.819$; all geographical populations of land bird species: $t_{143} = 0.531$, $P = 0.596$; strongly migratory populations only: $t_{148} = 0.153$, $P = 0.879$; strongly migratory populations of land bird species only: $t_{109} = 1.205$, $P = 0.231$). These diagnostics thus indicate that the results of our analyses are robust.

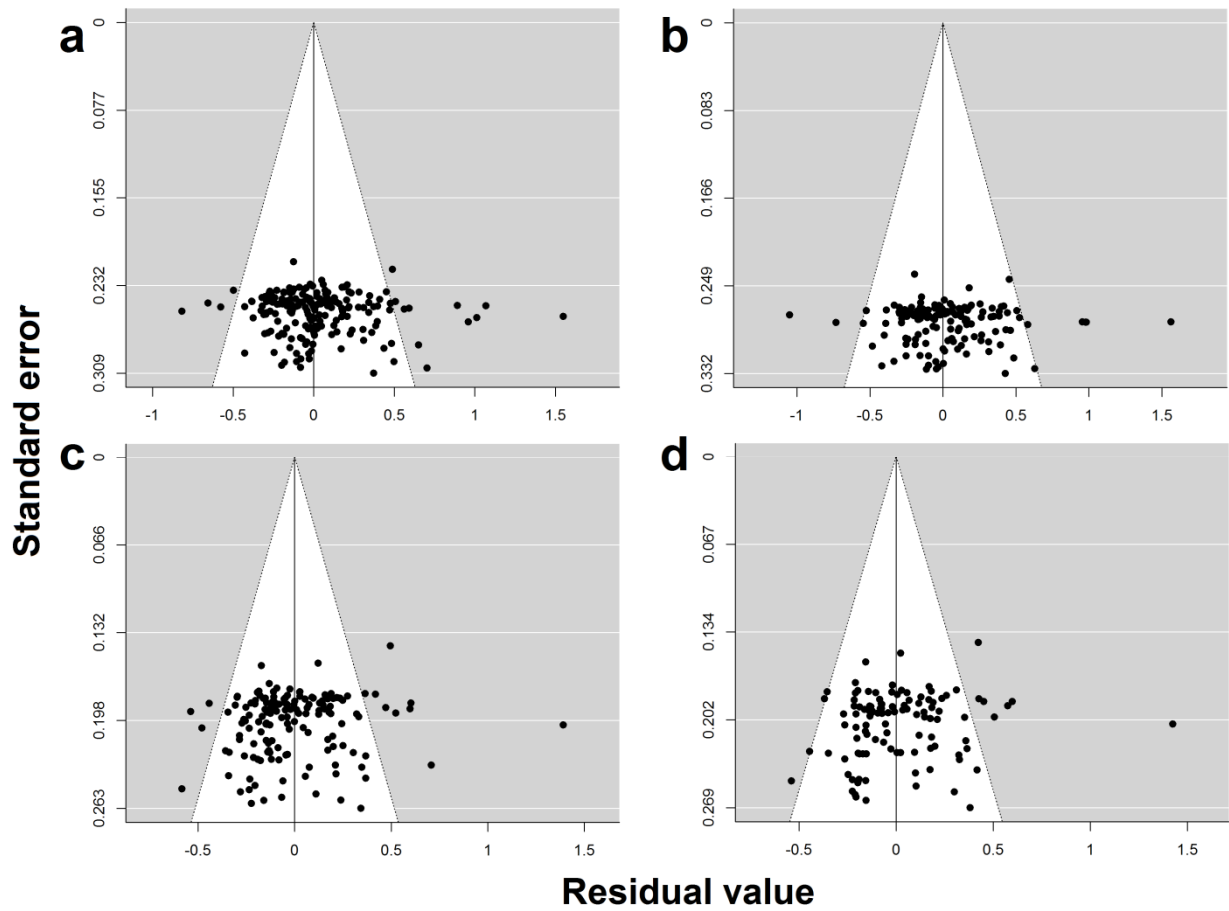


Figure S6. Funnel plots for the analyses conducted on all geographical populations (a), all geographical populations of land bird species (b), strongly migratory populations (c) and strongly migratory populations of land bird species (d).

Appendix S11. *Analysis testing the effect of dispersal ability on migratory connectivity*

Several weakly migratory populations showed a weaker migratory connectivity than that expected for their relatively short mean migration distance (e.g. *Alca torda*, *Fulica atra*, *Panurus biarmicus*; see Fig. 2, main text), implying high seasonal mobility within population range for these species. To evaluate whether this pattern may be due to some degree of dispersal (e.g. post-breeding dispersal), we re-run our model concerning both strongly and weakly migratory populations by including an additional predictor that would be able to account for interspecific differences in dispersal ability. We used the species-specific data on avian dispersal ability available from Sheard et al. (2021). Considering 10,338 bird species, this study has shown that avian dispersal ability was strongly predicted by the hand-wing-index (HWI), as a standardised biometric index of dispersal (see Sheard et al. 2021, and references therein). When we included this predictor, our model's results were unaffected, and HWI did not influence the strength of migratory connectivity (coefficient estimate \pm SE: 0.008 ± 0.034 ; $t_{72} = 0.228$; $P = 0.820$; observed vs predicted values: $R^2 = 0.80$).

Appendix S12. *Sensitivity analysis according to spatially-uneven sampling of ringing-recoveries in the nonbreeding ground and reduced sample size*

For each species, we performed a sensitivity analysis by rarefying the overall sample of individuals according to a spatially stratified subsampling, to assess whether our estimates of migratory connectivity were affected by uneven sampling in the nonbreeding range. Given that reporting rates of ring recoveries (i.e., sampling effort) differ between countries (Korner-Nievergelt et al. 2010), the spatial strata were represented by countries to account for geographic variation in the sampling effort. We performed a subsampling where the sampling probability was inversely proportional to the number of observations recorded in each country in the nonbreeding range. Thus, our stratified sampling assigned a lower sampling probability to countries with a greater number of records in the nonbreeding period, testing the robustness of migratory connectivity analysis in a situation corresponding to a spatially unbalanced sampling in the nonbreeding range. For each species, the sample of records was rarefied at the minimum possible sample size used in our analysis, i.e. 30 individuals. For two species having 30 individuals in the original dataset, the sample was rarefied at 29 individuals. Individuals were drawn from the original dataset without replacement. For each species, we simulated 100 different datasets and performed the migratory connectivity analyses. Simulations were implemented in R 3.6.2. We investigated the potential effects of uneven sampling in the nonbreeding range coupled with reduced sample size on the estimate of migratory connectivity strength, i.e. the Mantel correlation coefficient (r_M), as well as on the power of the Mantel permutation test (i.e., the relative frequency of simulations showing significant connectivity, if the analysis on the whole sample of that species was significant; the latter included $N = 78$ species). For each simulated dataset, we calculated Δr_M as the absolute value of the difference between the r_M value obtained from the simulation and that obtained from the original dataset. For each species, we averaged Δr_M values across the simulated datasets (to obtain mean Δr_M) and calculated the power of the Mantel test as the proportion of simulations showing significant migratory connectivity. Hence, we tested whether mean Δr_M and the power were associated to the mean nonbreeding latitude ($^\circ$). If low sample size coupled with uneven sampling in the nonbreeding range tends to affect migratory connectivity estimates and the power of the analysis, both Δr_M and the power should be correlated to nonbreeding latitude, indicating larger errors and/or lower power at the southernmost or northernmost latitudes.

For most (68%) species having their sample size reduced to the minimum number of individuals with uneven sampling in the nonbreeding range, we found that the mean Δr_M was still below 0.15 (corresponding to an error of about 15% on the possible range of r_M). Also, for 70% species among those showing significant connectivity, the power of the Mantel test was still above the 80% threshold. Most importantly, neither the mean Δr_M nor the power were correlated to nonbreeding latitude (Δr_M : $r = 0.15$, $P = 0.160$; power: $r = 0.15$, $P = 0.202$), suggesting that biases were unlikely to occur more often for species wintering farther south or farther north.

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