

# Migratory connectivity analysis

by EURING Migration Atlas

*Cinclus cinclus* (EURING code 10500)

## 1.1 Connectivity between individuals

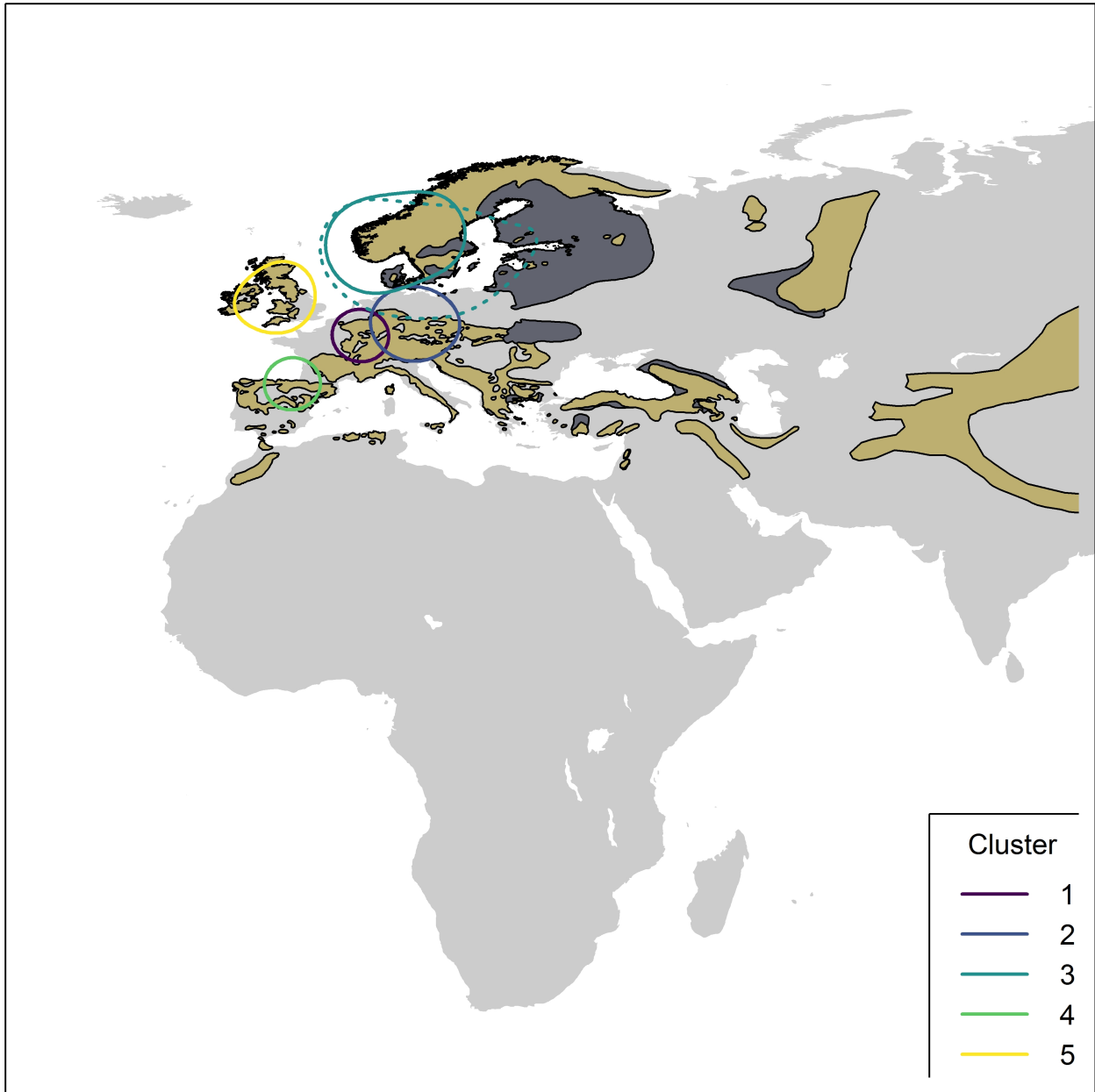
The analysis evaluated 1799 individuals (3598 encounters) filtered from a total of 64536 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from clustering, with a number of first-level clusters = 5 (Table 10500-1; Figure 10500-1).

**Table 10500-1.** 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	1799	0.939	0.001	0.932	0.946	5	0.621
1	1	302	0.993	0.001	0.989	0.995	4	0.746
2	1	507	0.996	0.001	0.992	0.998	5	0.687
3	1	549	0.641	0.001	0.567	0.700	9	0.468
4	1	54	0.999	0.001	0.998	1.000	4	0.919
5	1	387	0.998	0.001	0.996	0.999	7	0.779
11	2	45	0.967	0.001	0.936	0.989	9	0.613
12	2	220	0.639	0.001	0.523	0.737	2	0.418
13	2	28	0.957	0.001	0.904	0.994	9	0.735
14	2	9	-	-	-	-	-	-
21	2	47	0.999	0.001	0.998	0.999	5	0.905
22	2	36	0.982	0.001	0.950	0.999	2	0.562
23	2	109	0.911	0.001	0.791	0.968	5	0.545
24	2	285	0.968	0.001	0.934	0.989	6	0.545
25	2	30	1.000	0.001	1.000	1.000	2	0.989
41	2	47	0.680	0.001	0.480	0.874	8	0.615
42	2	5	-	-	-	-	-	-
43	2	1	-	-	-	-	-	-
44	2	1	-	-	-	-	-	-
51	2	26	0.791	0.001	0.518	0.994	8	0.694
52	2	29	0.981	0.001	0.954	0.996	8	0.638
53	2	93	0.976	0.001	0.945	0.994	2	0.716
54	2	123	0.873	0.001	0.798	0.929	2	0.489
55	2	19	-	-	-	-	-	-
56	2	71	0.787	0.001	0.529	0.910	3	0.447
57	2	26	0.668	0.001	0.486	0.873	7	0.486
111	3	7	-	-	-	-	-	-

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
112	3	10	-	-	-	-	-	-
113	3	2	-	-	-	-	-	-
114	3	7	-	-	-	-	-	-
115	3	8	-	-	-	-	-	-
116	3	3	-	-	-	-	-	-
117	3	3	-	-	-	-	-	-
118	3	2	-	-	-	-	-	-
119	3	3	-	-	-	-	-	-
131	3	4	-	-	-	-	-	-
132	3	8	-	-	-	-	-	-
133	3	1	-	-	-	-	-	-
134	3	1	-	-	-	-	-	-
135	3	2	-	-	-	-	-	-
136	3	7	-	-	-	-	-	-
137	3	2	-	-	-	-	-	-
138	3	1	-	-	-	-	-	-
139	3	2	-	-	-	-	-	-
211	3	36	0.369	0.001	0.181	0.703	8	0.612
212	3	6	-	-	-	-	-	-
213	3	1	-	-	-	-	-	-
214	3	2	-	-	-	-	-	-
215	3	2	-	-	-	-	-	-
221	3	18	-	-	-	-	-	-
222	3	18	-	-	-	-	-	-
231	3	23	0.547	0.001	0.226	0.783	2	0.542
232	3	1	-	-	-	-	-	-
233	3	11	-	-	-	-	-	-
234	3	33	0.551	0.001	0.356	0.803	3	0.485
235	3	41	0.736	0.001	0.586	0.874	4	0.404
241	3	21	0.894	0.001	0.764	0.985	3	0.615
242	3	144	0.847	0.001	0.630	0.920	3	0.522
243	3	23	0.705	0.008	0.111	0.946	2	0.770
244	3	72	0.868	0.001	0.295	0.963	2	0.900
245	3	6	-	-	-	-	-	-
246	3	19	-	-	-	-	-	-
251	3	28	-	-	-	-	-	-
252	3	2	-	-	-	-	-	-
411	3	2	-	-	-	-	-	-
412	3	7	-	-	-	-	-	-
413	3	10	-	-	-	-	-	-
414	3	9	-	-	-	-	-	-
415	3	10	-	-	-	-	-	-
416	3	1	-	-	-	-	-	-
417	3	7	-	-	-	-	-	-
418	3	1	-	-	-	-	-	-
511	3	3	-	-	-	-	-	-
512	3	3	-	-	-	-	-	-
513	3	1	-	-	-	-	-	-
514	3	2	-	-	-	-	-	-
515	3	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
516	3	1	-	-	-	-	-	-
517	3	11	-	-	-	-	-	-
518	3	1	-	-	-	-	-	-
521	3	4	-	-	-	-	-	-
522	3	1	-	-	-	-	-	-
523	3	7	-	-	-	-	-	-
524	3	8	-	-	-	-	-	-
525	3	2	-	-	-	-	-	-
526	3	3	-	-	-	-	-	-
527	3	3	-	-	-	-	-	-
528	3	1	-	-	-	-	-	-
531	3	13	-	-	-	-	-	-
532	3	80	0.978	0.001	0.950	0.989	8	0.587

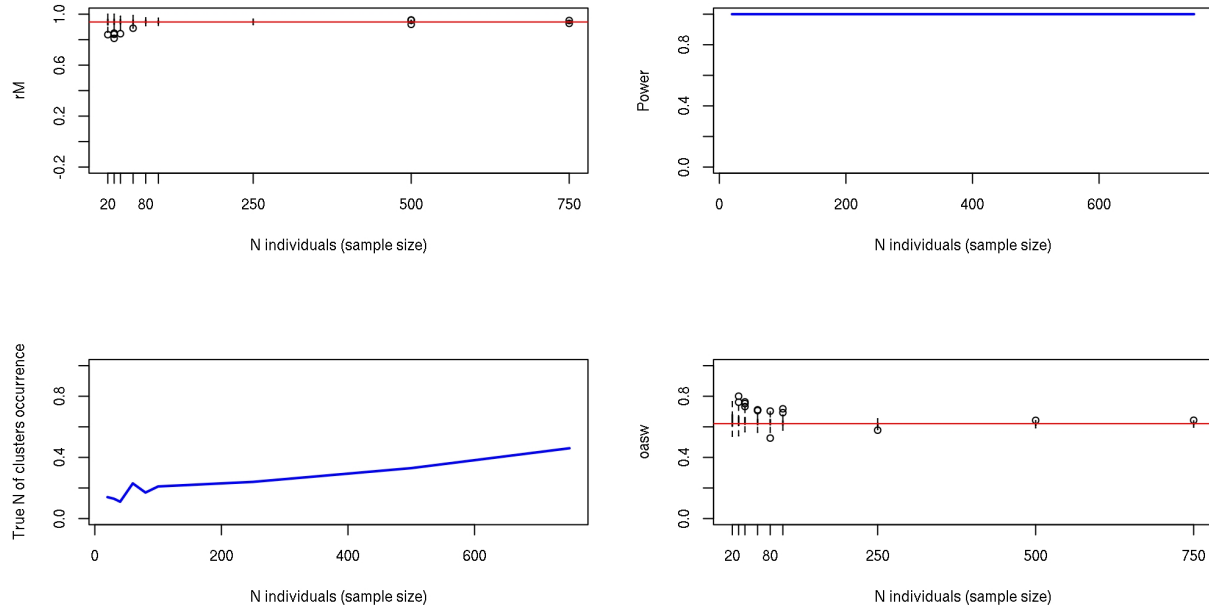


**Figure 10500-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

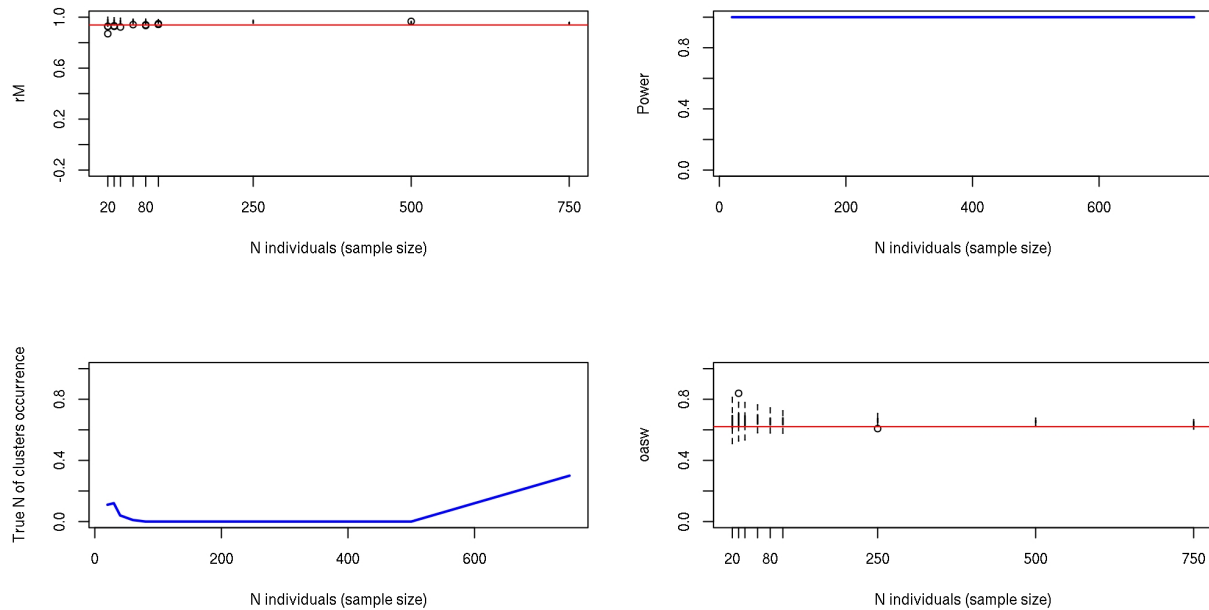
## 1.2 Sensitivity analysis

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 10500-2) and stratified sampling of individuals within the breeding range (Figure 10500-3) and the non breeding range (Figure 10500-4). 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.

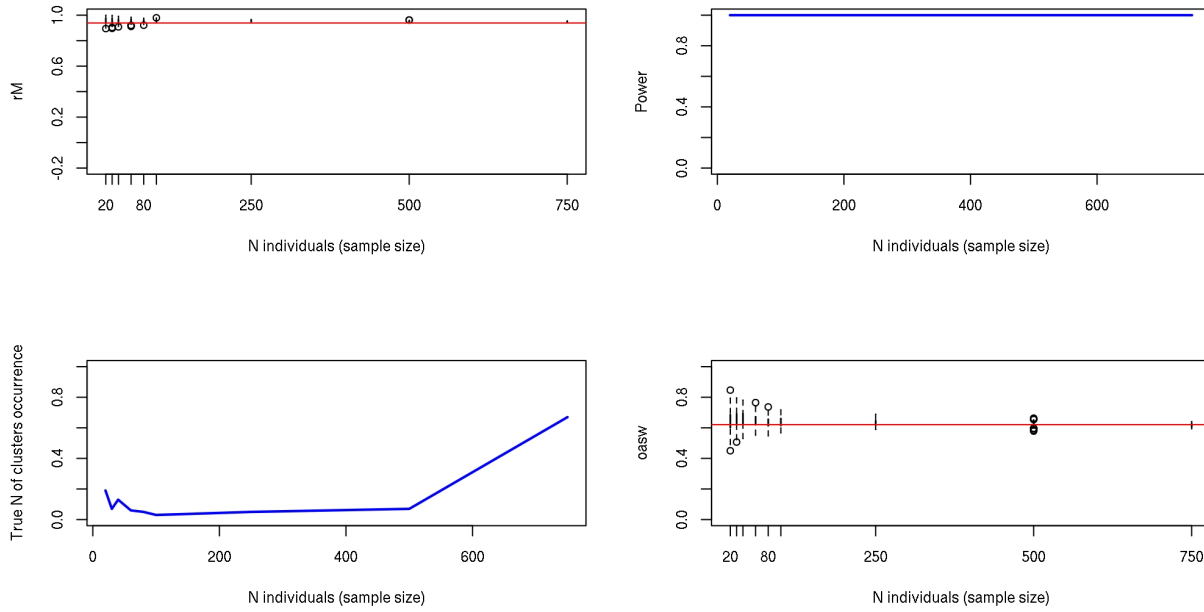


**Figure 10500-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



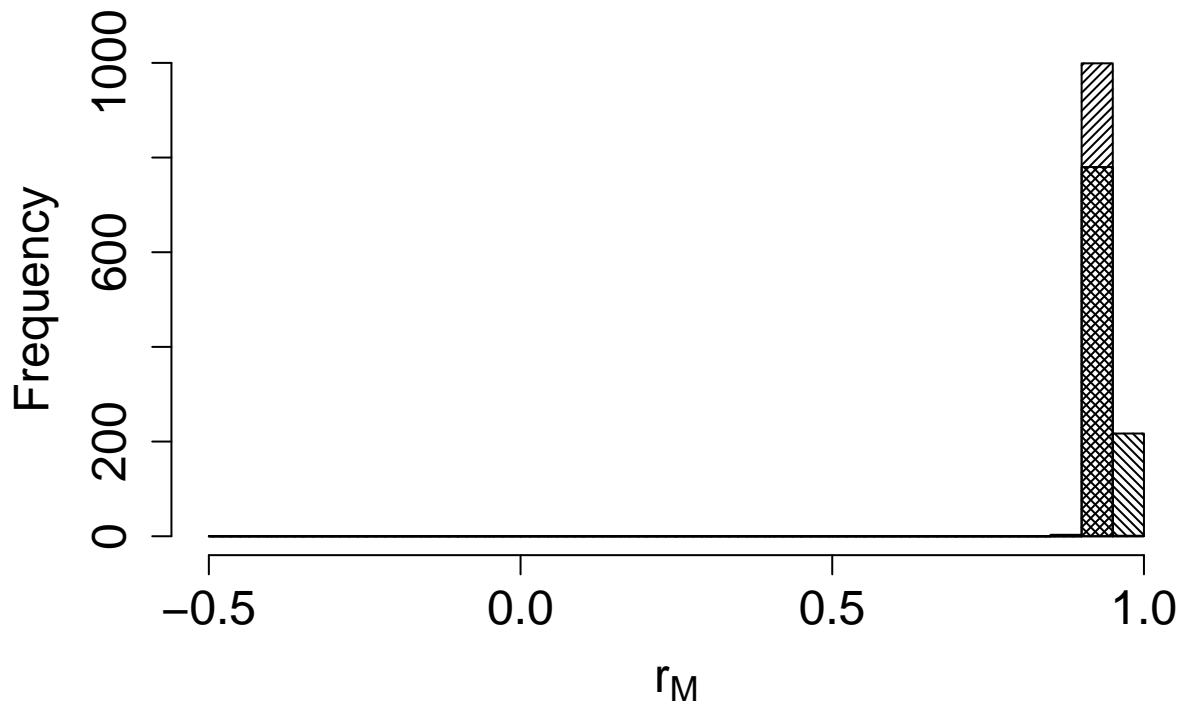
**Figure 10500-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 10500-4.** 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 not significant ( $p = 0.781$ ); Figure 10500-5).



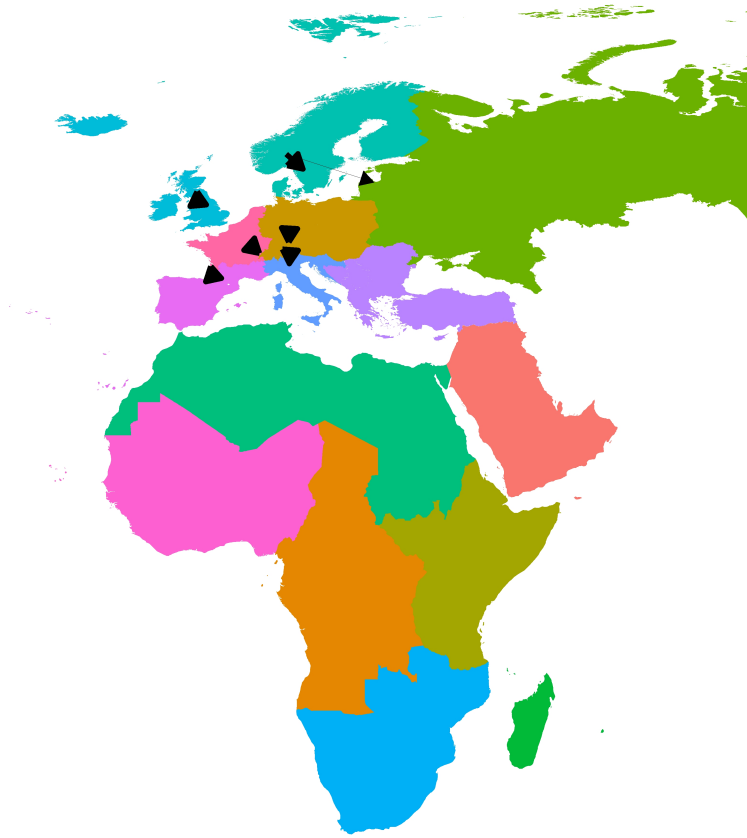
**Figure 10500-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

## 2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 0.985; MC = 0.985 when adjusted for absolute abundance) between 6 breeding regions and 7 non breeding regions (Table 10500-2; Figure 10500-6).

**Table 10500-2.** 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	65355	Central Europe	1.000
North Europe	71302	East Europe	0.033
North Europe	71302	North Europe	0.967
North-west Europe	33020	North-west Europe	1.000
South-central Europe	47224	South-central Europe	1.000
South-west Europe	33610	South-west Europe	1.000
West Europe	25076	West Europe	1.000



**Figure 10500-6.** 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>.