

# Migratory connectivity analysis

by EURING Migration Atlas

*Corvus monedula* (EURING code 15600)

## 1.1 Connectivity between individuals

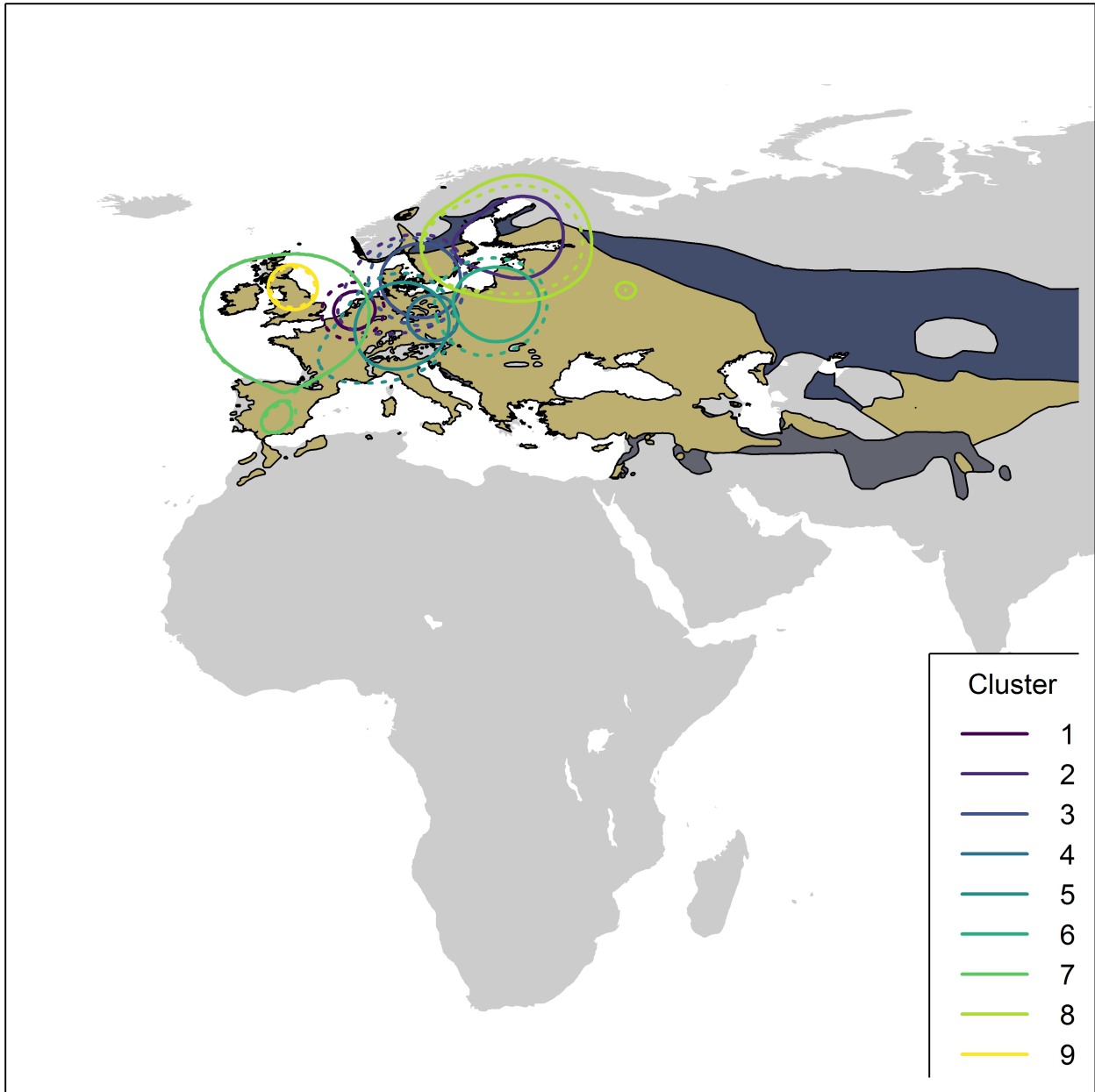
The analysis evaluated 1557 individuals (3114 encounters) filtered from a total of 82411 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from clustering, with a number of first-level clusters = 9 (Table 15600-1; Figure 15600-1).

**Table 15600-1.** 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	1557	0.850	0.001	0.822	0.876	9	0.535
1	1	382	0.680	0.001	0.551	0.794	7	0.566
2	1	62	0.217	0.029	0.033	0.473	2	0.460
3	1	146	0.768	0.001	0.673	0.891	5	0.525
4	1	373	0.871	0.001	0.796	0.942	9	0.647
5	1	163	0.669	0.001	0.588	0.766	3	0.693
6	1	63	0.800	0.001	0.693	0.915	6	0.682
7	1	130	0.995	0.001	0.988	0.998	2	0.810
8	1	117	0.920	0.001	0.863	0.955	2	0.807
9	1	121	0.753	0.001	0.625	0.998	8	0.864
11	2	123	0.775	0.001	0.650	0.910	5	0.490
12	2	32	0.738	0.001	0.524	0.932	2	0.636
13	2	111	0.783	0.001	0.689	0.972	7	0.788
14	2	11	-	-	-	-	-	-
15	2	29	0.788	0.001	0.696	0.968	8	0.516
16	2	7	-	-	-	-	-	-
17	2	69	0.871	0.001	0.773	0.974	9	0.726
31	2	6	-	-	-	-	-	-
32	2	48	0.806	0.001	0.634	0.951	9	0.569
33	2	18	-	-	-	-	-	-
34	2	54	0.614	0.001	0.358	0.880	8	0.439
35	2	20	0.641	0.001	0.558	0.918	2	0.485
41	2	25	0.871	0.001	0.476	0.967	2	0.574
42	2	14	-	-	-	-	-	-
43	2	6	-	-	-	-	-	-
44	2	39	0.430	0.009	0.270	0.782	4	0.677
45	2	37	0.470	0.006	0.034	0.990	5	0.862

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
46	2	63	0.548	0.001	0.321	0.765	9	0.472
47	2	159	0.243	0.030	-0.043	0.565	8	0.955
48	2	25	0.957	0.001	0.926	0.995	2	0.888
49	2	5	-	-	-	-	-	-
51	2	18	-	-	-	-	-	-
52	2	110	0.825	0.001	0.722	0.957	5	0.695
53	2	35	0.478	0.001	0.194	0.761	9	0.489
61	2	4	-	-	-	-	-	-
62	2	6	-	-	-	-	-	-
63	2	7	-	-	-	-	-	-
64	2	8	-	-	-	-	-	-
65	2	27	0.999	0.001	0.962	1.000	2	0.879
66	2	11	-	-	-	-	-	-
71	2	9	-	-	-	-	-	-
72	2	121	0.963	0.001	0.927	0.988	3	0.672
81	2	107	0.638	0.001	0.442	0.811	3	0.615
82	2	10	-	-	-	-	-	-
91	2	2	-	-	-	-	-	-
92	2	7	-	-	-	-	-	-
93	2	7	-	-	-	-	-	-
94	2	3	-	-	-	-	-	-
95	2	97	0.998	0.001	0.998	1.000	4	0.979
96	2	1	-	-	-	-	-	-
97	2	3	-	-	-	-	-	-
98	2	1	-	-	-	-	-	-
121	3	28	0.528	0.002	0.258	0.873	9	0.406
122	3	4	-	-	-	-	-	-
131	3	3	-	-	-	-	-	-
132	3	10	-	-	-	-	-	-
133	3	74	0.780	0.001	0.686	0.966	2	0.895
134	3	4	-	-	-	-	-	-
135	3	7	-	-	-	-	-	-
136	3	12	-	-	-	-	-	-
137	3	1	-	-	-	-	-	-
151	3	1	-	-	-	-	-	-
152	3	3	-	-	-	-	-	-
153	3	1	-	-	-	-	-	-
154	3	4	-	-	-	-	-	-
155	3	5	-	-	-	-	-	-
156	3	8	-	-	-	-	-	-
157	3	4	-	-	-	-	-	-
158	3	3	-	-	-	-	-	-
171	3	1	-	-	-	-	-	-
172	3	1	-	-	-	-	-	-
173	3	15	-	-	-	-	-	-
174	3	33	0.981	0.001	0.857	0.994	2	0.861
175	3	7	-	-	-	-	-	-
176	3	2	-	-	-	-	-	-
177	3	1	-	-	-	-	-	-
178	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
179	3	2	-	-	-	-	-	-
321	3	10	-	-	-	-	-	-
322	3	5	-	-	-	-	-	-
323	3	21	0.498	0.082	0.310	1.000	3	0.853
324	3	7	-	-	-	-	-	-
325	3	1	-	-	-	-	-	-
326	3	1	-	-	-	-	-	-
327	3	1	-	-	-	-	-	-
328	3	1	-	-	-	-	-	-
329	3	1	-	-	-	-	-	-
411	3	21	0.341	0.044	0.242	0.740	4	0.379
412	3	4	-	-	-	-	-	-
441	3	1	-	-	-	-	-	-
442	3	4	-	-	-	-	-	-
443	3	29	0.218	0.109	-0.009	0.876	-	-
444	3	5	-	-	-	-	-	-
451	3	2	-	-	-	-	-	-
452	3	30	0.064	0.172	-0.061	0.303	-	-
453	3	1	-	-	-	-	-	-
454	3	2	-	-	-	-	-	-
455	3	2	-	-	-	-	-	-
471	3	140	0.376	0.017	-0.021	0.964	2	0.979
472	3	3	-	-	-	-	-	-
473	3	8	-	-	-	-	-	-
474	3	1	-	-	-	-	-	-
475	3	2	-	-	-	-	-	-
476	3	3	-	-	-	-	-	-
477	3	1	-	-	-	-	-	-
478	3	1	-	-	-	-	-	-
481	3	6	-	-	-	-	-	-
482	3	19	-	-	-	-	-	-
521	3	8	-	-	-	-	-	-
522	3	15	-	-	-	-	-	-
523	3	80	0.586	0.001	0.408	0.808	2	0.752
524	3	3	-	-	-	-	-	-
525	3	4	-	-	-	-	-	-
651	3	25	0.993	0.001	0.600	1.000	2	0.881
652	3	2	-	-	-	-	-	-
721	3	67	0.855	0.001	0.699	0.985	9	0.492
722	3	37	0.996	0.001	0.951	1.000	2	0.949
723	3	17	-	-	-	-	-	-
811	3	82	0.671	0.001	0.432	0.873	7	0.471
812	3	15	-	-	-	-	-	-
813	3	10	-	-	-	-	-	-
951	3	92	-	-	-	-	-	-
952	3	1	-	-	-	-	-	-
953	3	1	-	-	-	-	-	-
954	3	3	-	-	-	-	-	-

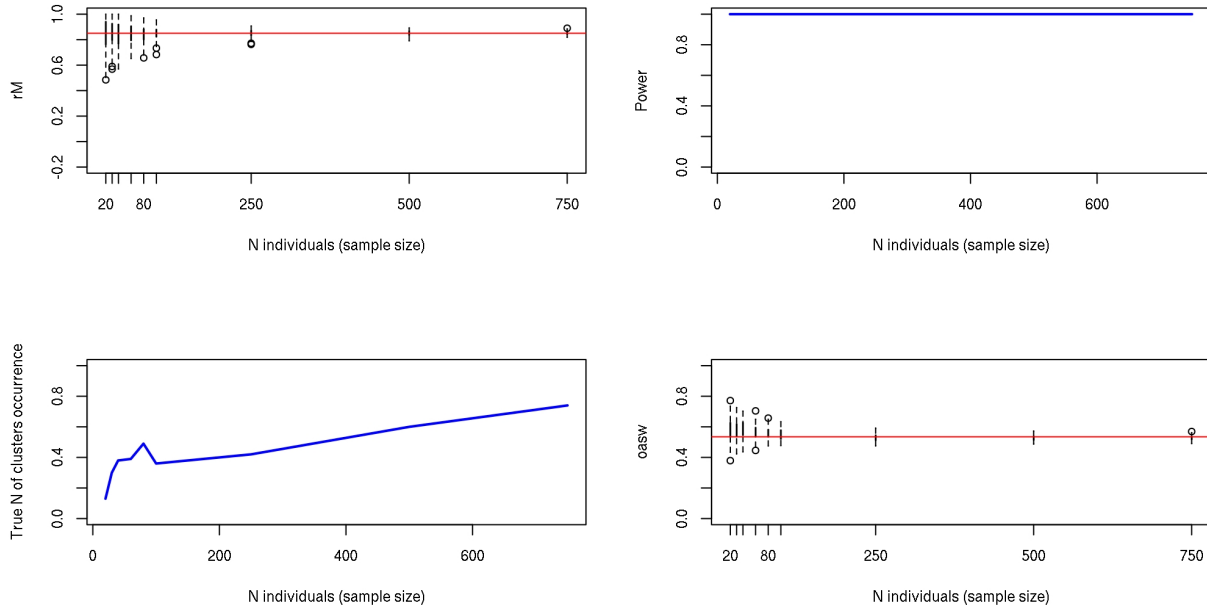


**Figure 15600-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

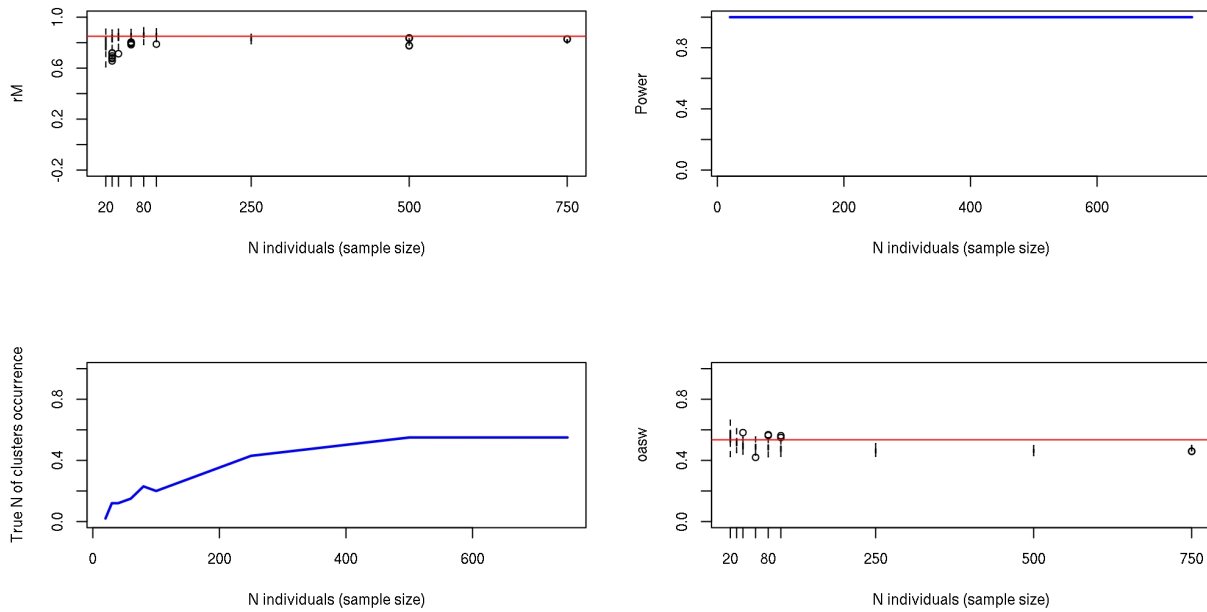
## 1.2 Sensitivity analysis

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 15600-2) and stratified sampling of individuals within the breeding range (Figure 15600-3) and the non breeding range (Figure 15600-4). 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.

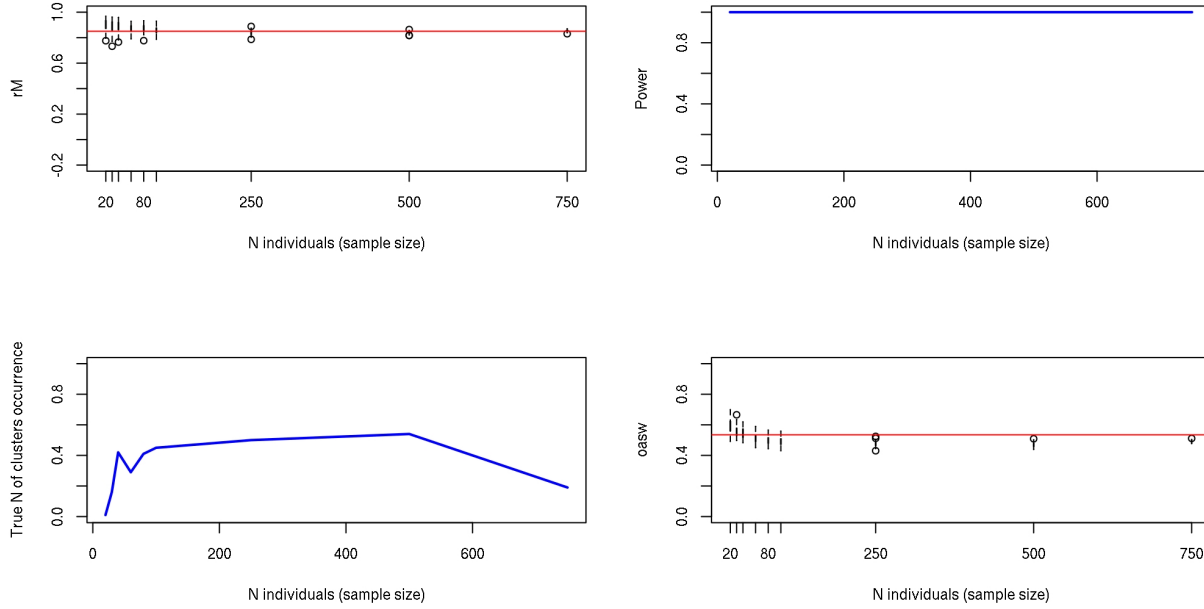


**Figure 15600-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



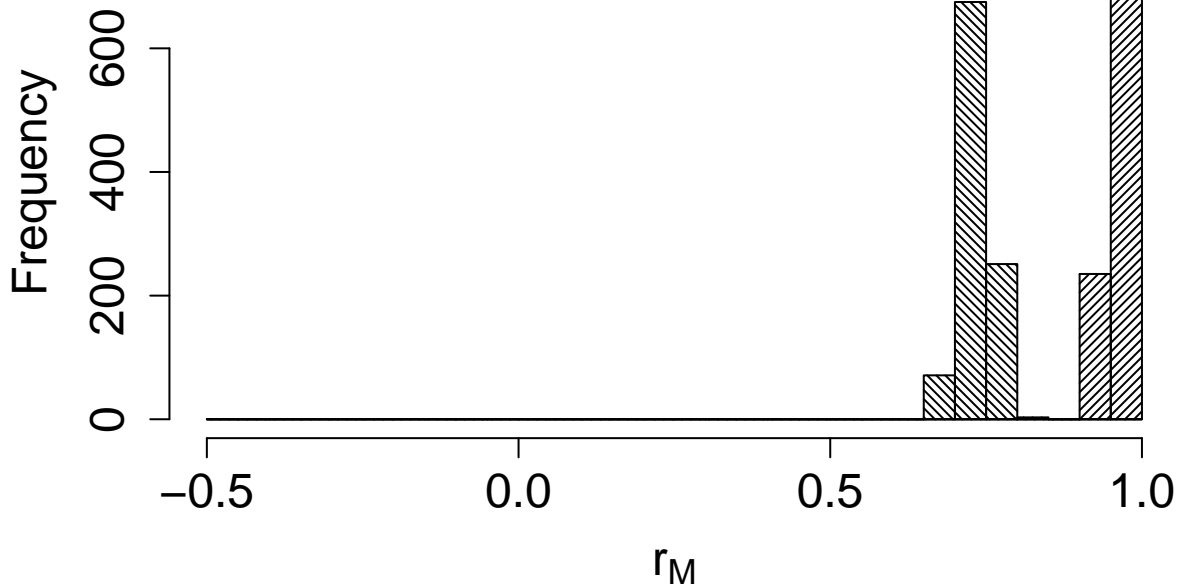
**Figure 15600-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 15600-4.** 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 ( $p < 0.001$ ); Figure 15600-5).



**Figure 15600-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

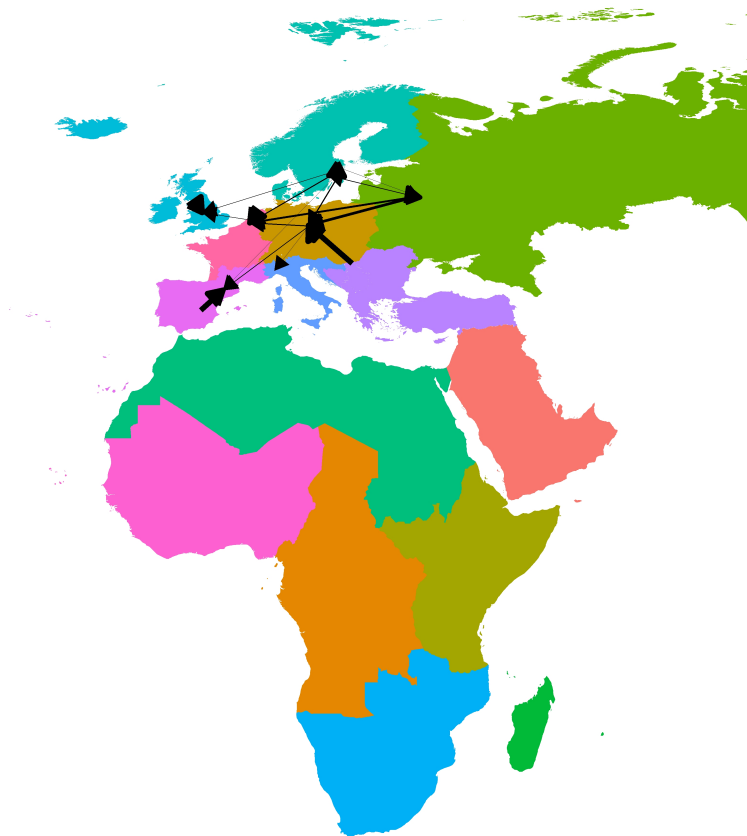
## 2. Connectivity between pre-defined regions

The species shows moderate/high connectivity ( $MC = 0.748$ ;  $MC = 0.748$  when adjusted for absolute abundance) between 7 breeding regions and 7 non breeding regions (Table 15600-2; Figure 15600-6).

**Table 15600-2.** 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	780550	Central Europe	0.942
Central Europe	780550	South-central Europe	0.002
Central Europe	780550	South-west Europe	0.019
Central Europe	780550	West Europe	0.038
East Europe	9229009	Central Europe	0.265
East Europe	9229009	East Europe	0.588
East Europe	9229009	North Europe	0.029
East Europe	9229009	West Europe	0.118
North Europe	905000	Central Europe	0.056
North Europe	905000	East Europe	0.004
North Europe	905000	North Europe	0.866
North Europe	905000	North-west Europe	0.011
North Europe	905000	South-west Europe	0.004

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	905000	West Europe	0.060
North-west Europe	5560050	North-west Europe	1.000
South-east Europe	8838250	Central Europe	1.000
South-west Europe	4291219	South-west Europe	1.000
West Europe	964522	North-west Europe	0.011
West Europe	964522	West Europe	0.989



**Figure 15600-6.** 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>.