Migratory connectivity analysis

by EURING Migration Atlas

Anser anser (EURING code 01610)

1.1 Connectivity between individuals

The analysis evaluated 285 individuals (570 encounters) filtered from a total of 196099 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 01610-1; Figure 01610-1).

Table 01610-1. 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	285	0.629	0.001	0.561	0.693	9	0.550
1	1	26	0.297	0.003	0.080	0.621	7	0.549
2	1	85	0.146	0.011	0.028	0.300	9	0.909
3	1	22	-0.107	0.660	-0.178	0.267	-	-
4	1	42	-0.050	0.730	-0.080	0.067	-	-
5	1	19	-	-	-	-	-	-
6	1	27	0.263	0.017	0.072	0.604	5	0.581
7	1	30	0.480	0.001	0.301	0.718	2	0.746
8	1	12	-	-	-	-	-	-
9	1	22	0.056	0.206	-0.047	0.409	-	-
11	2	2	-	-	-	-	-	-
12	2	3	-	-	-	-	-	-
13	2	3	-	-	-	-	-	-
14	2	11	-	-	-	-	-	-
15	2	2	-	-	-	-	-	-
16	2	1	-	-	-	-	-	-
17	2	4	-	-	-	-	-	-
21	2	14	-	-	-	-	-	-
22	2	3	-	-	-	-	-	-
23	2	43	-0.115	1.000	-0.168	-0.069	-	-
24	2	4	-	-	-	-	-	-
25	2	7	-	-	-	-	-	-
26	2	8	-	-	-	-	-	-
27	2	2	-	-	-	-	-	-
28	2	2	-	-	-	-	-	-
29	2	2	-	-	-	-	-	-
61	2	16	-	-	-	-	-	-

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
62	2	4	-	-	-	-	-	-
63	2	2	-	-	-	-	-	-
64	2	1	-	-	-	-	-	-
65	2	4	-	-	-	-	-	-
71	2	29	0.494	0.002	0.192	0.726	7	0.612
72	2	1	-	-	-	-	-	-
711	3	3	-	-	-	-	-	-
712	3	2	-	-	-	-	-	-
713	3	9	-	-	-	-	-	-
714	3	8	-	-	-	-	-	-
715	3	2	-	-	-	-	-	-
716	3	2	-	-	-	-	-	-
717	3	3	-	-	-	-	-	-

Figure 01610-1. 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 01610-2) and stratified sampling of individuals within the breeding range (Figure 01610-3) and the non breeding range (Figure 01610-4). 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.
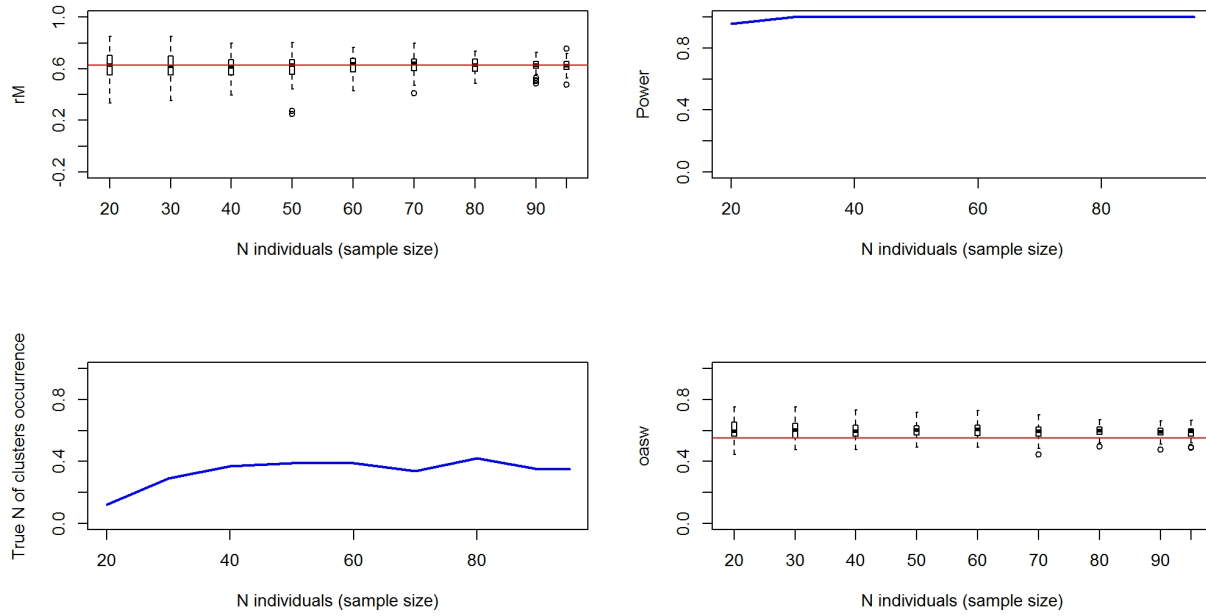

Figure 01610-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
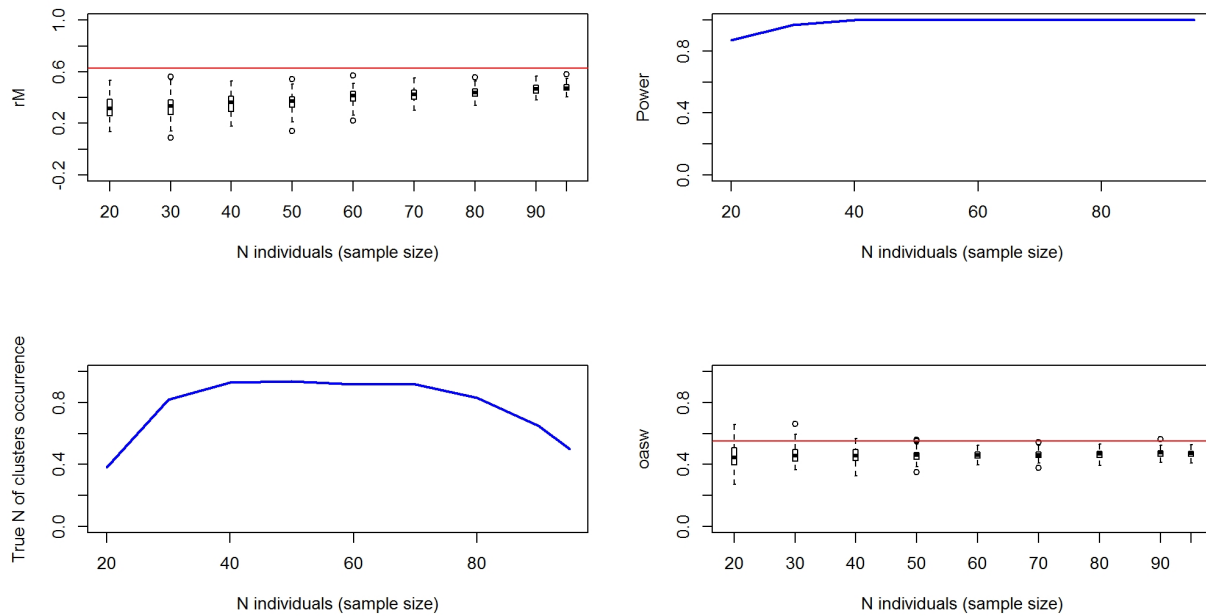

Figure 01610-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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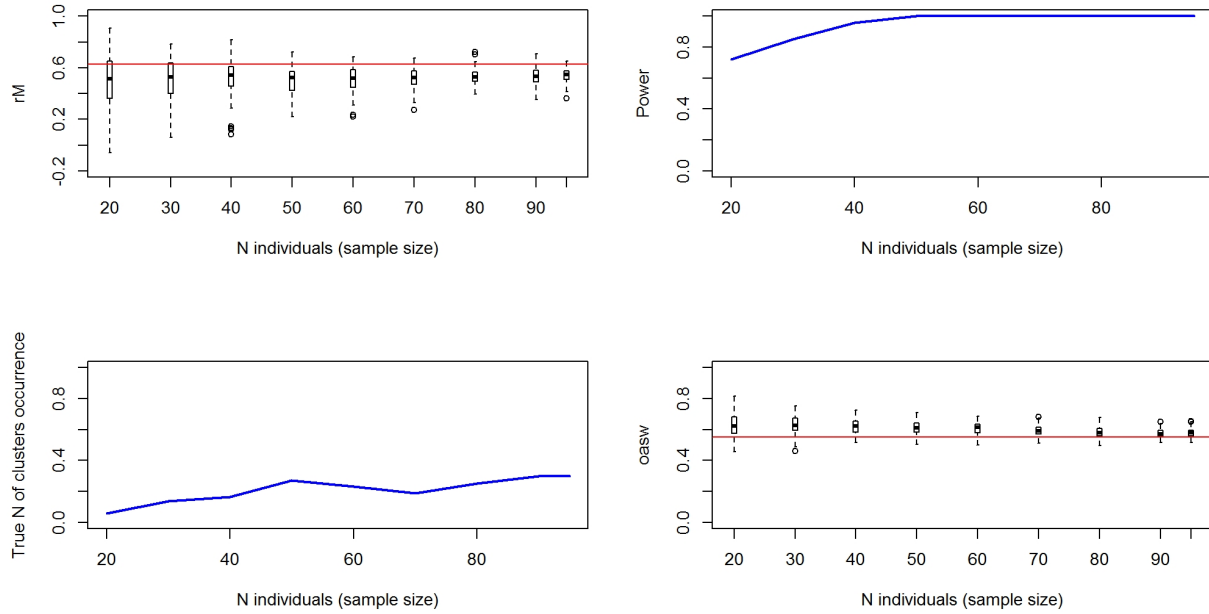

Figure 01610-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 = 0.654); Figure 01610-5).
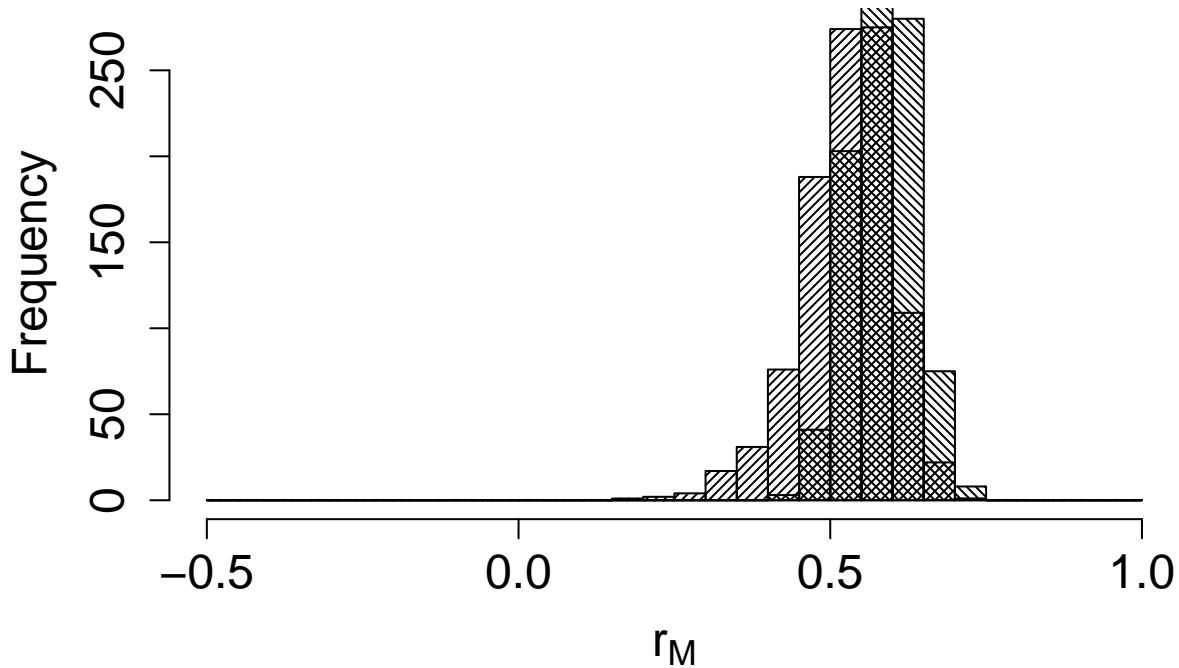
Figure 01610-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows moderate/high connectivity (MC = 0.63; MC = 0.627 when adjusted for absolute abundance) between 5 breeding regions and 7 non breeding regions (Table 01610-2; Figure 01610-6).

Table 01610-2. 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	86798	Central Europe	0.094
Central Europe	86798	North Africa	0.443
Central Europe	86798	South-central Europe	0.333
Central Europe	86798	South-west Europe	0.052
Central Europe	86798	West Europe	0.078
East Europe	59400	North Africa	0.333
East Europe	59400	South-central Europe	0.667
North Europe	146854	North Africa	0.061
North Europe	146854	South-east Europe	0.041
North Europe	146854	South-west Europe	0.367
North Europe	146854	West Europe	0.531
North-west Europe	142000	North-west Europe	1.000
West Europe	236764	South-central Europe	0.111

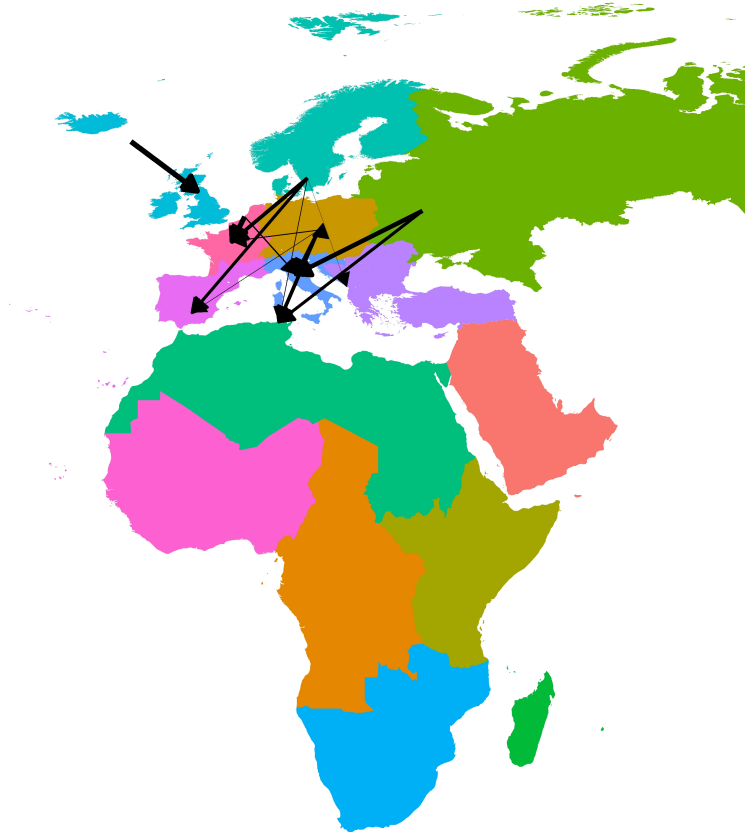| Breeding region	Abundance	Non breeding region	Transition probability
West Europe	236764	West Europe	0.889

Figure 01610-6. 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.