

# Migratory connectivity analysis

by EURING Migration Atlas

*Troglodytes troglodytes* (EURING code 10660)

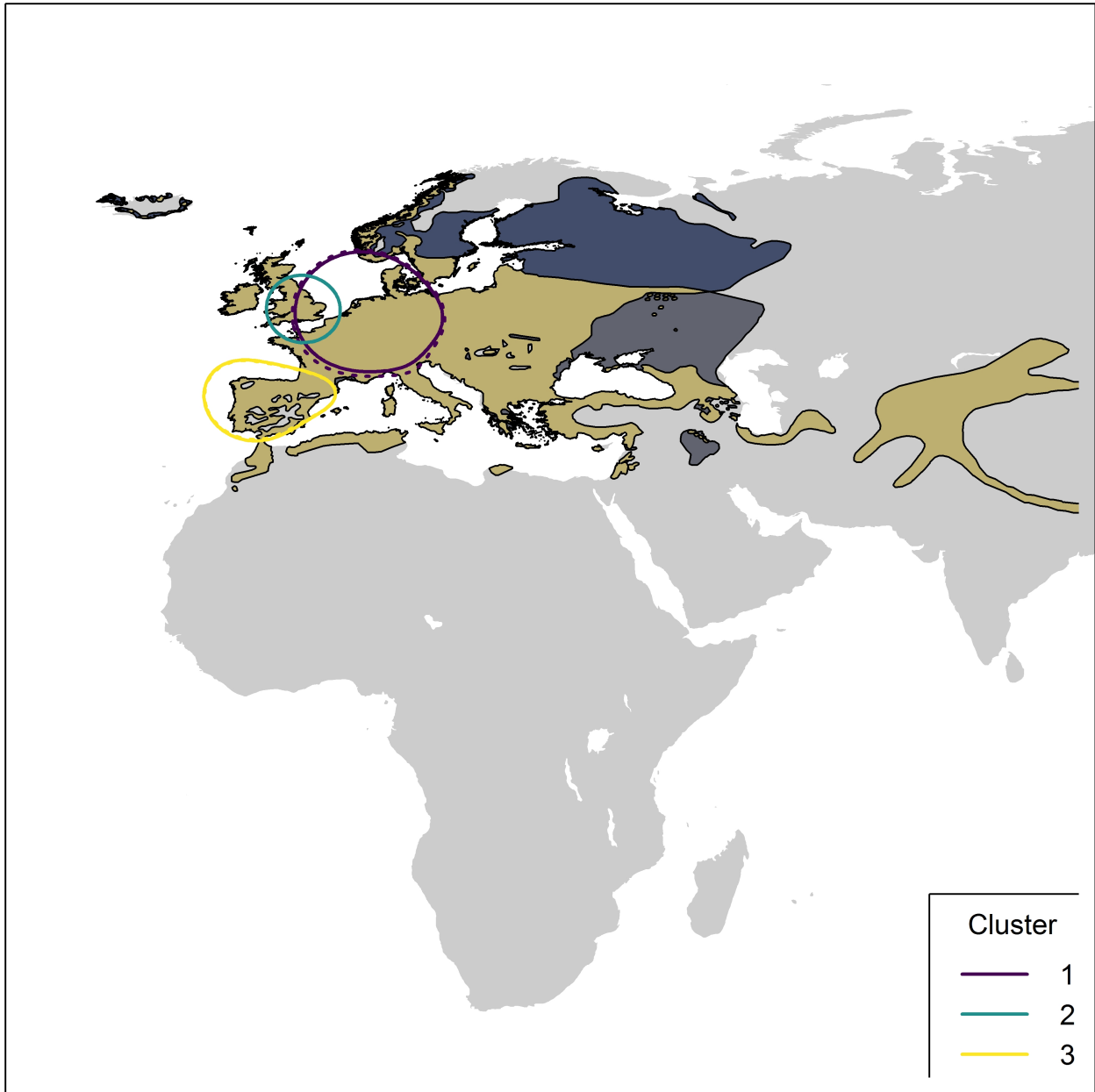
## 1.1 Connectivity between individuals

The analysis evaluated 3310 individuals (6620 encounters) filtered from a total of 294954 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 10660-1; Figure 10660-1).

**Table 10660-1.** 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	3310	0.991	0.001	0.987	0.994	3	0.576
1	1	737	0.949	0.001	0.921	0.976	2	0.648
2	1	2425	0.990	0.001	0.983	0.995	7	0.453
3	1	148	0.985	0.001	0.951	1.000	7	0.734
11	2	617	0.856	0.001	0.740	0.950	9	0.469
12	2	120	0.787	0.001	0.691	0.903	8	0.585
31	2	25	1.000	0.001	1.000	1.000	9	0.876
32	2	42	1.000	0.001	1.000	1.000	8	0.872
33	2	19	-	-	-	-	-	-
34	2	12	-	-	-	-	-	-
35	2	5	-	-	-	-	-	-
36	2	26	0.963	0.001	0.909	1.000	5	0.736
37	2	19	-	-	-	-	-	-
121	3	20	0.521	0.008	0.365	1.000	2	0.695
122	3	6	-	-	-	-	-	-
123	3	31	0.994	0.001	0.991	1.000	8	0.670
124	3	17	-	-	-	-	-	-
125	3	14	-	-	-	-	-	-
126	3	14	-	-	-	-	-	-
127	3	12	-	-	-	-	-	-
128	3	6	-	-	-	-	-	-
311	3	1	-	-	-	-	-	-
312	3	2	-	-	-	-	-	-
313	3	3	-	-	-	-	-	-
314	3	4	-	-	-	-	-	-
315	3	7	-	-	-	-	-	-
316	3	4	-	-	-	-	-	-

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
317	3	2	-	-	-	-	-	-
318	3	1	-	-	-	-	-	-
319	3	1	-	-	-	-	-	-
321	3	3	-	-	-	-	-	-
322	3	7	-	-	-	-	-	-
323	3	1	-	-	-	-	-	-
324	3	1	-	-	-	-	-	-
325	3	24	1.000	0.051	1.000	1.000	2	0.958
326	3	1	-	-	-	-	-	-
327	3	4	-	-	-	-	-	-
328	3	1	-	-	-	-	-	-
361	3	19	-	-	-	-	-	-
362	3	1	-	-	-	-	-	-
363	3	2	-	-	-	-	-	-
364	3	3	-	-	-	-	-	-
365	3	1	-	-	-	-	-	-

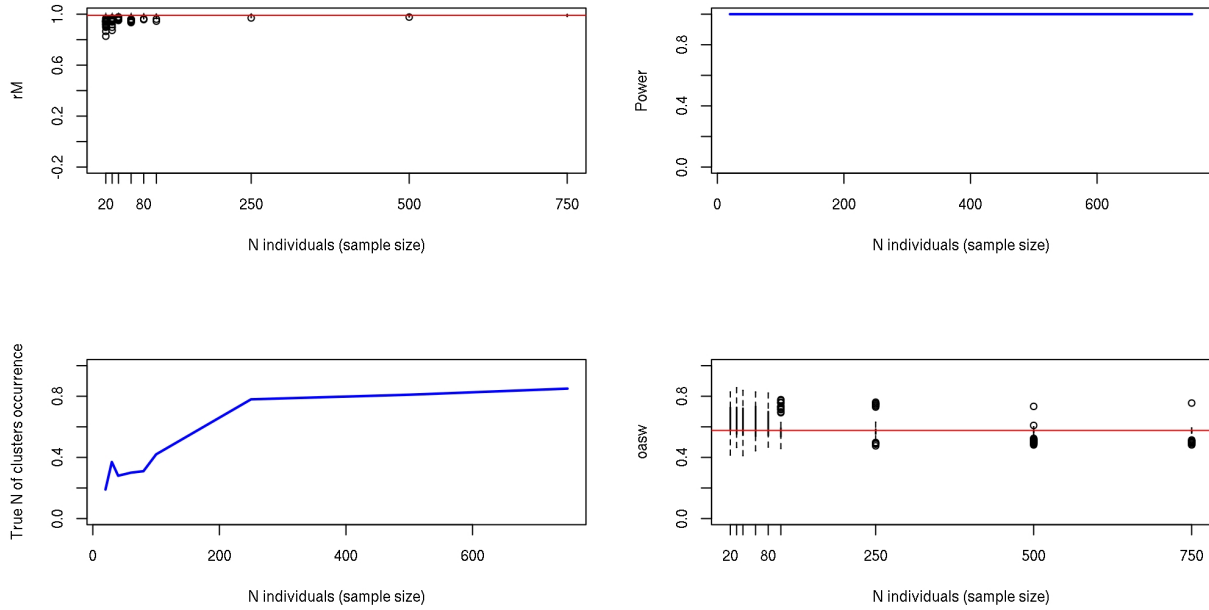


**Figure 10660-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

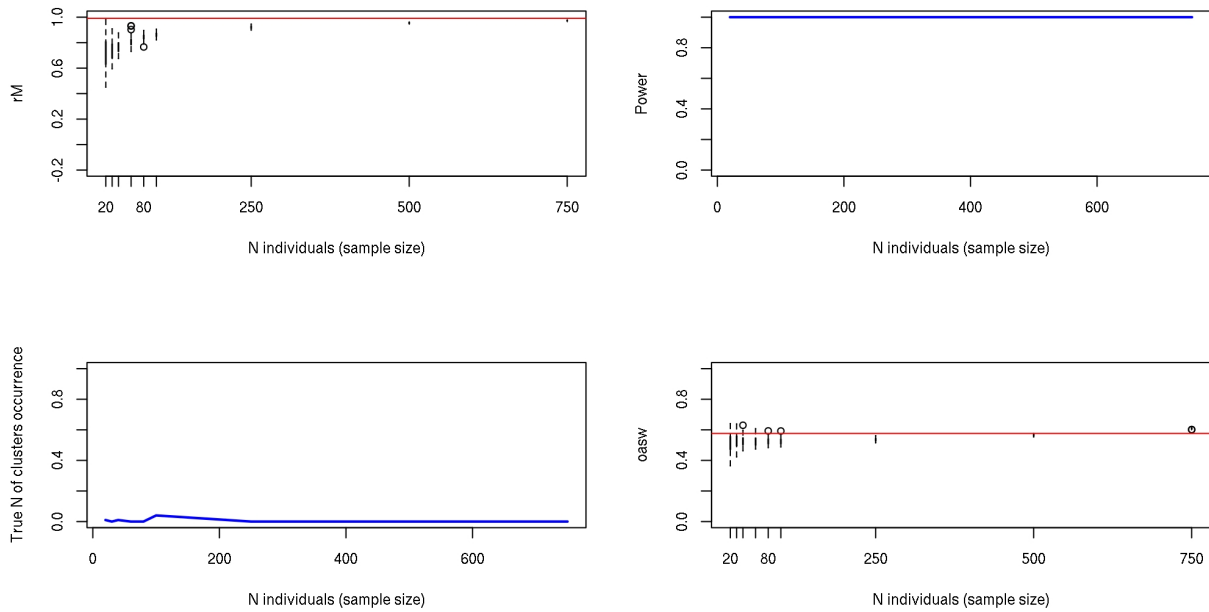
## 1.2 Sensitivity analysis

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 10660-2) and stratified sampling of individuals within the breeding range (Figure 10660-3) and the non breeding range (Figure 10660-4). 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.

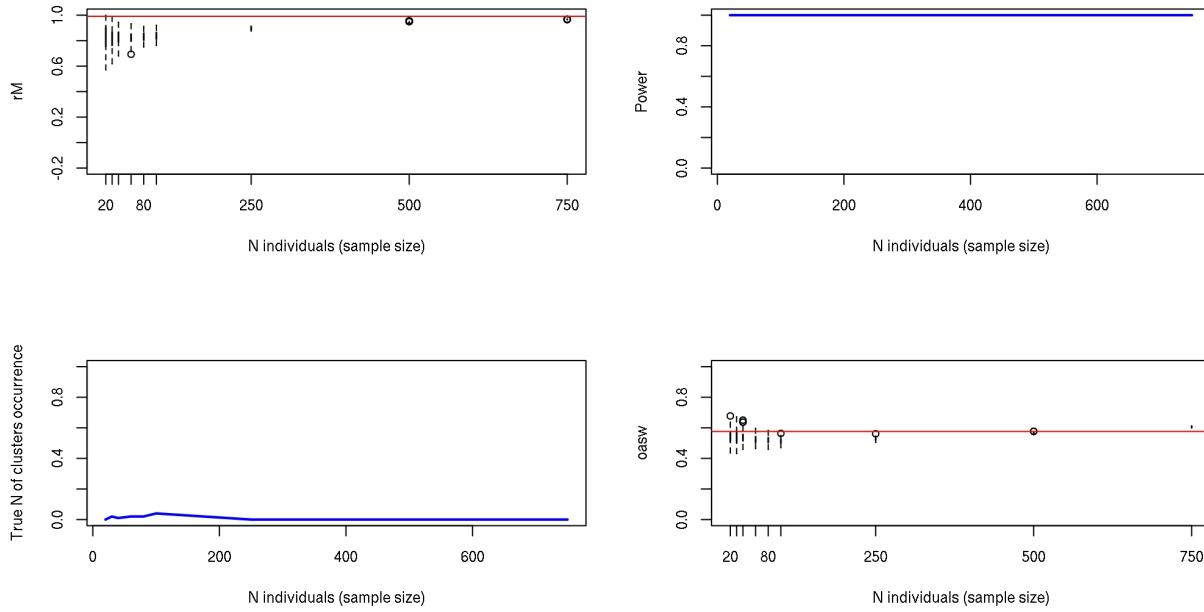


**Figure 10660-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



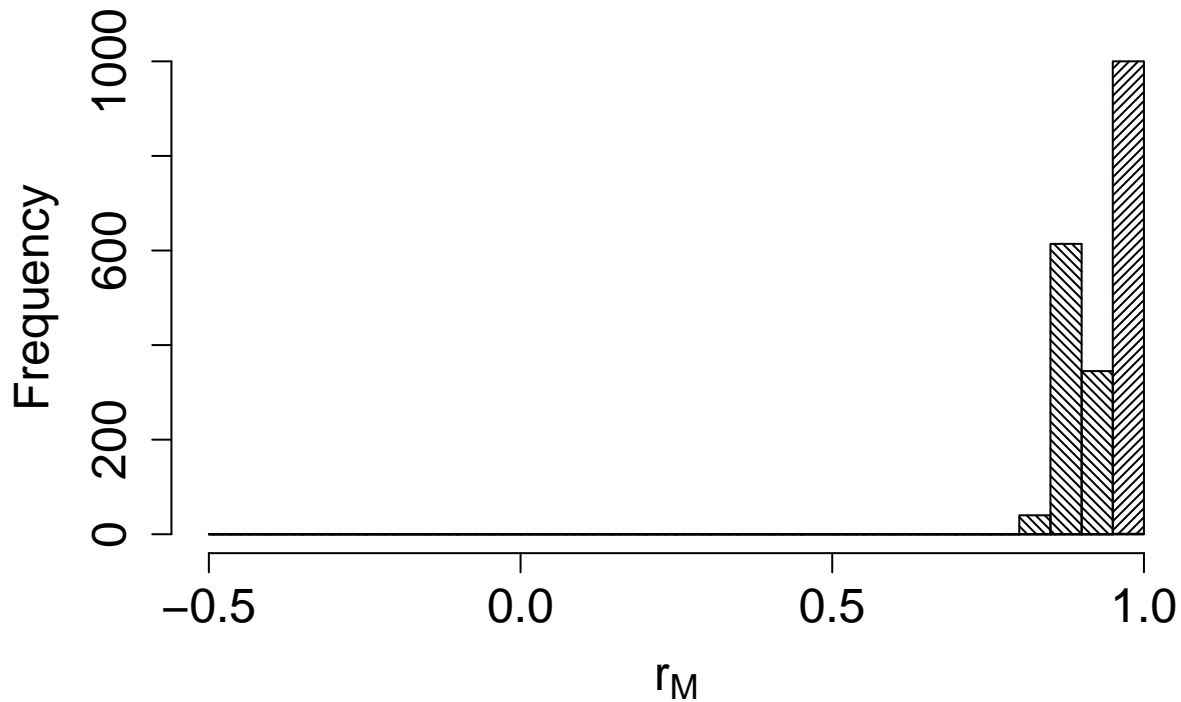
**Figure 10660-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 10660-4.** 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 10660-5).



**Figure 10660-5.** 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 = 0.959; MC = 0.959 when adjusted for absolute abundance) between 6 breeding regions and 6 non breeding regions (Table 10660-2; Figure 10660-6).

**Table 10660-2.** 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	9016600	Central Europe	0.933
Central Europe	9016600	South-west Europe	0.017
Central Europe	9016600	West Europe	0.050
North Europe	2222450	North Europe	0.583
North Europe	2222450	South-west Europe	0.250
North Europe	2222450	West Europe	0.167
North-west Europe	34125928	North-west Europe	1.000
North-west Europe	34125928	West Europe	0.000
South-central Europe	4174622	South-central Europe	1.000
South-west Europe	15520784	South-west Europe	1.000
West Europe	9755799	Central Europe	0.002
West Europe	9755799	South-west Europe	0.003
West Europe	9755799	West Europe	0.995



**Figure 10660-6.** 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>.