

Migratory connectivity analysis

by EURING Migration Atlas

Larus melanocephalus (EURING code 05750)

1.1 Connectivity between individuals

The analysis evaluated 1099 individuals (2198 encounters) filtered from a total of 65661 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from clustering, with a number of first-level clusters = 9 (Table 05750-1; Figure 05750-1).

Table 05750-1. Results from the migratory connectivity analysis. For each cluster, the degree of connectivity (r_M), its statistical significance (p-value) and 95% confidence interval limits are shown. When the p-value is less than or equal to 0.1, the degree of clustering structure (oasw) and the best number of clusters identified are reported.

Cluster name	Level of clustering	N individuals	Migratory connectivity (r_M)	p-value	Lower 95% confidence limit	Upper 95% confidence limit	Best number of clusters	oasw
0	0	1099	0.346	0.001	0.320	0.377	9	0.533
1	1	182	0.077	0.033	-0.008	0.184	9	0.567
2	1	55	0.128	0.016	0.010	0.321	9	0.600
3	1	72	0.116	0.065	-0.069	0.323	8	0.700
4	1	79	0.025	0.349	-0.123	0.223	-	-
5	1	171	0.013	0.263	-0.025	0.064	-	-
6	1	198	0.135	0.001	0.028	0.249	9	0.808
7	1	135	0.089	0.096	0.004	0.472	2	0.694
8	1	93	-0.001	0.447	-0.128	0.168	-	-
9	1	114	0.232	0.050	0.000	0.417	7	0.790
11	2	57	-0.054	0.565	-0.106	0.136	-	-
12	2	27	0.310	0.056	-0.115	0.786	7	0.676
13	2	21	-0.093	0.962	-0.136	0.190	-	-
14	2	6	-	-	-	-	-	-
15	2	13	-	-	-	-	-	-
16	2	31	0.441	0.038	0.198	0.739	4	0.823
17	2	10	-	-	-	-	-	-
18	2	6	-	-	-	-	-	-
19	2	11	-	-	-	-	-	-
21	2	3	-	-	-	-	-	-
22	2	9	-	-	-	-	-	-
23	2	9	-	-	-	-	-	-
24	2	11	-	-	-	-	-	-
25	2	7	-	-	-	-	-	-
26	2	5	-	-	-	-	-	-
27	2	5	-	-	-	-	-	-
28	2	4	-	-	-	-	-	-

Cluster name	Level of clustering	N individuals	Migratory connectivity (r_M)	p-value	Lower 95% confidence limit	Upper 95% confidence limit	Best number of clusters	oasw
29	2	2	-	-	-	-	-	-
31	2	1	-	-	-	-	-	-
32	2	3	-	-	-	-	-	-
33	2	11	-	-	-	-	-	-
34	2	20	-0.093	0.420	-0.148	0.675	-	-
35	2	17	-	-	-	-	-	-
36	2	14	-	-	-	-	-	-
37	2	3	-	-	-	-	-	-
38	2	3	-	-	-	-	-	-
61	2	2	-	-	-	-	-	-
62	2	28	-0.071	0.408	-0.121	-0.009	-	-
63	2	65	0.014	0.240	-0.106	0.153	-	-
64	2	27	-0.049	0.526	-0.158	0.129	-	-
65	2	38	-0.066	0.669	-0.113	0.155	-	-
66	2	14	-	-	-	-	-	-
67	2	11	-	-	-	-	-	-
68	2	3	-	-	-	-	-	-
69	2	10	-	-	-	-	-	-
71	2	118	0.049	0.153	-0.013	0.118	-	-
72	2	17	-	-	-	-	-	-
91	2	7	-	-	-	-	-	-
92	2	14	-	-	-	-	-	-
93	2	11	-	-	-	-	-	-
94	2	6	-	-	-	-	-	-
95	2	25	-0.041	0.440	-0.124	0.134	-	-
96	2	50	-0.036	1.000	-0.071	-0.020	-	-
97	2	1	-	-	-	-	-	-
121	3	4	-	-	-	-	-	-
122	3	15	-	-	-	-	-	-
123	3	1	-	-	-	-	-	-
124	3	3	-	-	-	-	-	-
125	3	1	-	-	-	-	-	-
126	3	1	-	-	-	-	-	-
127	3	2	-	-	-	-	-	-
161	3	7	-	-	-	-	-	-
162	3	5	-	-	-	-	-	-
163	3	17	-	-	-	-	-	-
164	3	2	-	-	-	-	-	-

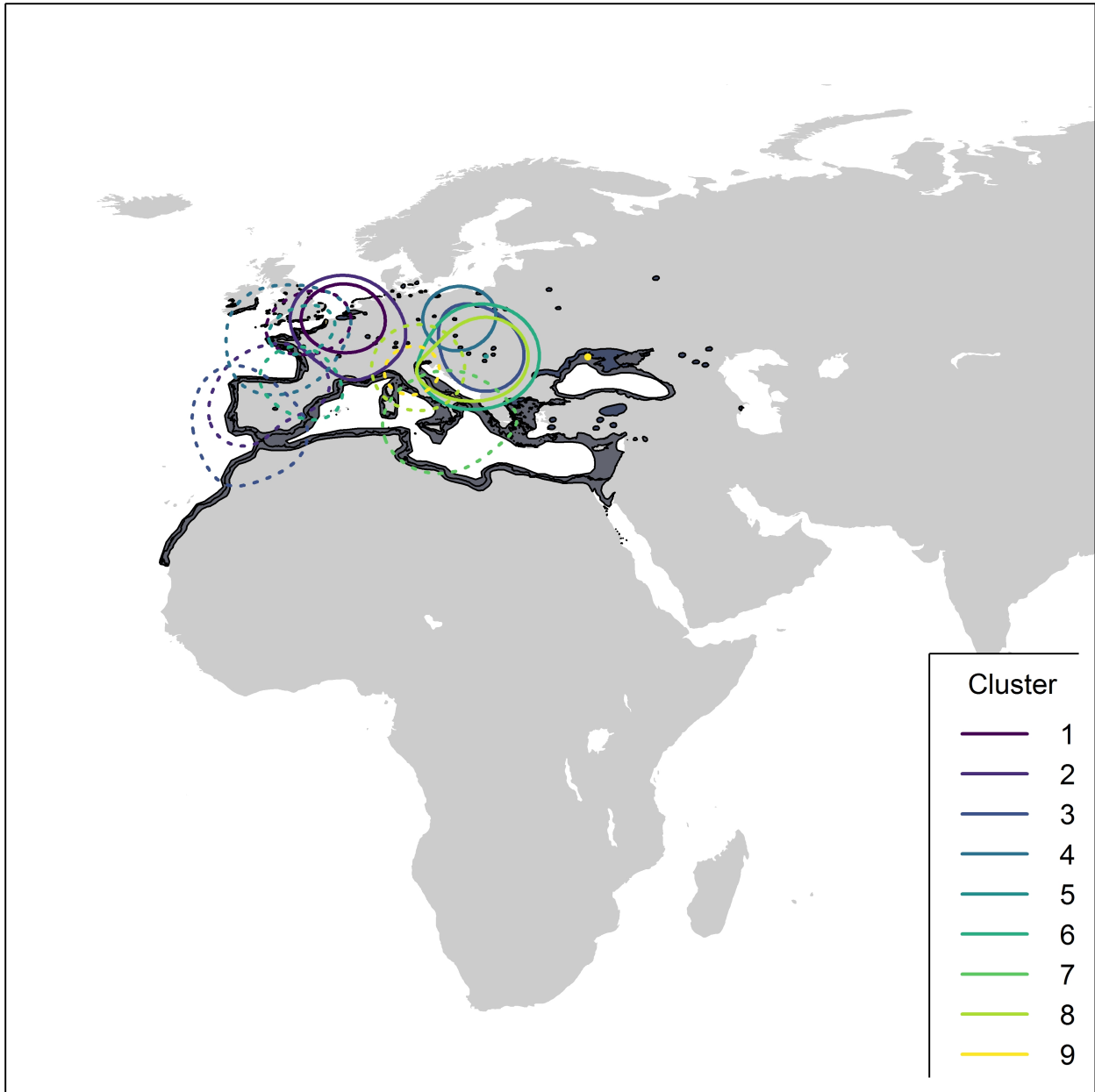


Figure 05750-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding range. Different contour colours correspond to different clusters, as reported in legend. The species distribution range is also shown (breeding range: blue; non-breeding range: dark grey; resident range: beige; from BirdLife International, 2019).

1.2 Sensitivity analysis

Results of power analysis and validation. Analyses at the species level were re-run on subsamples of individuals of decreasing size (100 repetitions per subsample size), according to simple random sampling of individuals (Figure 05750-2) and stratified sampling of individuals within the breeding range (Figure 05750-3) and the non breeding range (Figure 05750-4). For stratified sampling, we selected individuals with a

probability inversely proportional to the number of observation in each country. Figures below report the results of the procedure.

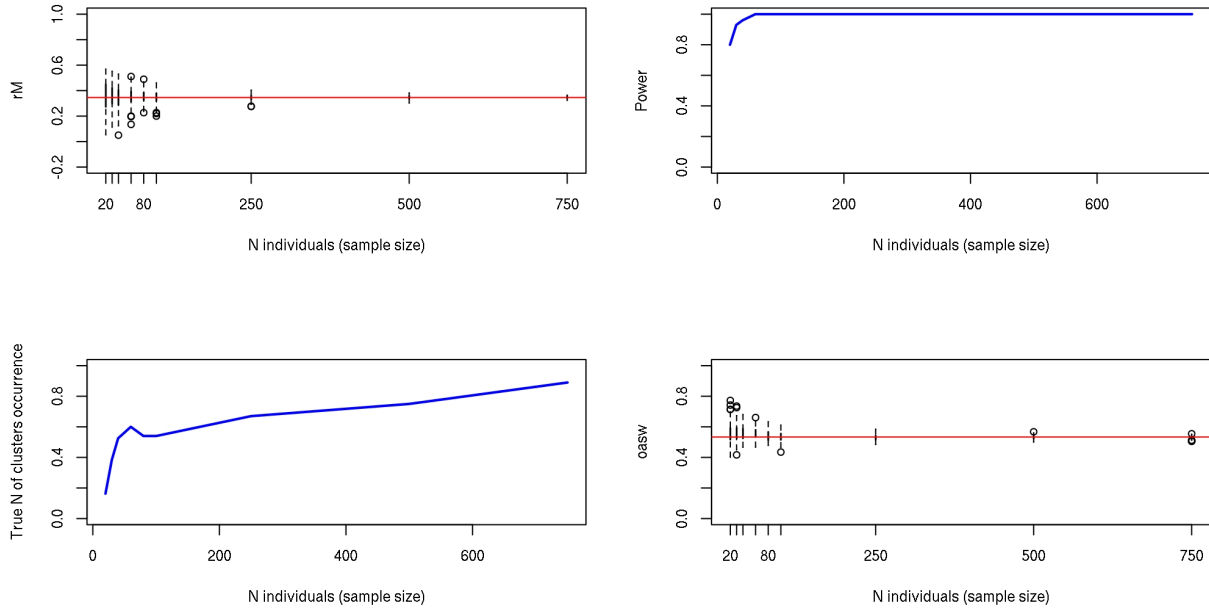


Figure 05750-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

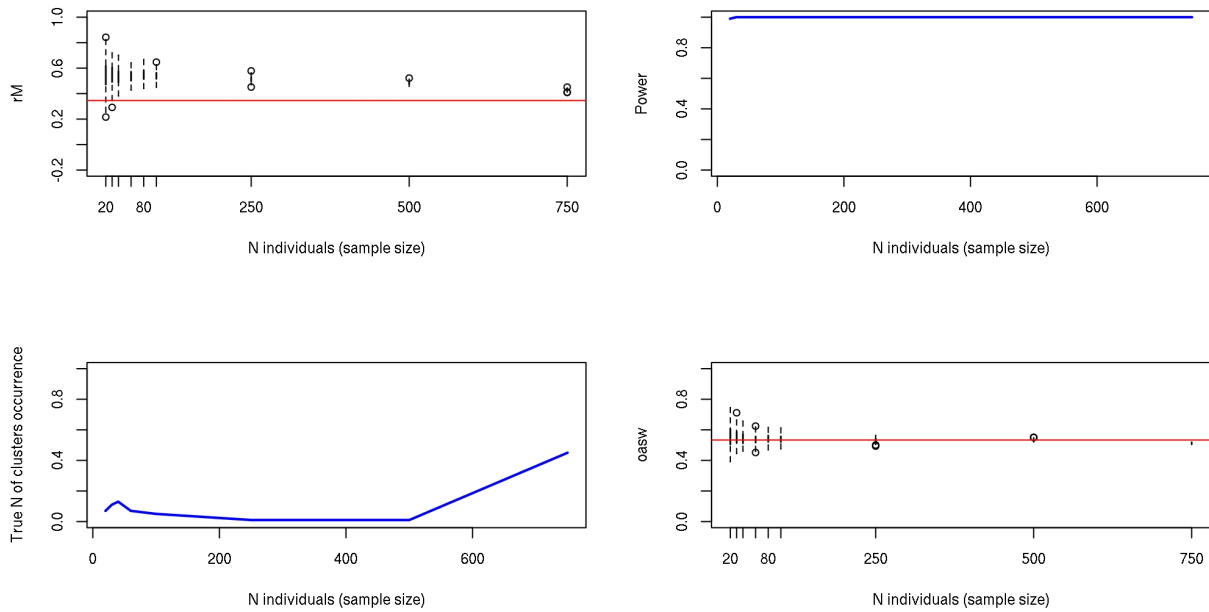


Figure 05750-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

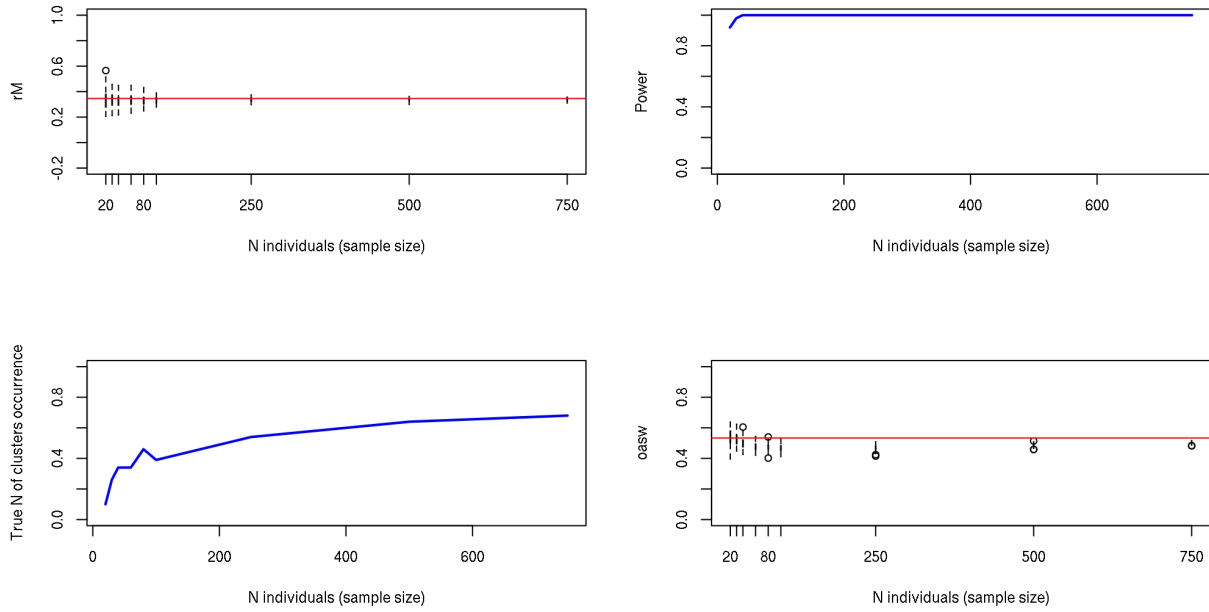


Figure 05750-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is significant ($p = 0.026$); Figure 05750-5).

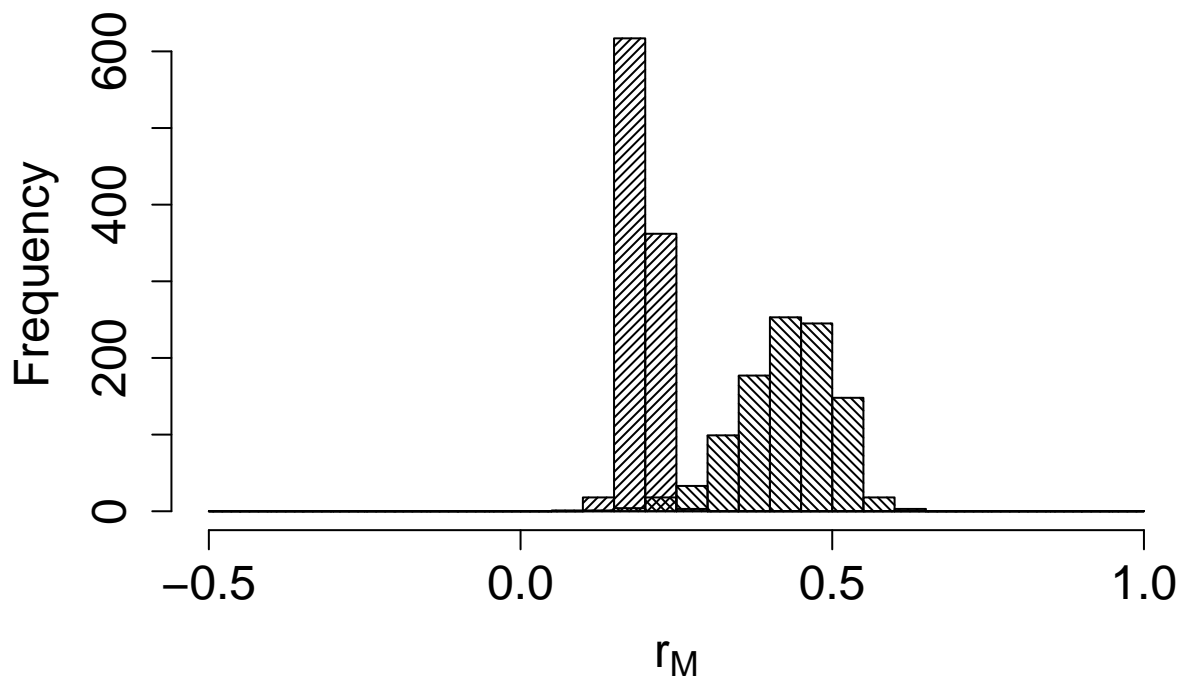


Figure 05750-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows moderate/high connectivity ($MC = 0.626$; $MC = 0.626$ when adjusted for absolute abundance) between 7 breeding regions and 7 non breeding regions (Table 05750-2; Figure 05750-6).

Table 05750-2. Transition probabilities between pre-defined regions. Estimated abundance (number of individuals) in each breeding region is also reported.

Breeding region	Abundance	Non breeding region	Transition probability
Central Europe	2034	North Africa	0.012
Central Europe	2034	North-west Europe	0.067
Central Europe	2034	South-central Europe	0.115
Central Europe	2034	South-west Europe	0.290
Central Europe	2034	West Europe	0.515
East Europe	406017	East Europe	0.008
East Europe	406017	North Africa	0.008
East Europe	406017	South-central Europe	0.916
East Europe	406017	South-east Europe	0.060
East Europe	406017	South-west Europe	0.008
North-west Europe	1280	North-west Europe	0.667
North-west Europe	1280	South-west Europe	0.056
North-west Europe	1280	West Europe	0.278

Breeding region	Abundance	Non breeding region	Transition probability
South-central Europe	6500	North Africa	0.073
South-central Europe	6500	North-west Europe	0.018
South-central Europe	6500	South-central Europe	0.436
South-central Europe	6500	South-west Europe	0.473
South-east Europe	9748	South-central Europe	0.667
South-east Europe	9748	South-east Europe	0.333
South-west Europe	7439	North-west Europe	0.143
South-west Europe	7439	South-west Europe	0.857
West Europe	12469	North Africa	0.011
West Europe	12469	North-west Europe	0.286
West Europe	12469	South-west Europe	0.173
West Europe	12469	West Europe	0.530

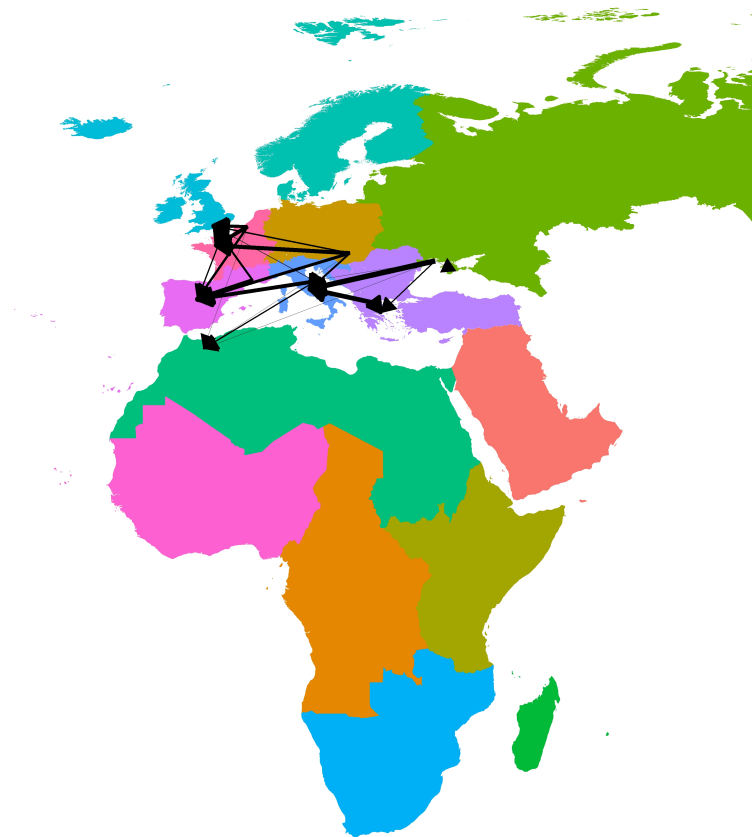


Figure 05750-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

Reference

BirdLife International and Handbook of the Birds of the World (2019). Bird species distribution maps of the world. Version 2019.1. Available at <http://datazone.birdlife.org/species/requestdis>.