Migratory connectivity analysis

by EURING Migration Atlas

Corvus corax **(EURING code 15720)**

1.1 Connectivity between individuals

The analysis evaluated 2907 individuals (5814 encounters) filtered from a total of 30564 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 = 3 (Table 15720-1; Figure 15720-1).

Table 15720-1. 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	2907	0.991	0.001	0.990	0.992	3	0.654
1	1	728	0.993	0.001	0.991	0.995	7	0.761
2	1	190	0.997	0.001	0.994	0.998	3	0.697
3	1	1989	0.942	0.001	0.932	0.950	2	0.551
11	2	27	0.967	0.001	0.941	0.991	3	0.663
12	2	346	0.817	0.001	0.603	0.906	2	0.769
13	2	74	0.525	0.001	0.378	0.702	3	0.447
14	2	62	0.941	0.001	0.817	0.979	2	0.845
15	2	142	0.775	0.001	0.471	0.892	2	0.409
16	2	46	0.756	0.001	0.456	0.909	3	0.582
17	2	31	0.995	0.026	-0.072	1.000	2	0.960
21	2	33	0.990	0.001	0.982	0.996	3	0.778
22	2	12	-	-	-	-	-	-
23	2	145	0.901	0.001	0.869	0.933	3	0.547
31	2	1593	0.904	0.001	0.880	0.925	2	0.586
32	2	396	0.871	0.001	0.837	0.903	2	0.528
111	3	3	-	-	-	-	-	-
112	3	19	-	-	-	-	-	-
113	3	5	-	-	-	-	-	-
121	3	330	0.812	0.001	0.263	0.932	2	0.347
122	3	16	-	-	-	-	-	-
141	3	58	0.708	0.001	0.433	0.887	3	0.619
142	3	4	-	-	-	-	-	-
161	3	10	-	-	-	-	-	-
162	3	2	-	-	-	-	-	-
163	3	34	0.209	0.008	0.090	0.515	2	0.396
171	3	30	-0.041	0.746	-0.087	0.267	-	-

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
172	3	1	-	-	-	-	-	-
211	3	9	-	-	-	-	-	-
212	3	13	-	-	-	-	-	-
213	3	11	-	-	-	-	-	-
231	3	56	0.765	0.001	0.555	0.886	2	0.408
232	3	49	0.880	0.001	0.842	0.925	4	0.622
233	3	40	0.760	0.001	0.599	0.892	3	0.658
311	3	1382	0.848	0.001	0.751	0.900	4	0.440
312	3	211	0.766	0.001	0.682	0.842	2	0.411
321	3	77	0.876	0.001	0.751	0.952	6	0.681
322	3	319	0.708	0.001	0.639	0.775	2	0.481
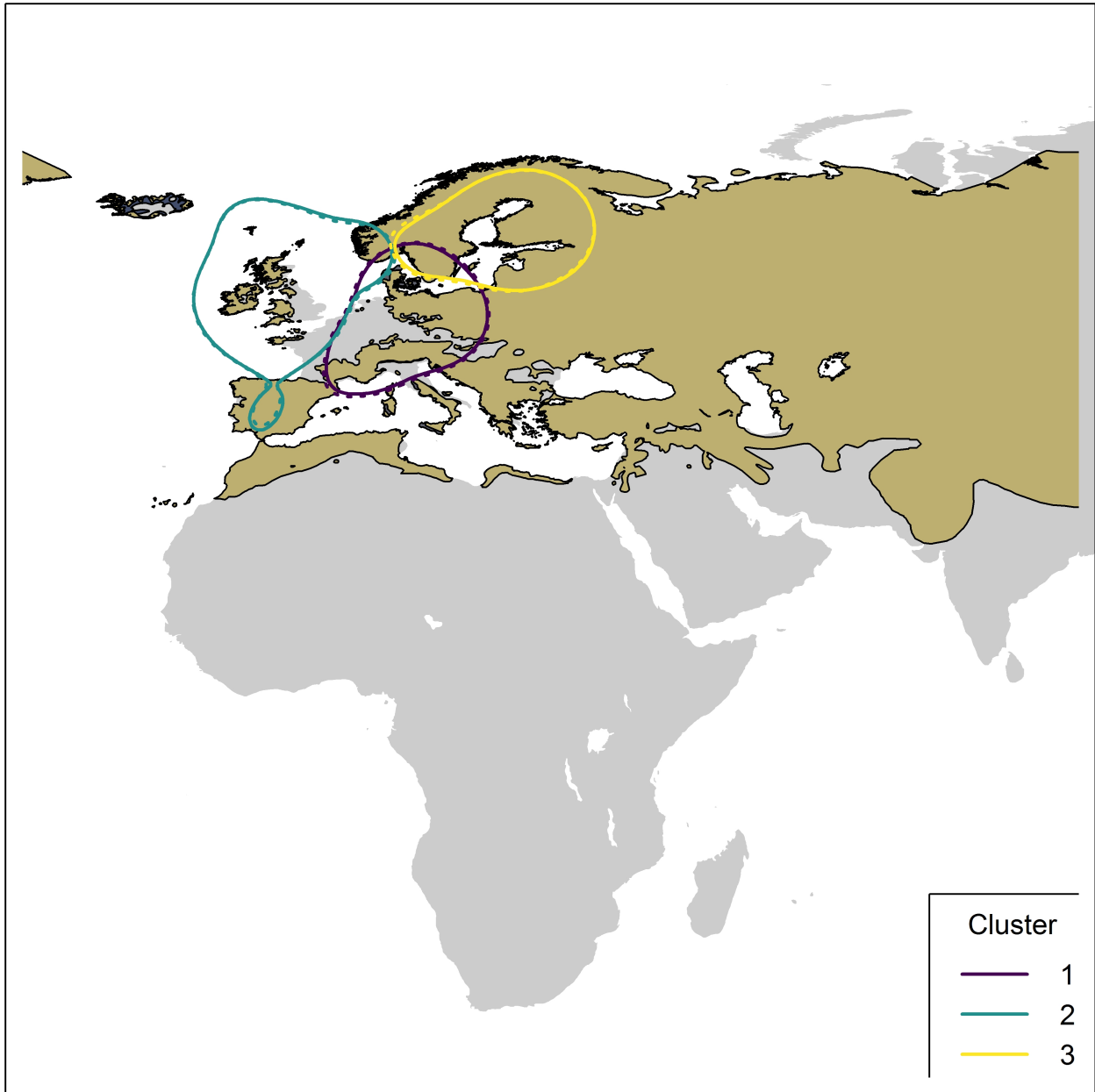
Figure 15720-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 15720-2) and stratified sampling of individuals within the breeding range (Figure 15720-3) and the non breeding range (Figure 15720-4). 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.
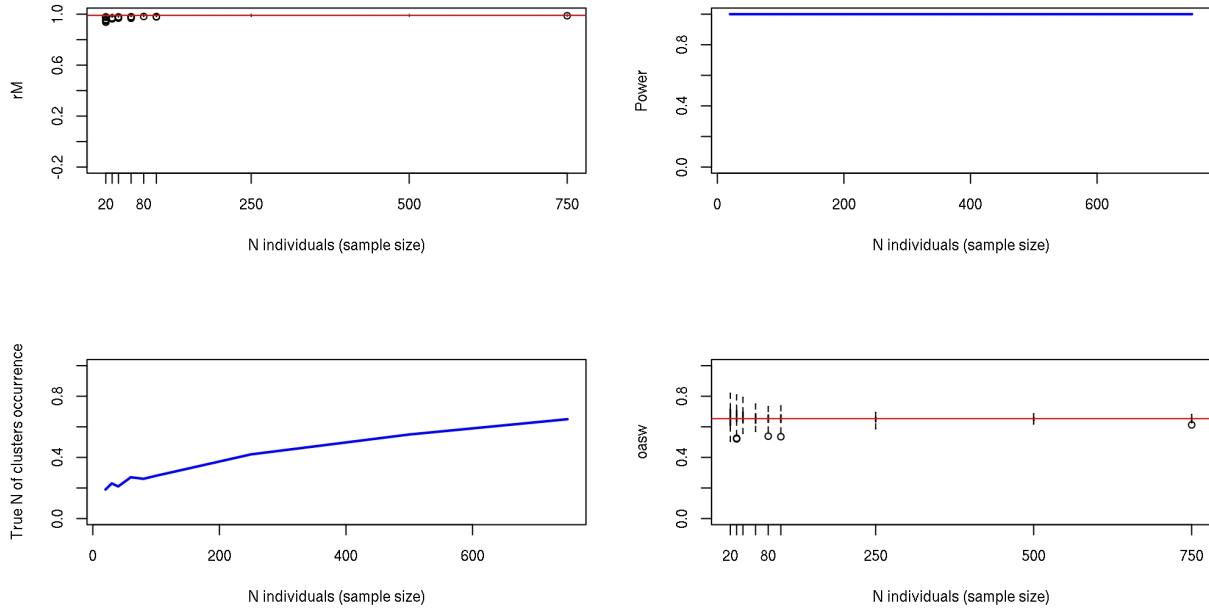

Figure 15720-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
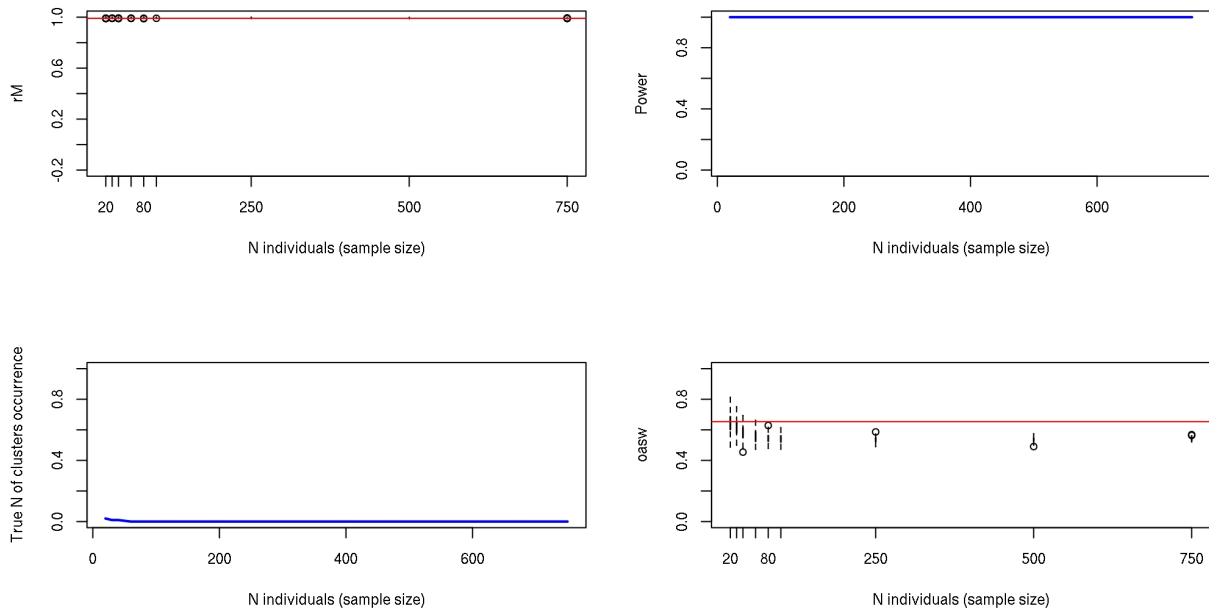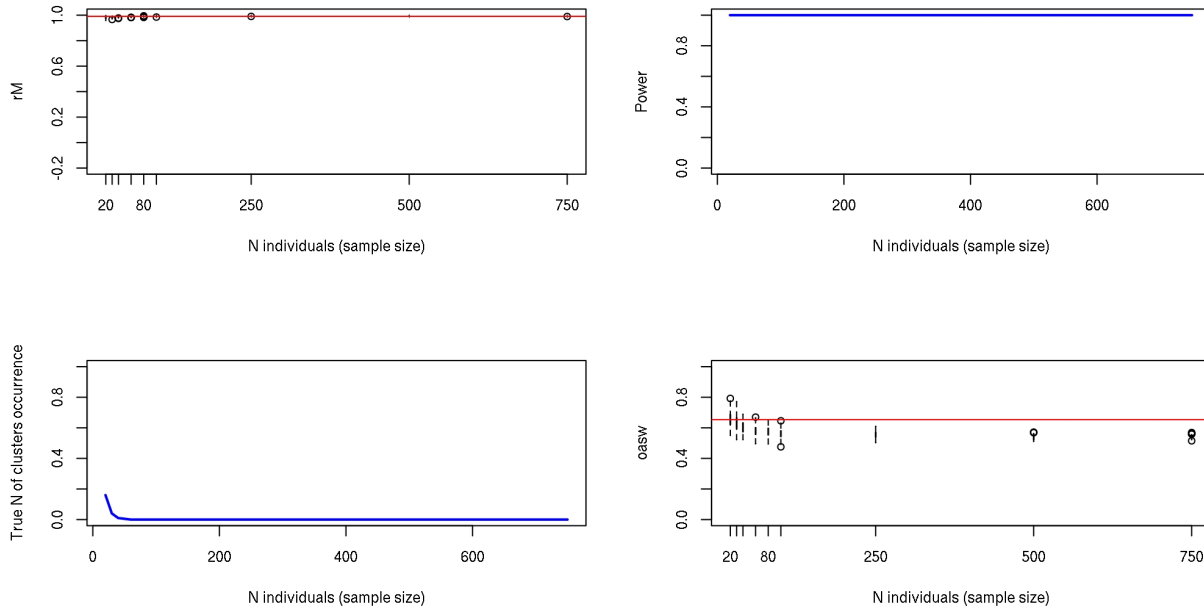

Figure 15720-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

Figure 15720-4. 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 = 1); Figure 15720-5).
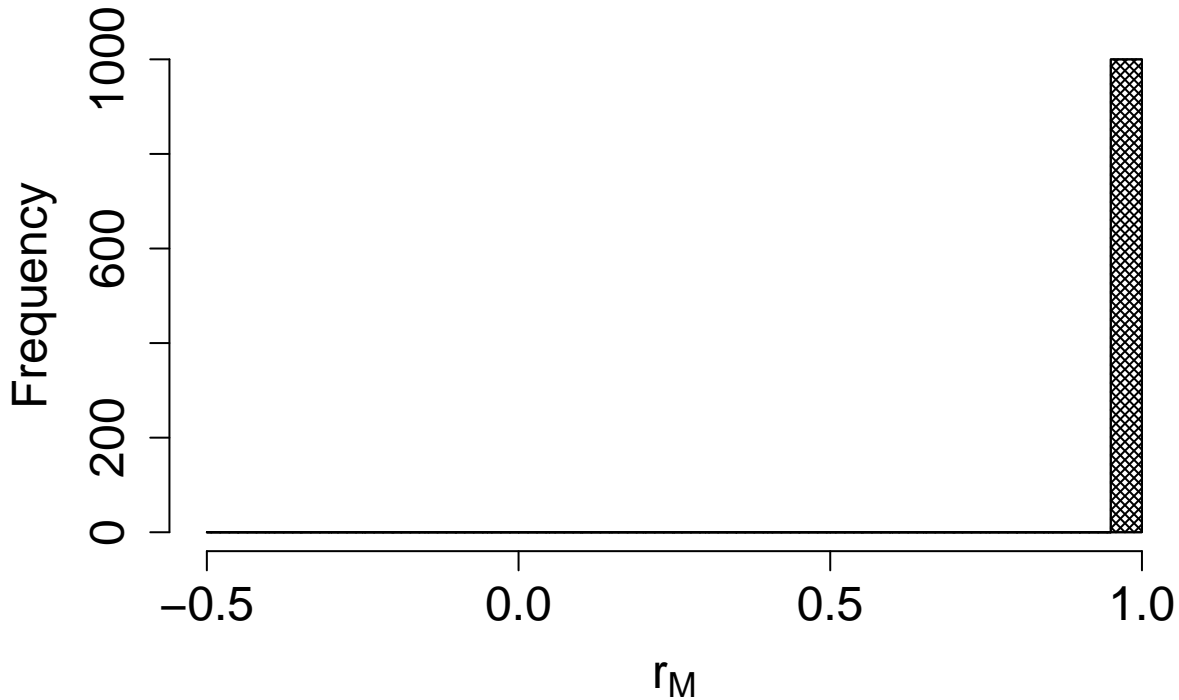
Figure 15720-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 0.997; MC = 0.997 when adjusted for absolute abundance) between 6 breeding regions and 7 non breeding regions (Table 15720-2; Figure 15720-6).

Table 15720-2. 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	132620	Central Europe	0.958
Central Europe	132620	North Europe	0.003
Central Europe	132620	South-central Europe	0.002
Central Europe	132620	West Europe	0.037
East Europe	775000	East Europe	1.000
North Europe	190000	Central Europe	0.012
North Europe	190000	East Europe	0.003
North Europe	190000	North Europe	0.985
North-west Europe	91108	North-west Europe	1.000
South-west Europe	277211	South-west Europe	1.000
West Europe	7046	Central Europe	0.333
West Europe	7046	West Europe	0.667
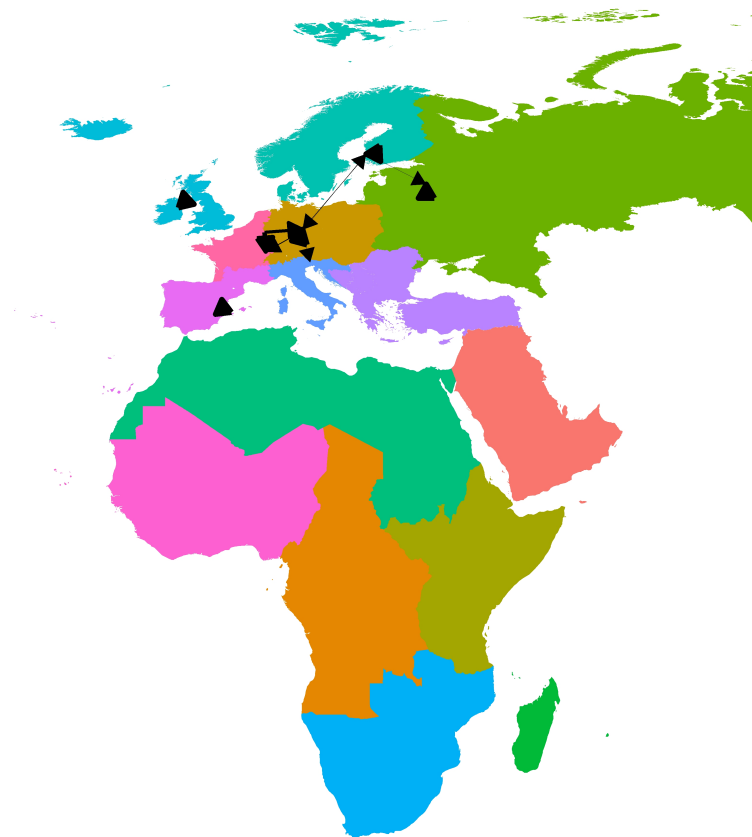
Figure 15720-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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.