

Migratory connectivity analysis

by EURING Migration Atlas

Streptopelia decaocto (EURING code 06840)

1.1 Connectivity between individuals

The analysis evaluated 378 individuals (756 encounters) filtered from a total of 21043 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 = 2 (Table 06840-1; Figure 06840-1).

Table 06840-1. 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	378	0.956	0.001	0.921	0.980	2	0.667
1	1	348	0.912	0.001	0.854	0.961	4	0.553
2	1	30	0.999	0.001	0.996	1.000	5	1.000
11	2	166	0.828	0.001	0.691	0.928	6	0.525
12	2	38	0.909	0.001	0.585	0.984	9	0.454
13	2	37	0.410	0.001	0.133	0.937	6	0.677
14	2	107	0.811	0.001	0.662	0.945	9	0.590
21	2	2	-	-	-	-	-	-
22	2	13	-	-	-	-	-	-
23	2	4	-	-	-	-	-	-
24	2	9	-	-	-	-	-	-
25	2	2	-	-	-	-	-	-
111	3	6	-	-	-	-	-	-
112	3	88	0.515	0.001	0.293	0.924	9	0.558
113	3	10	-	-	-	-	-	-
114	3	35	0.715	0.001	0.509	0.948	9	0.548
115	3	4	-	-	-	-	-	-
116	3	23	0.999	0.001	0.997	1.000	4	0.897
131	3	8	-	-	-	-	-	-
132	3	2	-	-	-	-	-	-
133	3	6	-	-	-	-	-	-
134	3	13	-	-	-	-	-	-
135	3	6	-	-	-	-	-	-
136	3	2	-	-	-	-	-	-
141	3	2	-	-	-	-	-	-
142	3	12	-	-	-	-	-	-
143	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
144	3	51	0.948	0.001	0.929	1.000	2	0.876
145	3	9	-	-	-	-	-	-
146	3	2	-	-	-	-	-	-
147	3	8	-	-	-	-	-	-
148	3	7	-	-	-	-	-	-
149	3	9	-	-	-	-	-	-

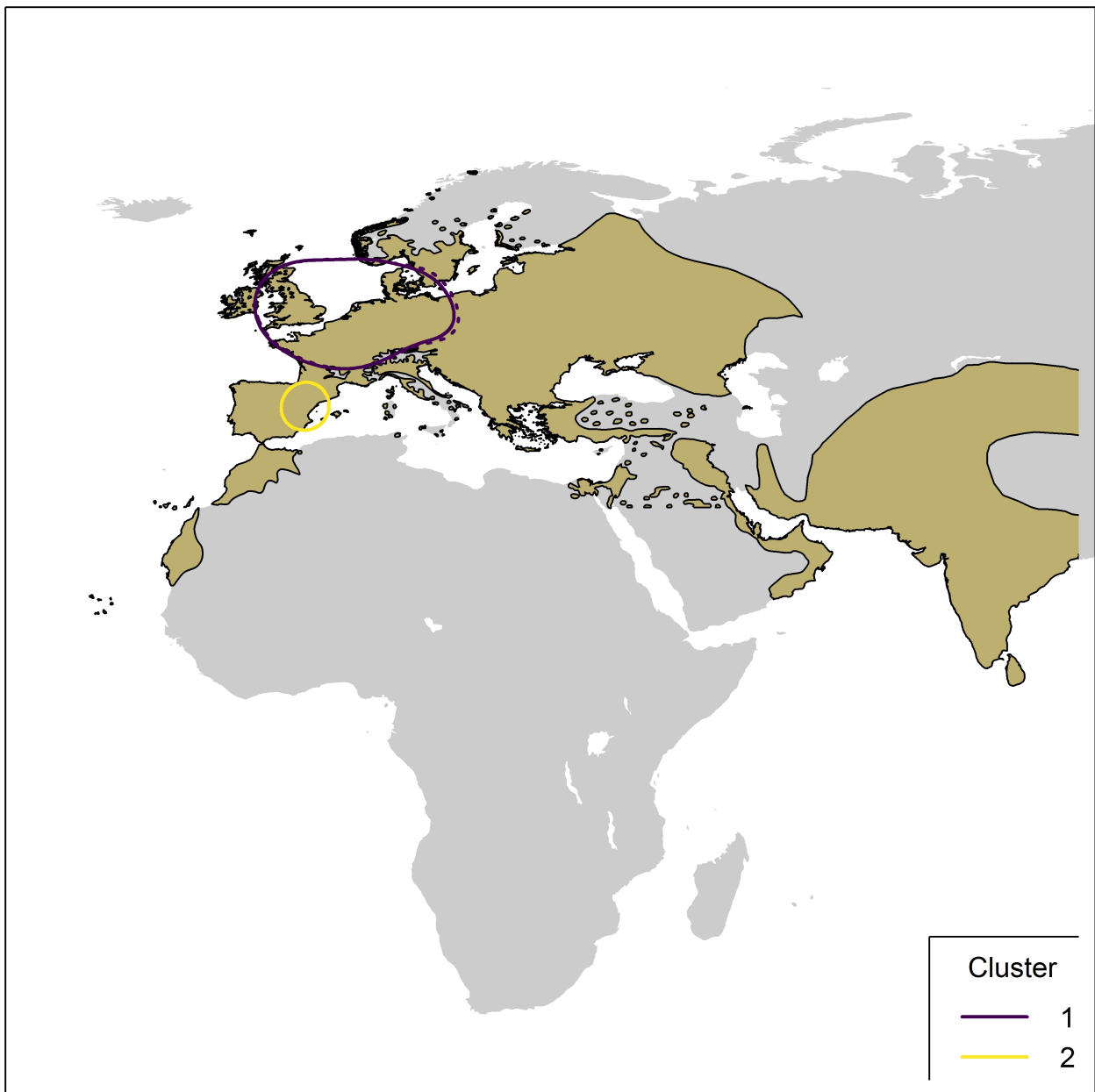


Figure 06840-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure.

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 06840-2) and stratified sampling of individuals within the breeding range (Figure 06840-3) and the non breeding range (Figure 06840-4). 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.

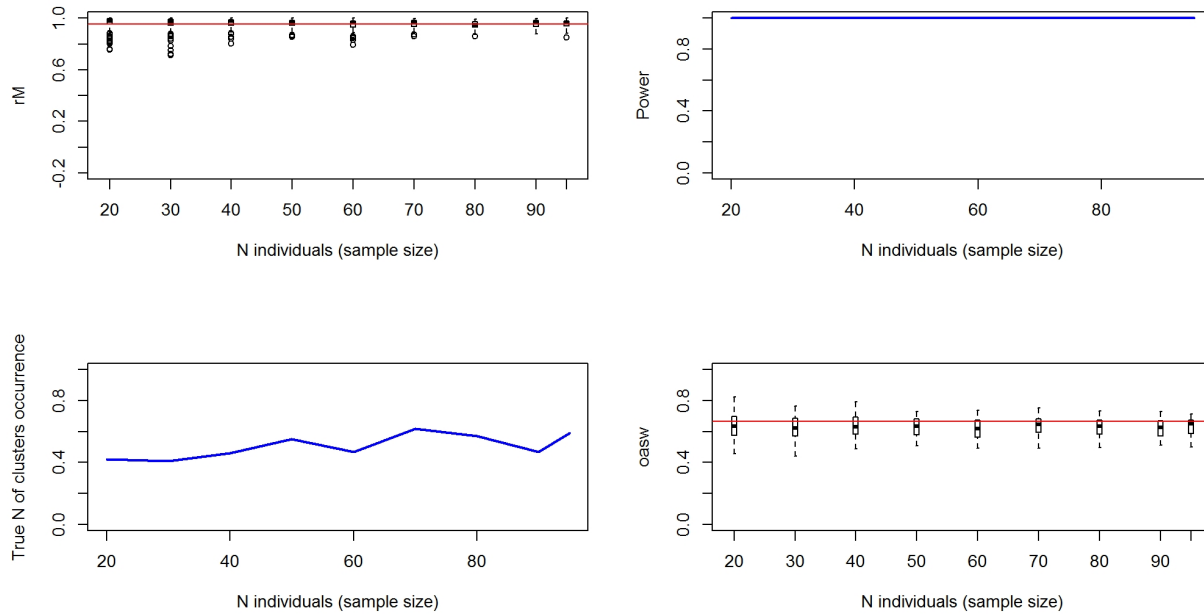


Figure 06840-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

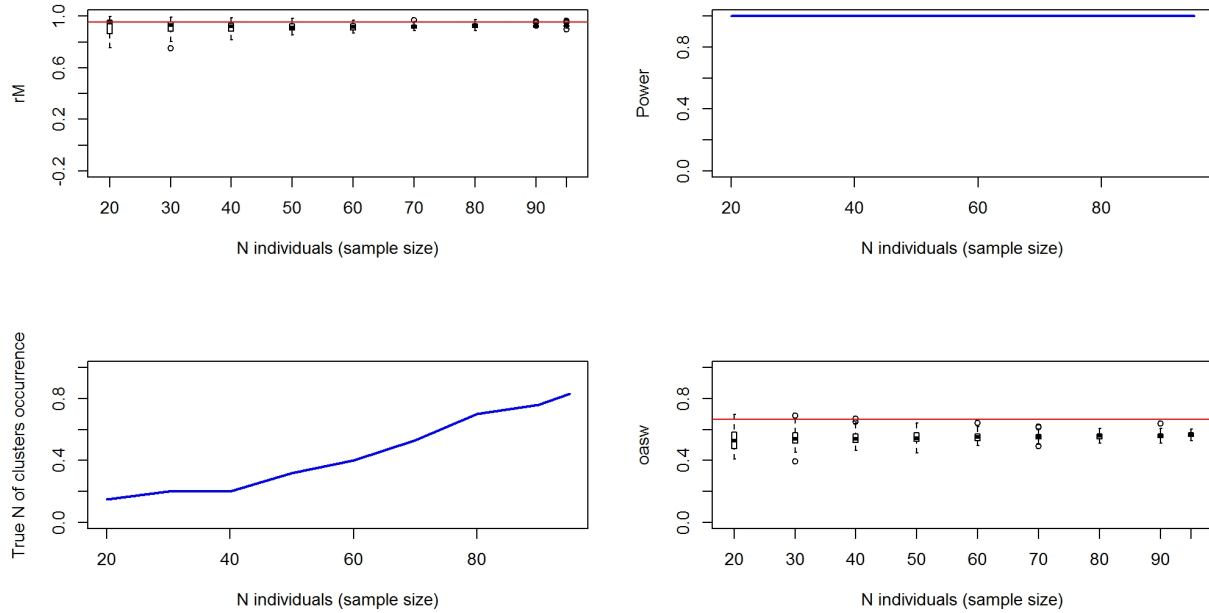


Figure 06840-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

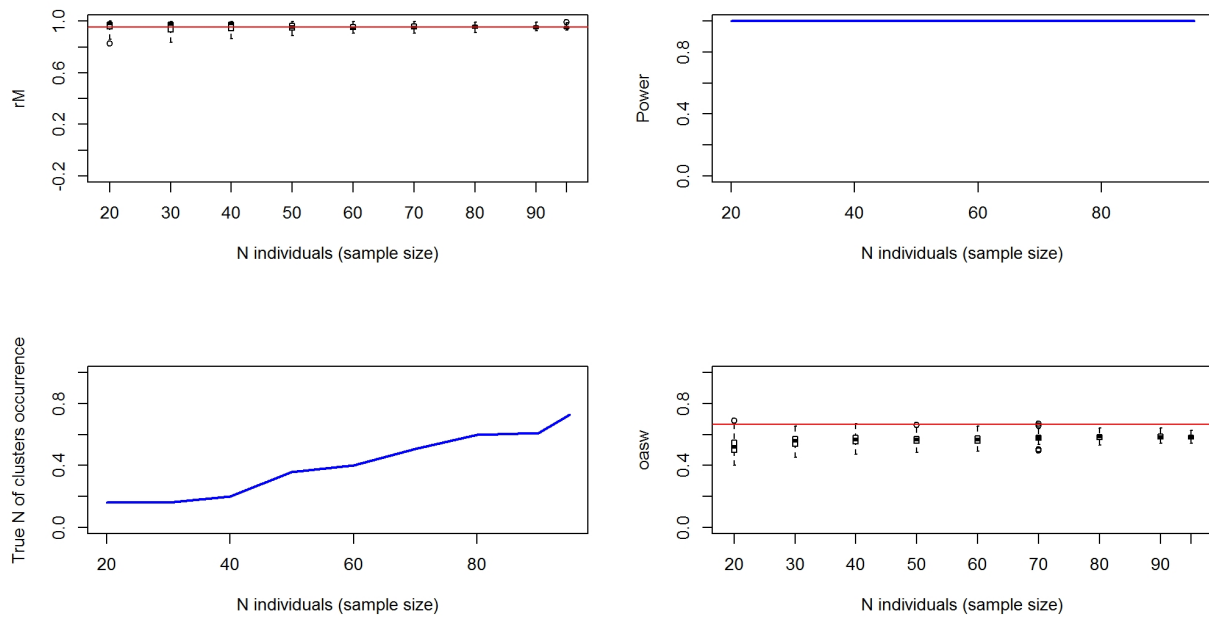


Figure 06840-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.108$); Figure 06840-5).

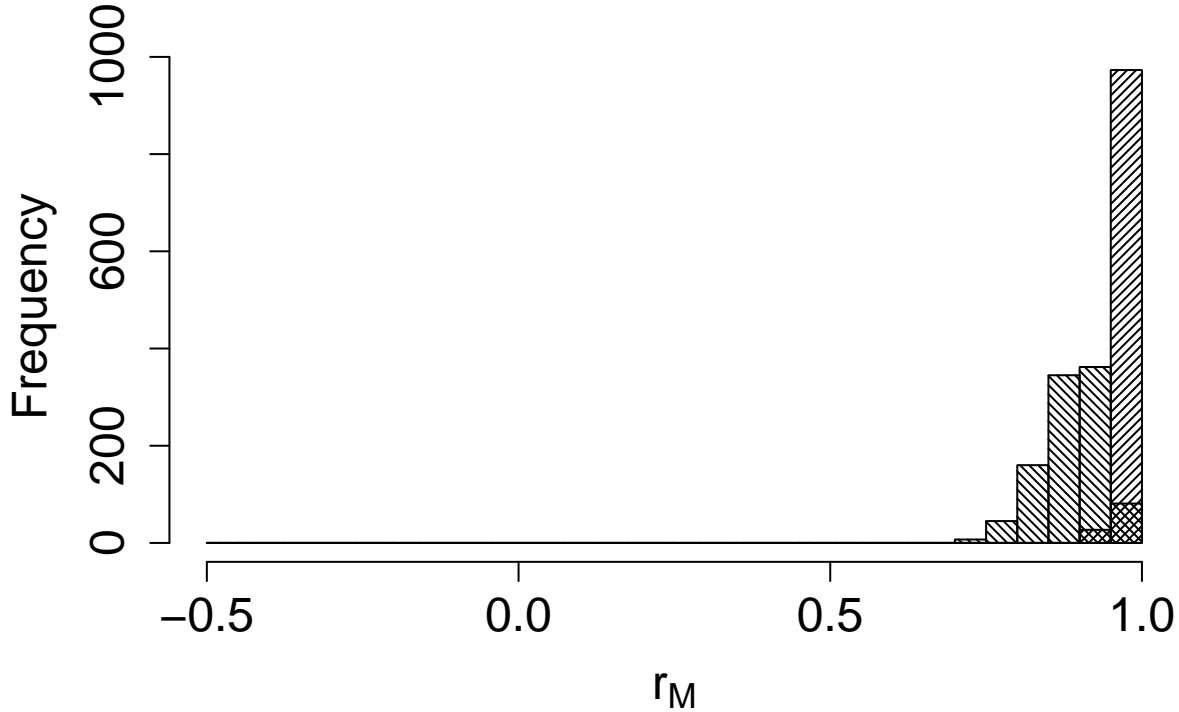


Figure 06840-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=37.5°).

2. Connectivity between pre-defined regions

The species shows high connectivity ($MC = 0.997$; $MC = 0.997$ when adjusted for absolute abundance) between 7 breeding regions and 7 non breeding regions (Table 06840-2; Figure 06840-6).

Table 06840-2. 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	3388050	Central Europe	0.979
Central Europe	3388050	North Europe	0.021
East Europe	1542366	East Europe	1.000
North Europe	60625	North Europe	1.000
North-west Europe	2246375	Central Europe	0.009
North-west Europe	2246375	North-west Europe	0.974
North-west Europe	2246375	West Europe	0.017
South-central Europe	1287977	South-central Europe	1.000
South-west Europe	4341881	South-west Europe	1.000
West Europe	2467925	West Europe	1.000



Figure 06840-6. 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>.