Migratory connectivity analysis

by EURING Migration Atlas

***Garrulus glandarius* (EURING code 15390)**

1.1 Connectivity between individuals

The analysis evaluated 519 individuals (1038 encounters) filtered from a total of 28549 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 = 7 (Table 15390-1; Figure 15390-1).

Table 15390-1. 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	519	0.985	0.001	0.975	0.994	7	0.508
1	1	152	0.850	0.001	0.729	0.977	3	0.464
2	1	94	0.815	0.001	0.696	0.937	2	0.523
3	1	39	0.857	0.001	0.617	0.997	9	0.545
4	1	39	0.961	0.001	0.856	0.999	2	0.686
5	1	23	0.976	0.001	0.934	1.000	5	0.411
6	1	148	0.980	0.001	0.956	0.993	2	0.460
7	1	24	0.984	0.001	0.968	0.998	2	0.445
21	2	21	0.596	0.001	0.465	0.879	4	0.464
22	2	73	0.715	0.001	0.572	0.885	2	0.473
31	2	1	-	-	-	-	-	-
32	2	9	-	-	-	-	-	-
33	2	4	-	-	-	-	-	-
34	2	1	-	-	-	-	-	-
35	2	1	-	-	-	-	-	-
36	2	3	-	-	-	-	-	-
37	2	7	-	-	-	-	-	-
38	2	4	-	-	-	-	-	-
39	2	9	-	-	-	-	-	-
41	2	35	0.868	0.001	0.679	0.998	8	0.558
42	2	4	-	-	-	-	-	-
411	3	9	-	-	-	-	-	-
412	3	5	-	-	-	-	-	-
413	3	5	-	-	-	-	-	-
414	3	4	-	-	-	-	-	-
415	3	1	-	-	-	-	-	-
416	3	5	-	-	-	-	-	-

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
417	3	4	-	-	-	-	-	-
418	3	2	-	-	-	-	-	-

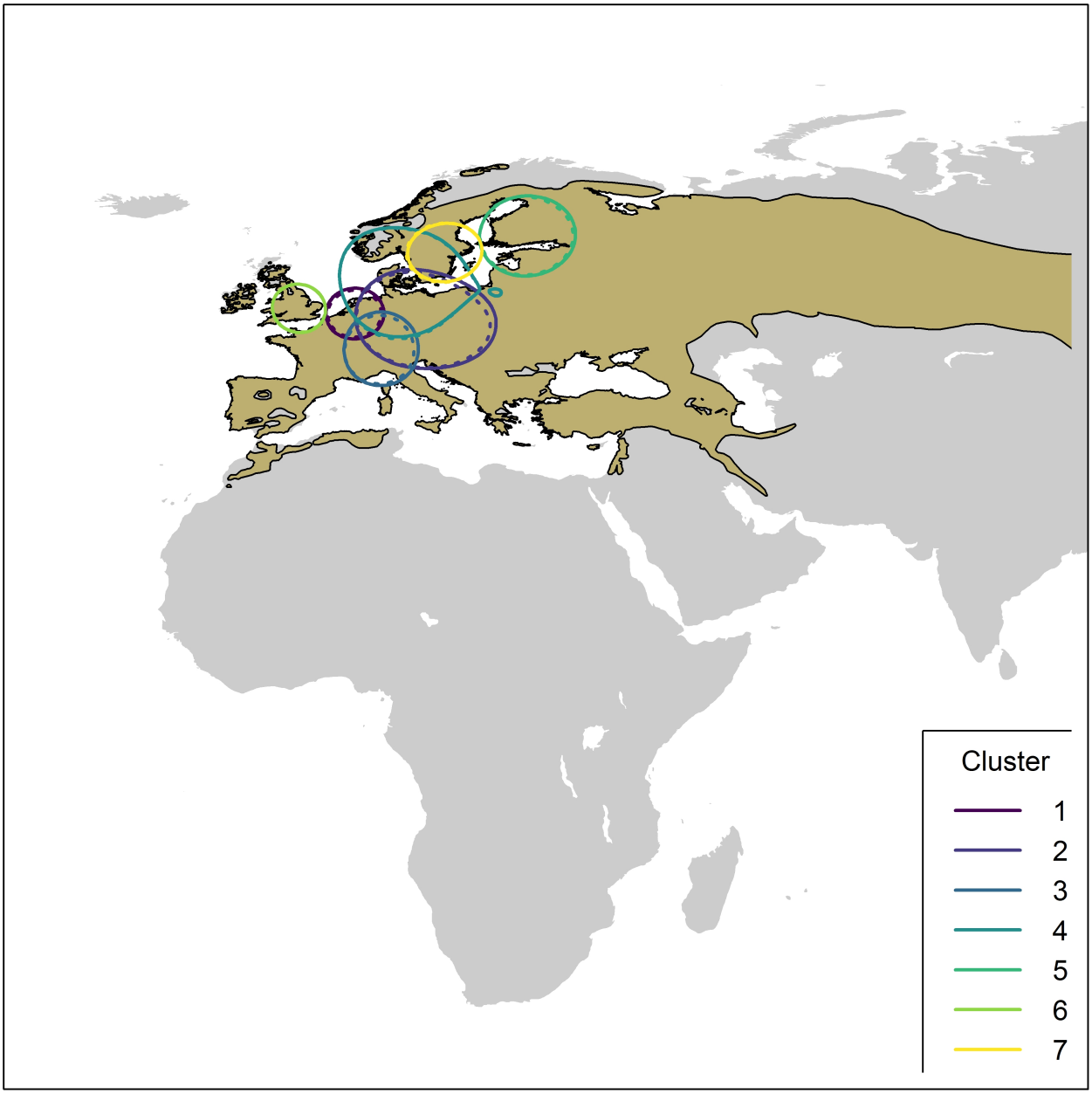

Figure 15390-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 15390-2) and stratified sampling of individuals within the breeding range (Figure 15390-3) and the non breeding range (Figure 15390-4). 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.

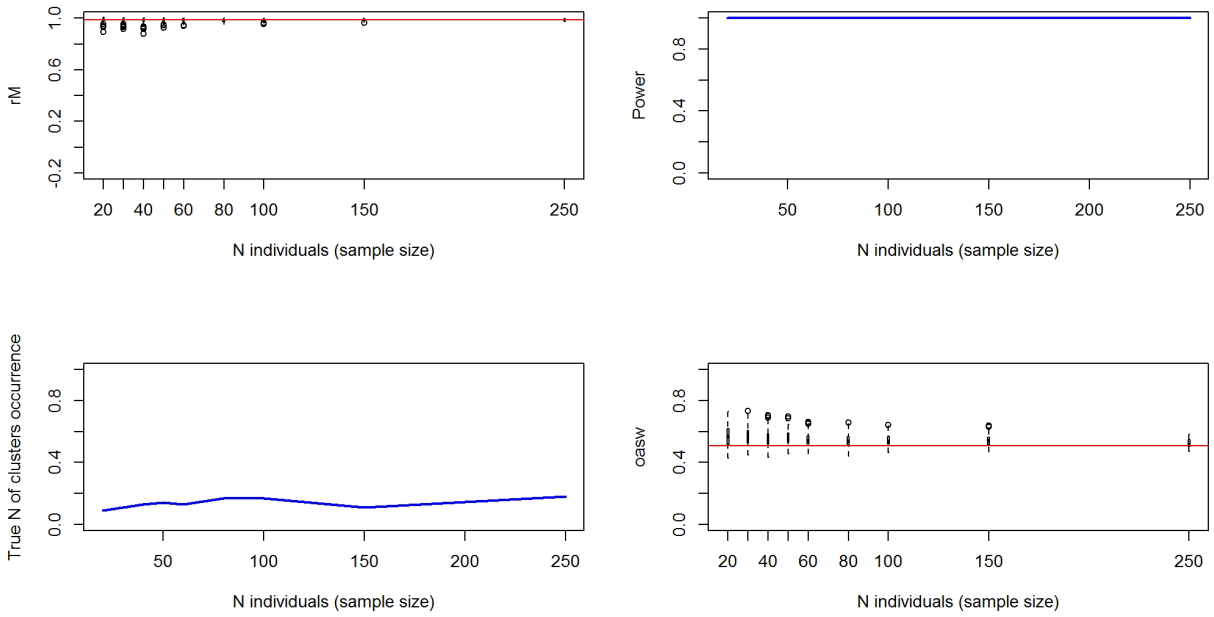

Figure 15390-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

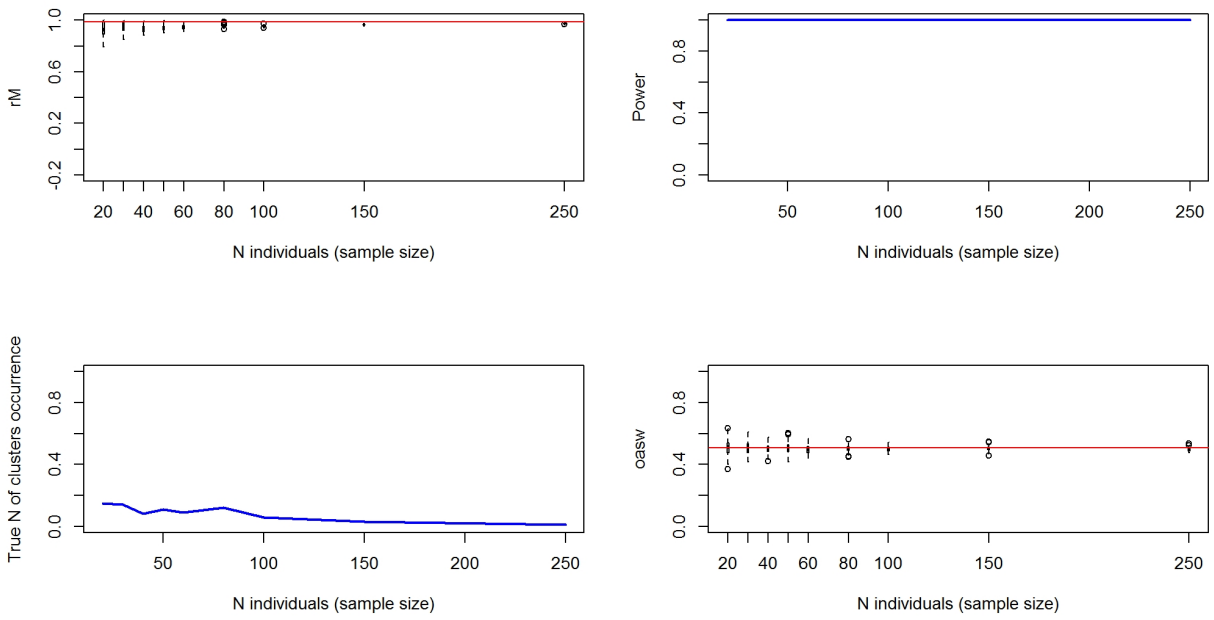

Figure 15390-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

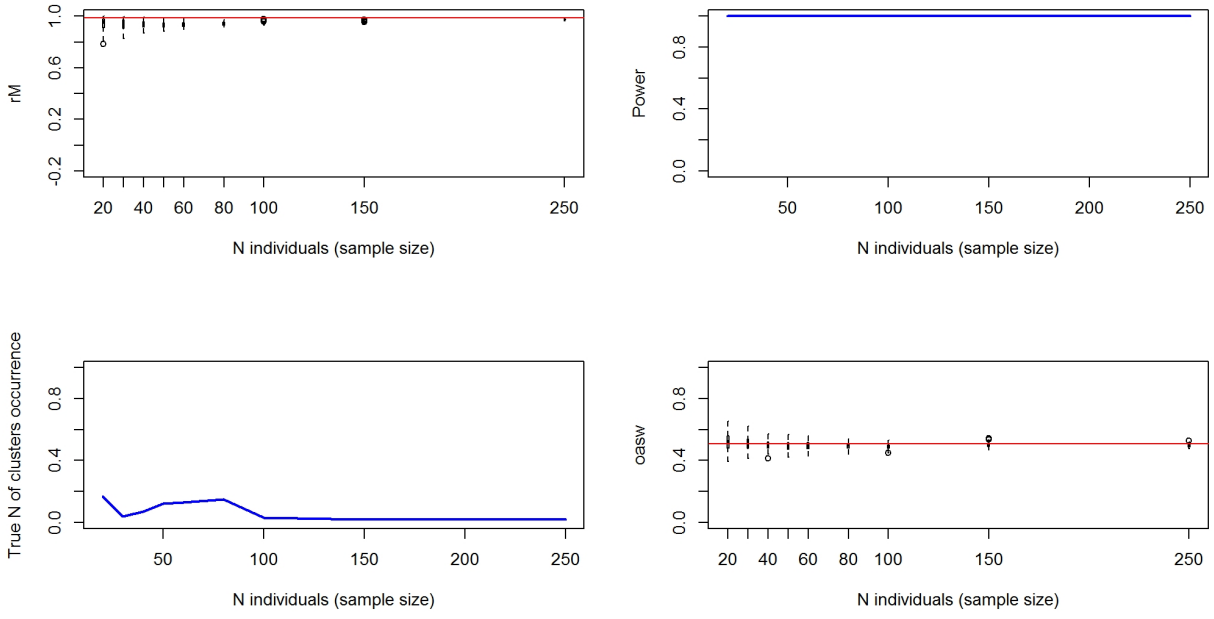

Figure 15390-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 15390-5).

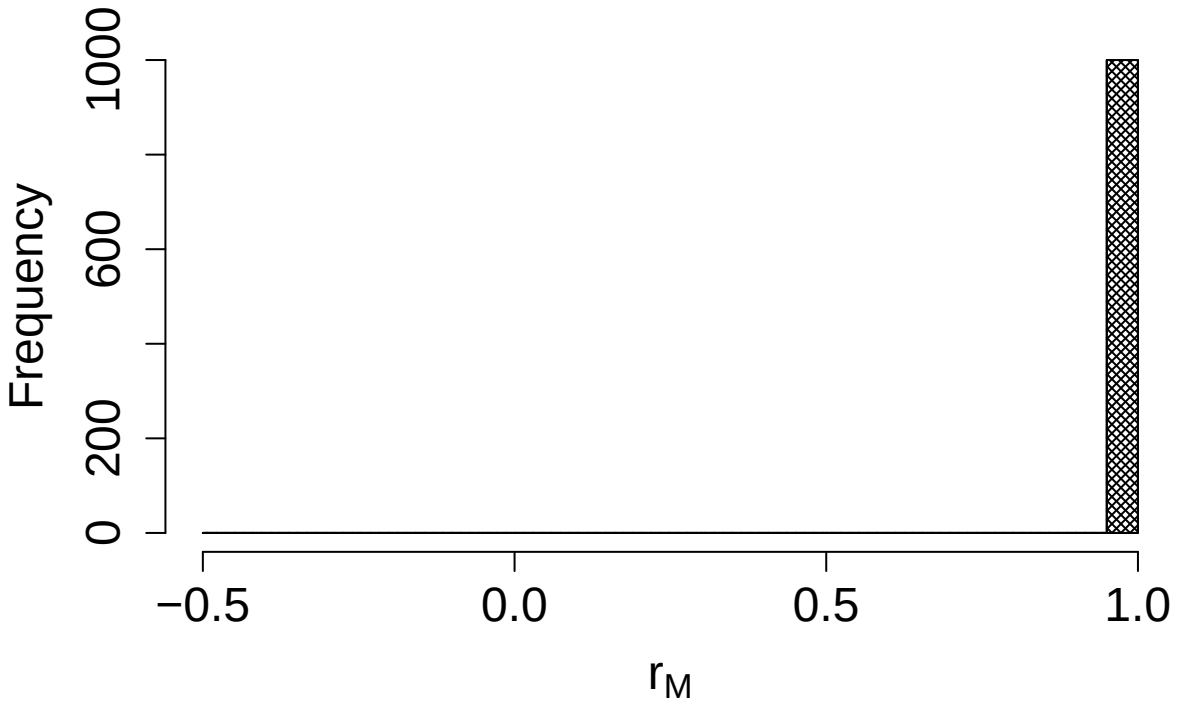

Figure 15390-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows moderate/high connectivity (MC = 0.677; MC = 0.675 when adjusted for absolute abundance) between 7 breeding regions and 7 non breeding regions (Table 15390-2; Figure 15390-6).

Table 15390-2. 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	3266450	Central Europe	0.962
Central Europe	3266450	South-west Europe	0.006
Central Europe	3266450	West Europe	0.032
East Europe	5669718	Central Europe	0.429
East Europe	5669718	East Europe	0.571
North Europe	1097000	Central Europe	0.015
North Europe	1097000	North Europe	0.985
North-west Europe	359999	North-west Europe	1.000
South-central Europe	1571879	South-central Europe	1.000
South-west Europe	3739860	South-west Europe	1.000

Breeding region	Abundance	Non breeding region	Transition probability
West Europe	1198769	Central Europe	0.024
West Europe	1198769	West Europe	0.976

Figure 15390-6. 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.