

# Migratory connectivity analysis

by EURING Migration Atlas

*Tadorna tadorna* (EURING code 01730)

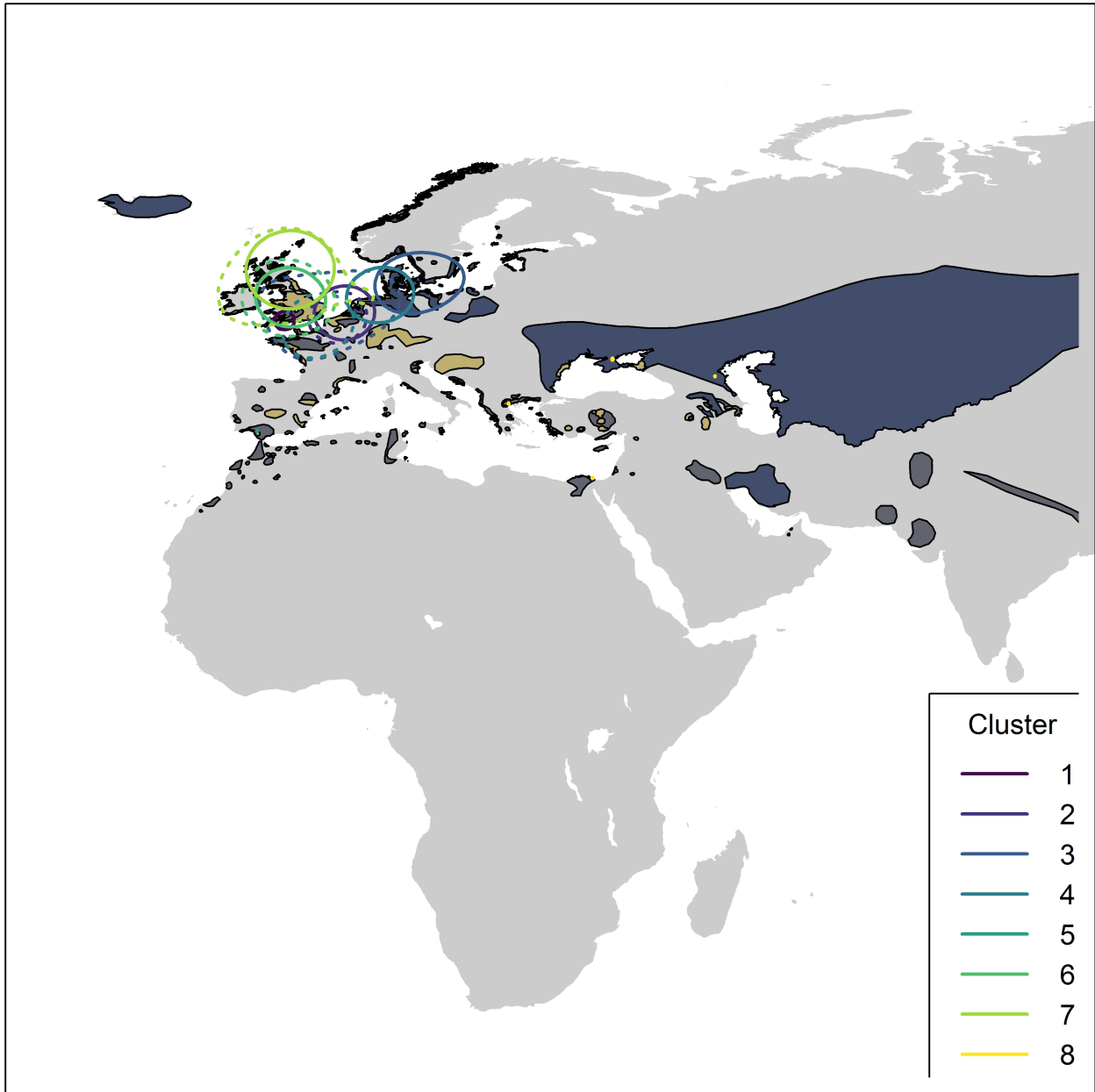
## 1.1 Connectivity between individuals

The analysis evaluated 335 individuals (670 encounters) filtered from a total of 16182 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 = 8 (Table 01730-1; Figure 01730-1).

**Table 01730-1.** 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	335	0.750	0.001	0.538	0.857	8	0.555
1	1	124	0.841	0.001	0.726	0.995	7	0.931
2	1	67	0.361	0.032	-0.040	0.836	9	0.560
3	1	33	0.128	0.075	0.049	0.365	4	0.428
4	1	36	0.046	0.300	-0.089	0.308	-	-
5	1	2	-	-	-	-	-	-
6	1	50	0.558	0.001	0.374	0.816	9	0.674
7	1	21	0.147	0.229	-0.202	0.540	-	-
8	1	2	-	-	-	-	-	-
11	2	1	-	-	-	-	-	-
12	2	1	-	-	-	-	-	-
13	2	114	-0.026	1.000	-0.061	-0.013	-	-
14	2	2	-	-	-	-	-	-
15	2	3	-	-	-	-	-	-
16	2	1	-	-	-	-	-	-
17	2	2	-	-	-	-	-	-
21	2	28	0.456	0.003	0.176	0.857	3	0.623
22	2	7	-	-	-	-	-	-
23	2	8	-	-	-	-	-	-
24	2	1	-	-	-	-	-	-
25	2	13	-	-	-	-	-	-
26	2	1	-	-	-	-	-	-
27	2	3	-	-	-	-	-	-
28	2	5	-	-	-	-	-	-
29	2	1	-	-	-	-	-	-
61	2	31	0.533	0.017	0.064	0.999	3	0.867
62	2	2	-	-	-	-	-	-

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
63	2	5	-	-	-	-	-	-
64	2	3	-	-	-	-	-	-
65	2	2	-	-	-	-	-	-
66	2	2	-	-	-	-	-	-
67	2	2	-	-	-	-	-	-
68	2	2	-	-	-	-	-	-
69	2	1	-	-	-	-	-	-
211	3	7	-	-	-	-	-	-
212	3	18	-	-	-	-	-	-
213	3	3	-	-	-	-	-	-
611	3	28	0.060	0.101	-0.070	1.000	-	-
612	3	2	-	-	-	-	-	-
613	3	1	-	-	-	-	-	-

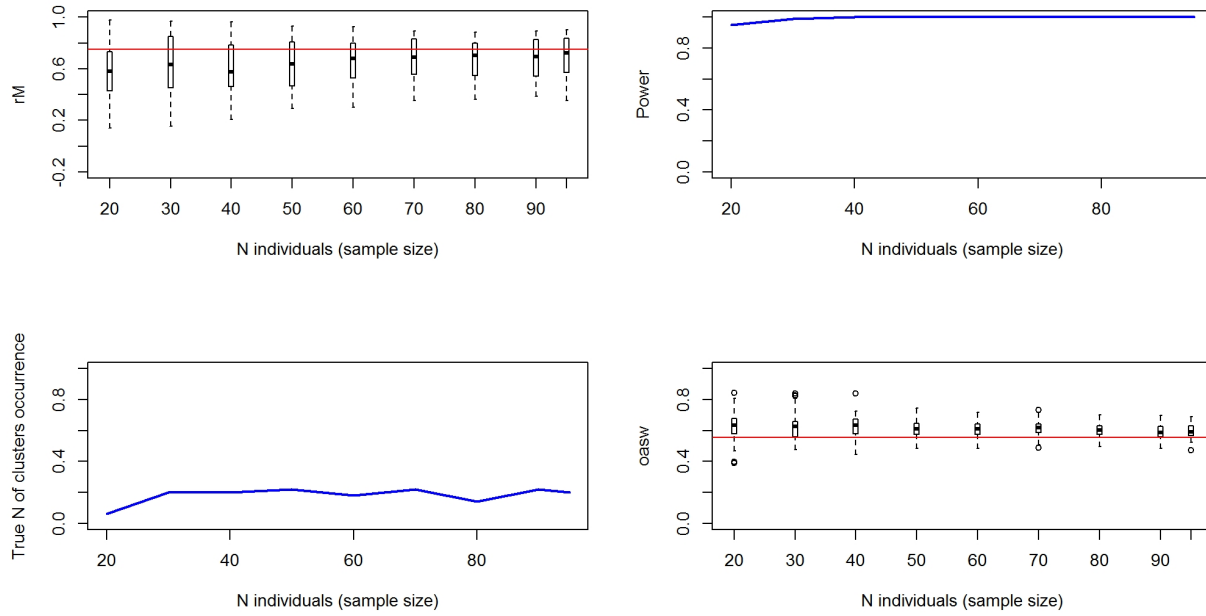


**Figure 01730-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

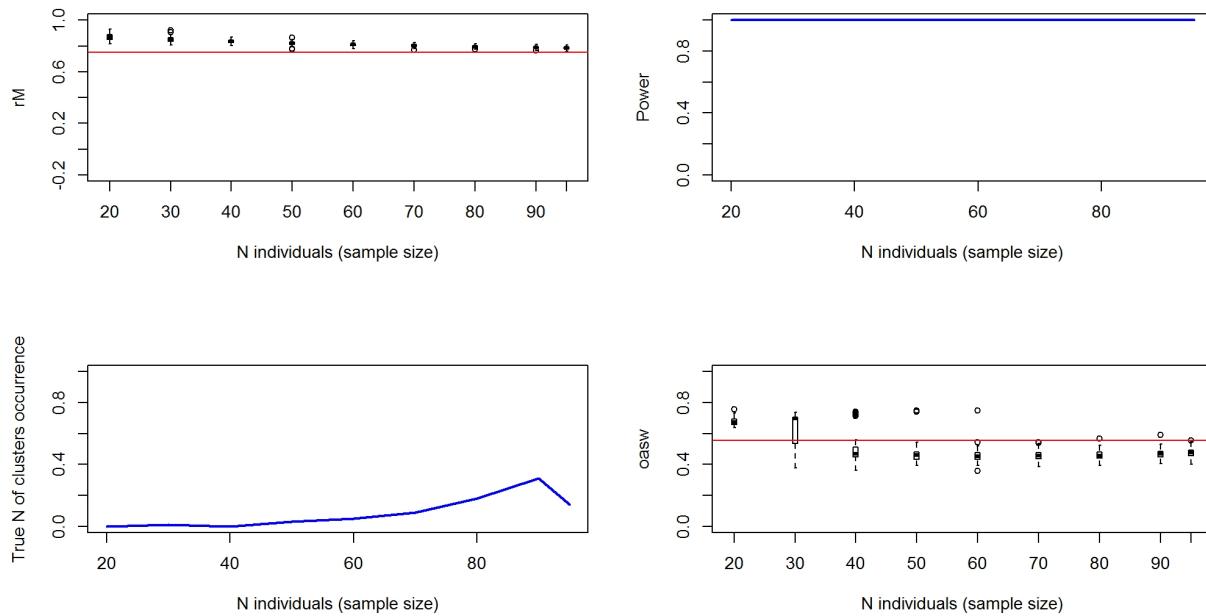
## 1.2 Sensitivity analysis

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 01730-2) and stratified sampling of individuals within the breeding range (Figure 01730-3) and the non breeding range (Figure 01730-4). 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.

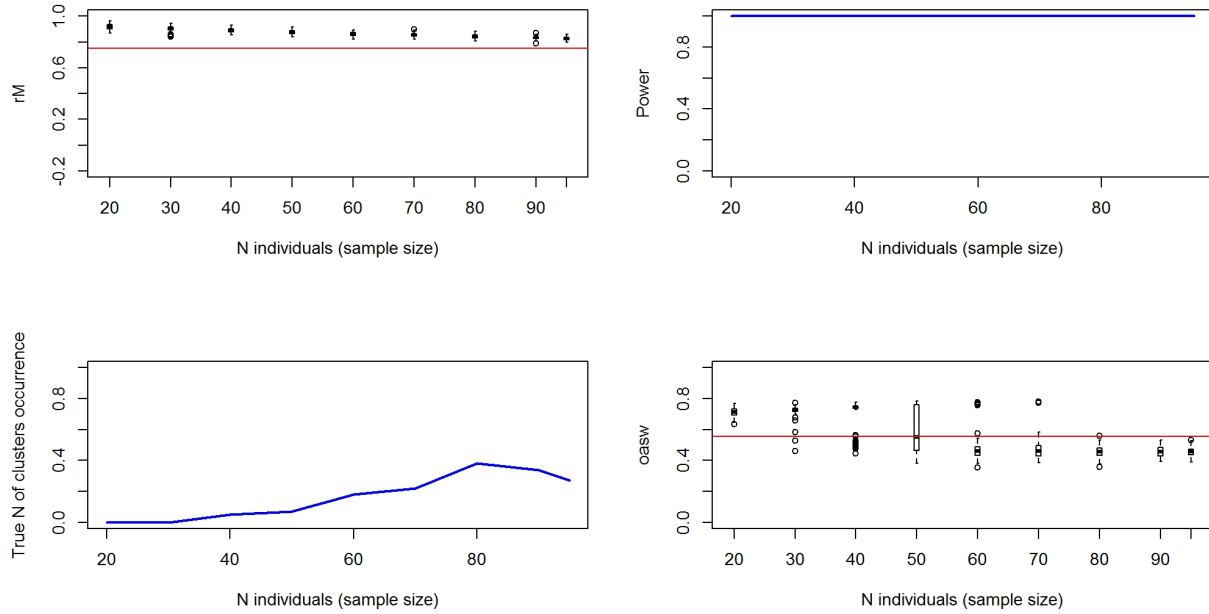


**Figure 01730-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



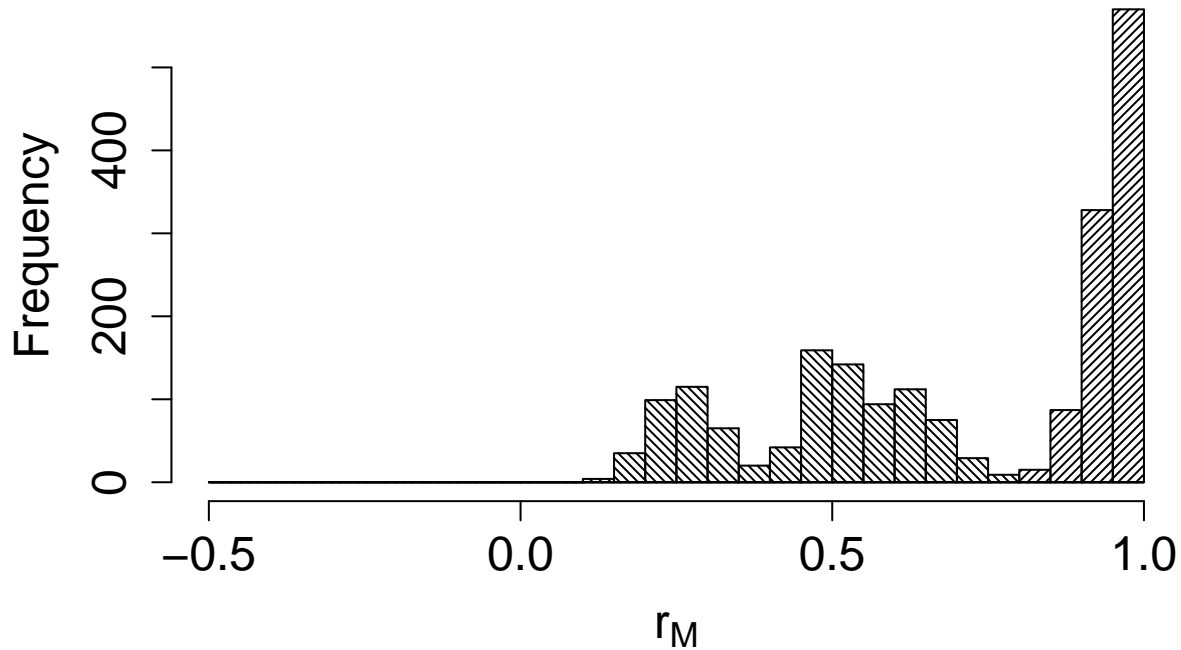
**Figure 01730-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 01730-4.** 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 01730-5).



**Figure 01730-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

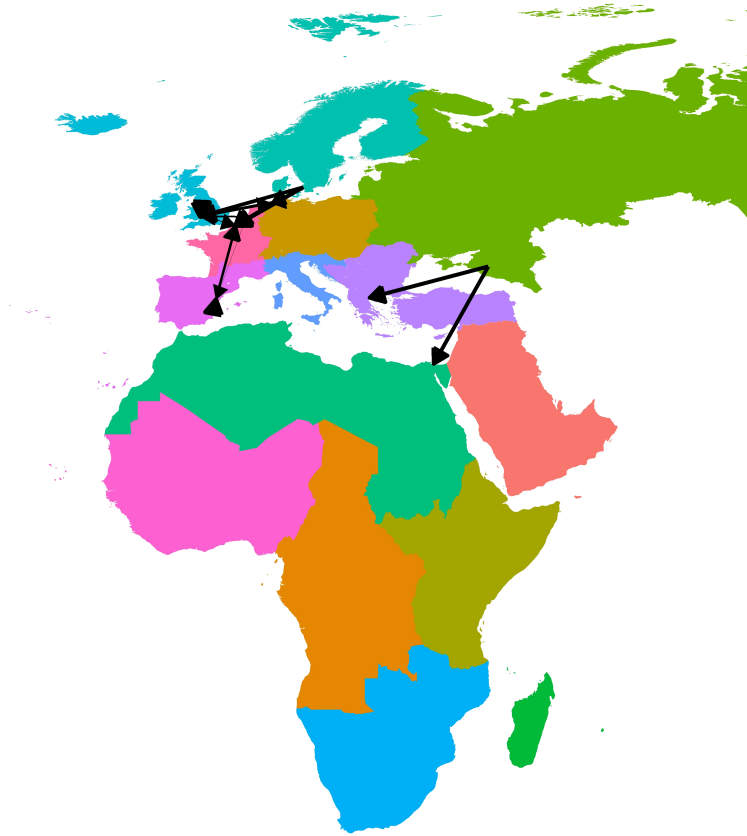
## 2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 0.874; MC = 0.874 when adjusted for absolute abundance) between 6 breeding regions and 6 non breeding regions (Table 01730-2; Figure 01730-6).

**Table 01730-2.** 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	14840	Central Europe	0.094
Central Europe	14840	North-west Europe	0.281
Central Europe	14840	West Europe	0.625
East Europe	18528	North Africa	0.500
East Europe	18528	South-east Europe	0.500
North Europe	23650	Central Europe	0.033
North Europe	23650	North-west Europe	0.467
North Europe	23650	West Europe	0.500
North-west Europe	32056	Central Europe	0.010
North-west Europe	32056	North-west Europe	0.955
North-west Europe	32056	West Europe	0.035
South-west Europe	4096	South-west Europe	0.750
South-west Europe	4096	West Europe	0.250

Breeding region	Abundance	Non breeding region	Transition probability
West Europe	21074	North-west Europe	0.116
West Europe	21074	South-west Europe	0.014
West Europe	21074	West Europe	0.870



**Figure 01730-6.** 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>.