

# Migratory connectivity analysis

by EURING Migration Atlas

*Certhia brachydactyla* (EURING code 14870)

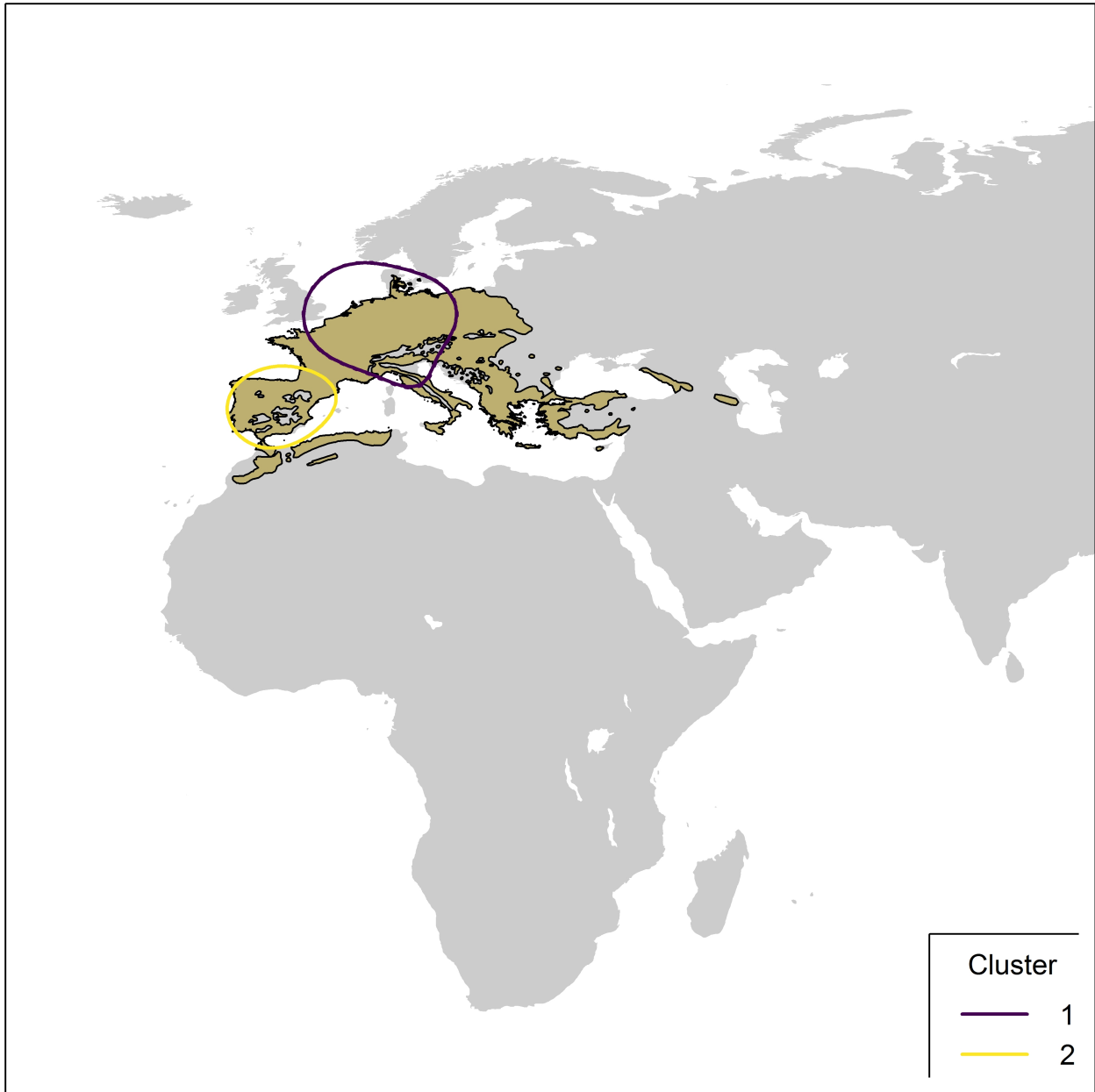
## 1.1 Connectivity between individuals

The analysis evaluated 1903 individuals (3806 encounters) filtered from a total of 22115 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 14870-1; Figure 14870-1).

**Table 14870-1.** 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	1903	1.000	0.001	0.999	1.000	2	0.706
1	1	1150	0.999	0.001	0.998	1.000	2	0.636
2	1	753	0.996	0.001	0.990	0.999	7	0.714
11	2	968	0.998	0.001	0.995	1.000	2	0.627
12	2	182	1.000	0.001	0.999	1.000	3	0.649
21	2	115	1.000	0.001	1.000	1.000	2	0.663
22	2	102	0.929	0.001	0.795	1.000	6	0.723
23	2	29	0.999	0.001	0.997	1.000	8	0.882
24	2	59	0.996	0.001	0.987	1.000	9	0.825
25	2	311	1.000	0.001	0.999	1.000	9	0.672
26	2	66	0.746	0.001	0.532	0.999	8	0.807
27	2	71	1.000	0.001	1.000	1.000	9	0.830
111	3	664	0.993	0.001	0.981	1.000	2	0.490
112	3	304	0.998	0.001	0.992	1.000	7	0.589
121	3	82	1.000	0.001	1.000	1.000	8	0.762
122	3	12	-	-	-	-	-	-
123	3	88	0.995	0.001	0.988	1.000	9	0.744
211	3	13	-	-	-	-	-	-
212	3	102	1.000	0.001	0.999	1.000	9	0.617
221	3	42	1.000	0.001	1.000	1.000	9	0.952
222	3	9	-	-	-	-	-	-
223	3	28	0.911	0.001	0.884	1.000	8	0.828
224	3	11	-	-	-	-	-	-
225	3	6	-	-	-	-	-	-
226	3	6	-	-	-	-	-	-
231	3	2	-	-	-	-	-	-
232	3	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
233	3	12	-	-	-	-	-	-
234	3	1	-	-	-	-	-	-
235	3	6	-	-	-	-	-	-
236	3	1	-	-	-	-	-	-
237	3	3	-	-	-	-	-	-
238	3	2	-	-	-	-	-	-
241	3	2	-	-	-	-	-	-
242	3	6	-	-	-	-	-	-
243	3	17	-	-	-	-	-	-
244	3	5	-	-	-	-	-	-
245	3	3	-	-	-	-	-	-
246	3	9	-	-	-	-	-	-
247	3	4	-	-	-	-	-	-
248	3	9	-	-	-	-	-	-
249	3	4	-	-	-	-	-	-
251	3	7	-	-	-	-	-	-
252	3	14	-	-	-	-	-	-
253	3	63	0.982	0.001	0.940	1.000	8	0.977
254	3	4	-	-	-	-	-	-
255	3	60	0.982	0.001	0.945	1.000	7	0.975
256	3	122	0.960	0.001	0.920	0.988	9	0.890
257	3	18	-	-	-	-	-	-
258	3	19	-	-	-	-	-	-
259	3	4	-	-	-	-	-	-
261	3	11	-	-	-	-	-	-
262	3	13	-	-	-	-	-	-
263	3	21	0.998	0.001	0.986	1.000	8	0.652
264	3	8	-	-	-	-	-	-
265	3	2	-	-	-	-	-	-
266	3	1	-	-	-	-	-	-
267	3	7	-	-	-	-	-	-
268	3	3	-	-	-	-	-	-
271	3	1	-	-	-	-	-	-
272	3	22	1.000	0.001	1.000	1.000	3	0.946
273	3	1	-	-	-	-	-	-
274	3	9	-	-	-	-	-	-
275	3	8	-	-	-	-	-	-
276	3	8	-	-	-	-	-	-
277	3	9	-	-	-	-	-	-
278	3	4	-	-	-	-	-	-
279	3	9	-	-	-	-	-	-

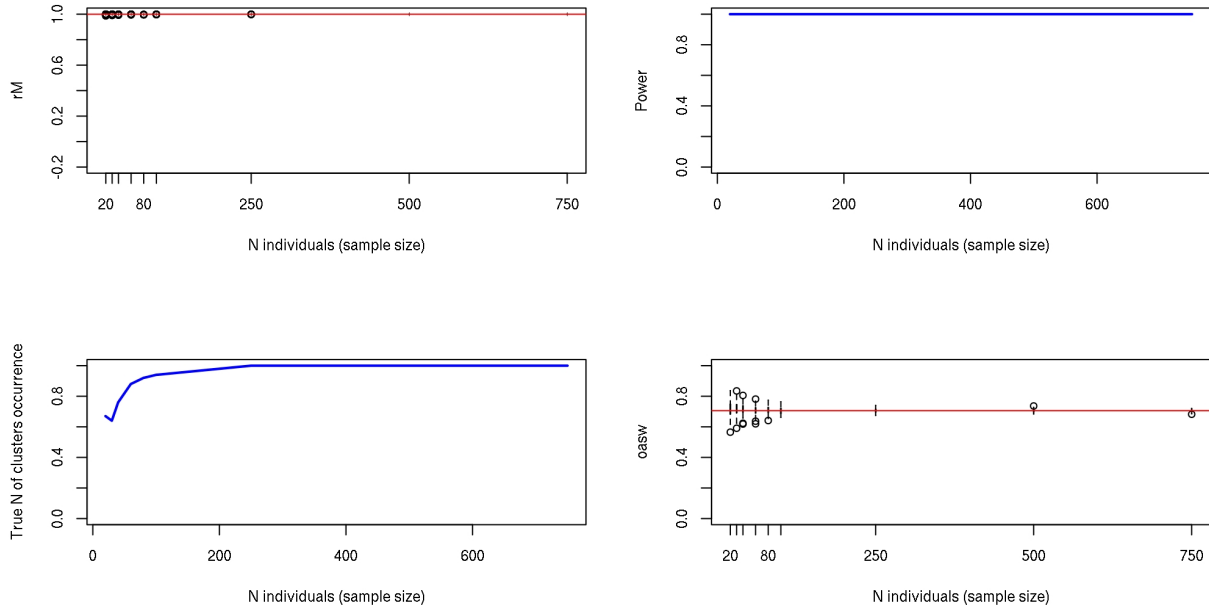


**Figure 14870-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

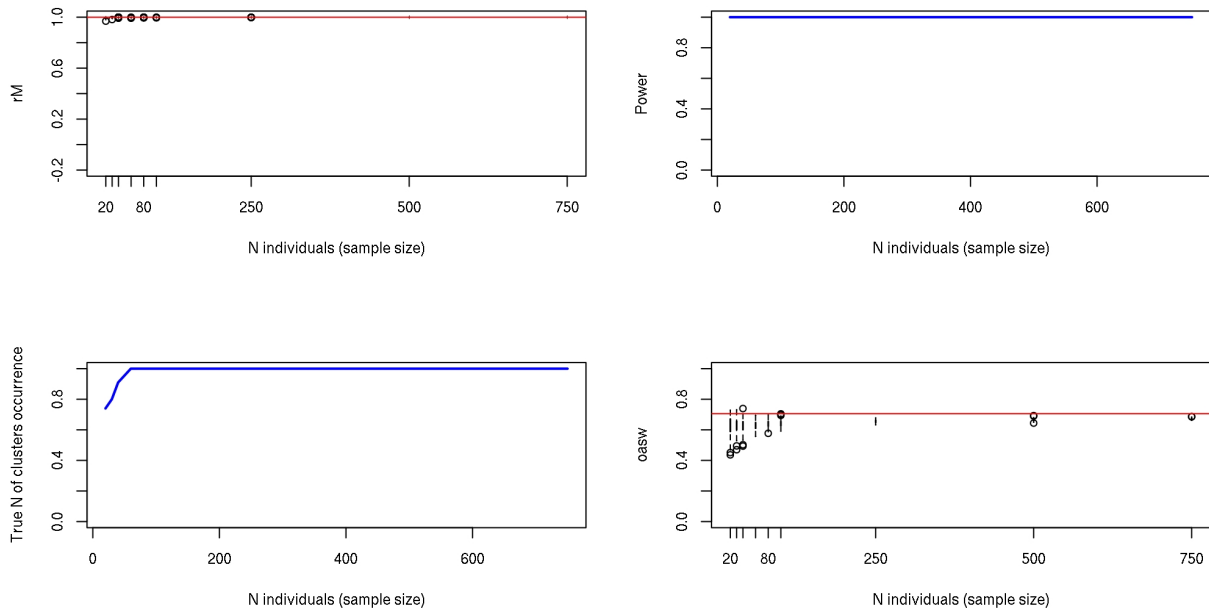
## 1.2 Sensitivity analysis

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 14870-2) and stratified sampling of individuals within the breeding range (Figure 14870-3) and the non breeding range (Figure 14870-4). 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.

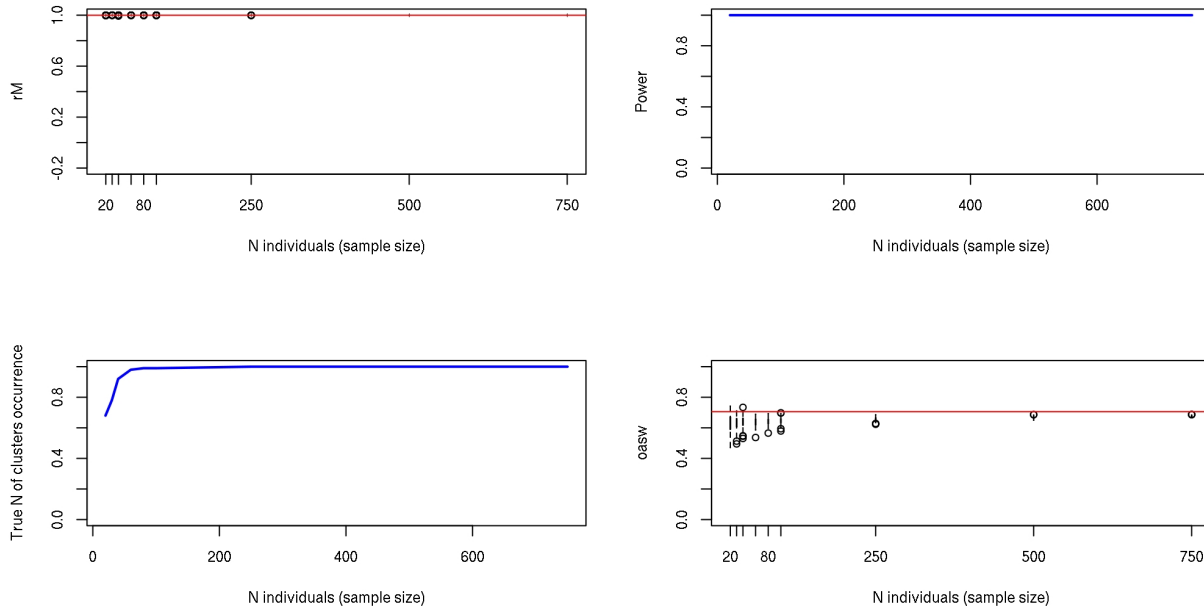


**Figure 14870-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



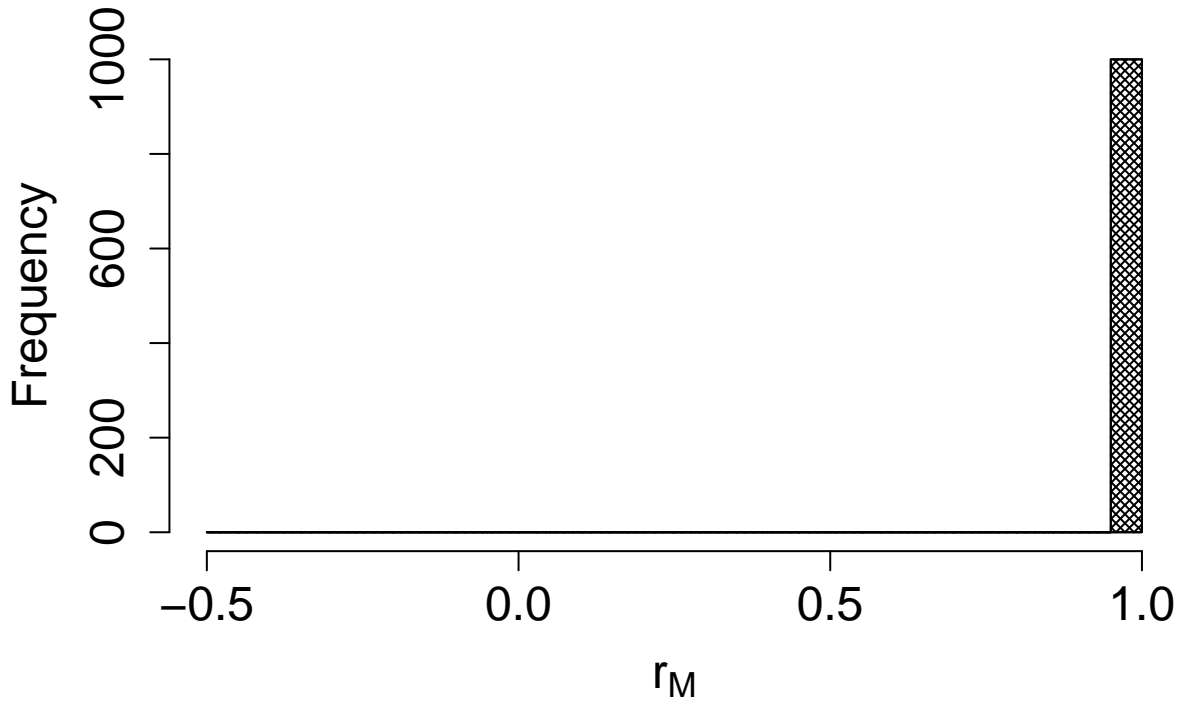
**Figure 14870-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 14870-4.** 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 14870-5).



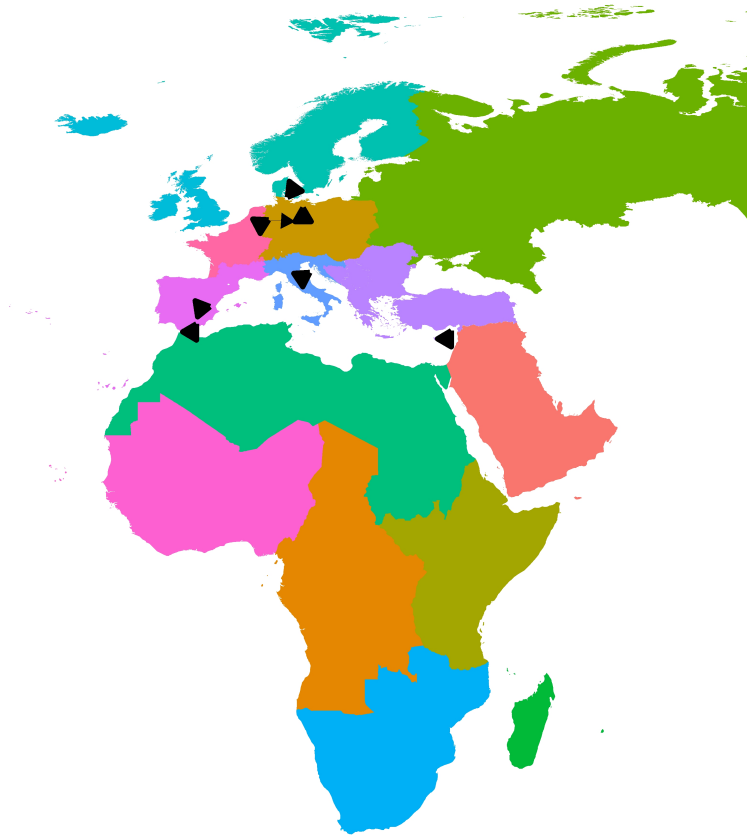
**Figure 14870-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

## 2. Connectivity between pre-defined regions

The species shows high connectivity ( $MC = 1$ ;  $MC = 1$  when adjusted for absolute abundance) between 7 breeding regions and 7 non breeding regions (Table 14870-2; Figure 14870-6).

**Table 14870-2.** 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	1513780	Central Europe	1.000
North Africa	1000	North Africa	1.000
North Europe	3000	North Europe	1.000
South-central Europe	1650000	South-central Europe	1.000
South-east Europe	1092250	South-east Europe	1.000
South-west Europe	7228981	South-west Europe	1.000
West Europe	2314584	Central Europe	0.002
West Europe	2314584	West Europe	0.998



**Figure 14870-6.** 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>.