

# Migratory connectivity analysis

by EURING Migration Atlas

*Certhia familiaris* (EURING code 14860)

## 1.1 Connectivity between individuals

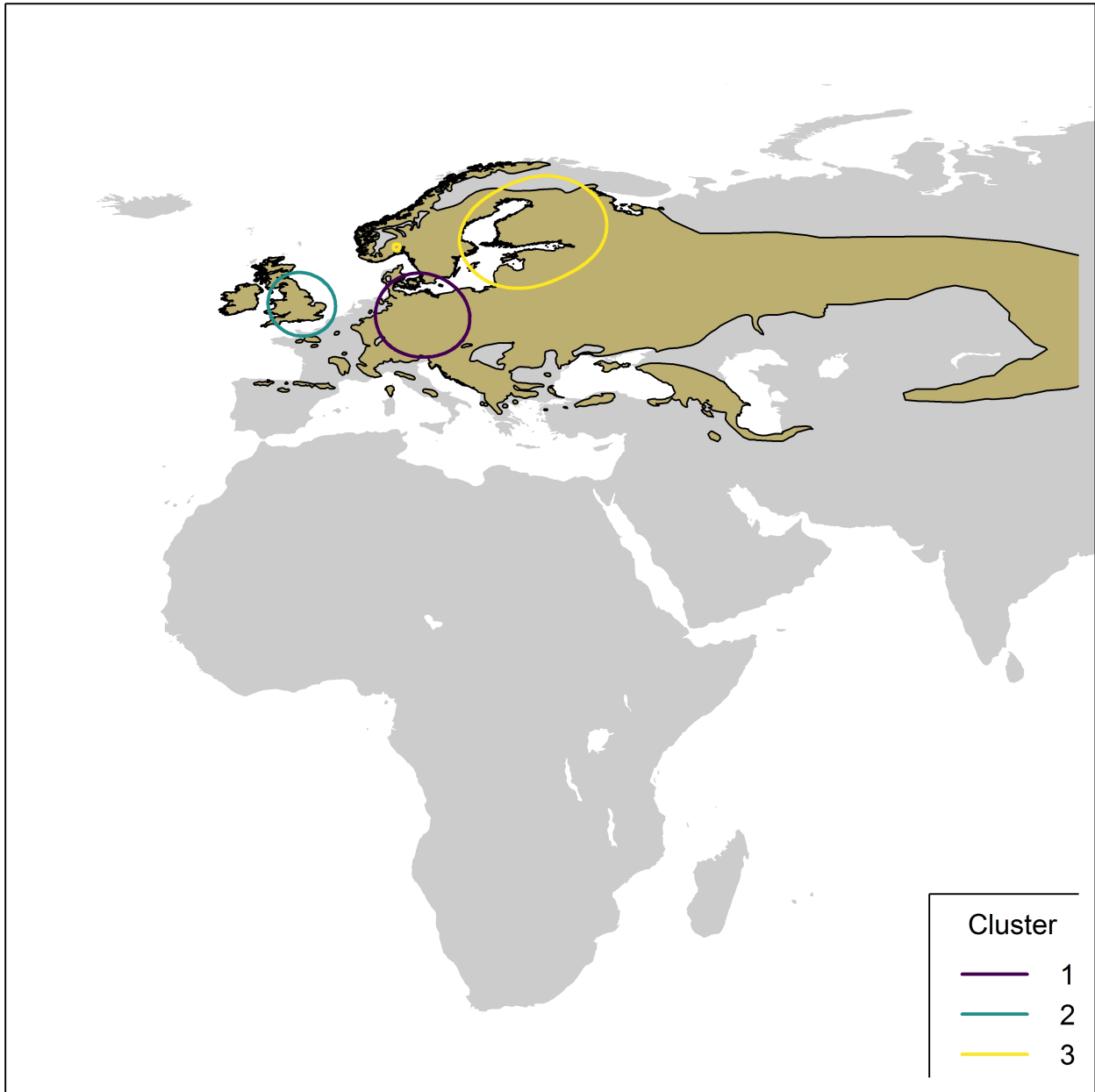
The analysis evaluated 558 individuals (1116 encounters) filtered from a total of 47573 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from clustering, with a number of first-level clusters = 3 (Table 14860-1; Figure 14860-1).

**Table 14860-1.** 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	558	1.000	0.001	1.000	1	3	0.781
1	1	66	0.998	0.001	0.993	1	4	0.575
2	1	460	1.000	0.001	1.000	1	8	0.587
3	1	32	1.000	0.001	1.000	1	9	0.779
11	2	19	-	-	-	-	-	-
12	2	42	0.997	0.001	0.980	1	8	0.780
13	2	3	-	-	-	-	-	-
14	2	2	-	-	-	-	-	-
21	2	45	1.000	0.001	1.000	1	9	0.862
22	2	110	1.000	0.001	0.999	1	9	0.770
23	2	138	1.000	0.001	1.000	1	8	0.941
24	2	29	1.000	0.001	1.000	1	2	0.554
25	2	31	1.000	0.001	1.000	1	9	0.632
26	2	45	1.000	0.001	1.000	1	8	0.648
27	2	40	0.999	0.001	0.997	1	9	0.616
28	2	22	0.998	0.001	0.982	1	2	0.848
31	2	3	-	-	-	-	-	-
32	2	9	-	-	-	-	-	-
33	2	1	-	-	-	-	-	-
34	2	6	-	-	-	-	-	-
35	2	3	-	-	-	-	-	-
36	2	5	-	-	-	-	-	-
37	2	1	-	-	-	-	-	-
38	2	1	-	-	-	-	-	-
39	2	3	-	-	-	-	-	-
121	3	4	-	-	-	-	-	-
122	3	3	-	-	-	-	-	-

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
123	3	6	-	-	-	-	-	-
124	3	6	-	-	-	-	-	-
125	3	6	-	-	-	-	-	-
126	3	7	-	-	-	-	-	-
127	3	9	-	-	-	-	-	-
128	3	1	-	-	-	-	-	-
211	3	1	-	-	-	-	-	-
212	3	4	-	-	-	-	-	-
213	3	15	-	-	-	-	-	-
214	3	6	-	-	-	-	-	-
215	3	2	-	-	-	-	-	-
216	3	6	-	-	-	-	-	-
217	3	1	-	-	-	-	-	-
218	3	4	-	-	-	-	-	-
219	3	6	-	-	-	-	-	-
221	3	18	-	-	-	-	-	-
222	3	16	-	-	-	-	-	-
223	3	14	-	-	-	-	-	-
224	3	22	1.000	0.001	1.000	1	9	0.739
225	3	12	-	-	-	-	-	-
226	3	5	-	-	-	-	-	-
227	3	9	-	-	-	-	-	-
228	3	10	-	-	-	-	-	-
229	3	4	-	-	-	-	-	-
231	3	115	1.000	0.001	1.000	1	2	1.000
232	3	1	-	-	-	-	-	-
233	3	7	-	-	-	-	-	-
234	3	3	-	-	-	-	-	-
235	3	2	-	-	-	-	-	-
236	3	4	-	-	-	-	-	-
237	3	4	-	-	-	-	-	-
238	3	2	-	-	-	-	-	-
241	3	17	-	-	-	-	-	-
242	3	12	-	-	-	-	-	-
251	3	9	-	-	-	-	-	-
252	3	4	-	-	-	-	-	-
253	3	1	-	-	-	-	-	-
254	3	2	-	-	-	-	-	-
255	3	2	-	-	-	-	-	-
256	3	3	-	-	-	-	-	-
257	3	3	-	-	-	-	-	-
258	3	5	-	-	-	-	-	-
259	3	2	-	-	-	-	-	-
261	3	13	-	-	-	-	-	-
262	3	4	-	-	-	-	-	-
263	3	4	-	-	-	-	-	-
264	3	2	-	-	-	-	-	-
265	3	11	-	-	-	-	-	-
266	3	2	-	-	-	-	-	-
267	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
268	3	5	-	-	-	-	-	-
271	3	4	-	-	-	-	-	-
272	3	3	-	-	-	-	-	-
273	3	3	-	-	-	-	-	-
274	3	3	-	-	-	-	-	-
275	3	8	-	-	-	-	-	-
276	3	4	-	-	-	-	-	-
277	3	5	-	-	-	-	-	-
278	3	6	-	-	-	-	-	-
279	3	4	-	-	-	-	-	-
281	3	20	0.984	0.001	0.965	1	8	0.629
282	3	2	-	-	-	-	-	-

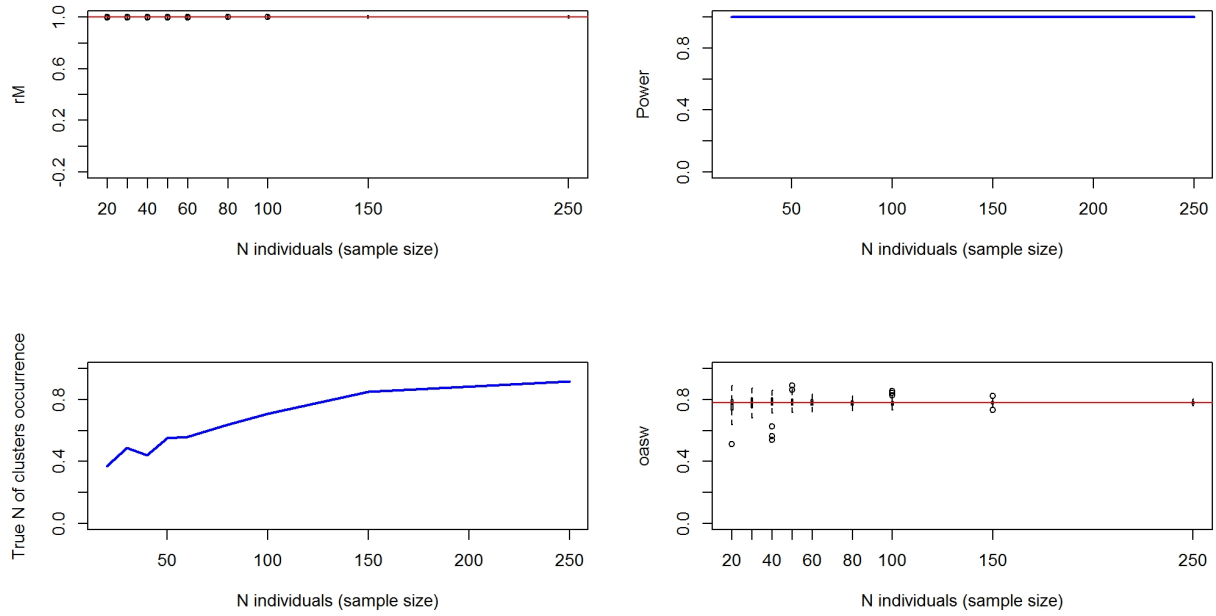


**Figure 14860-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

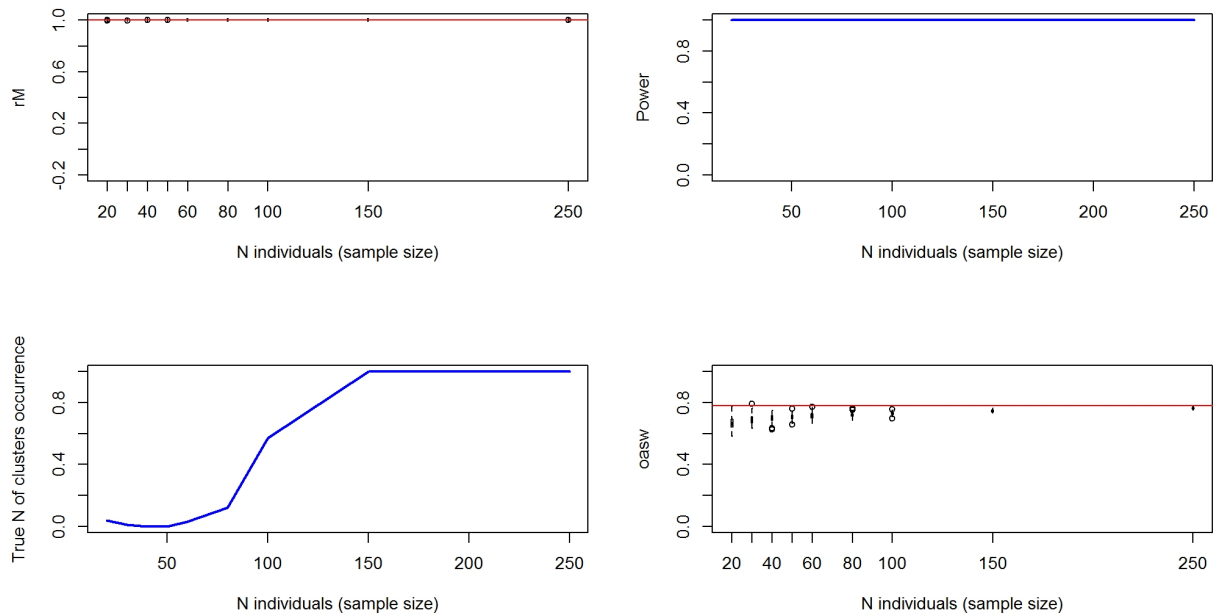
## 1.2 Sensitivity analysis

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 14860-2) and stratified sampling of individuals within the breeding range (Figure 14860-3) and the non breeding range (Figure 14860-4). 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.

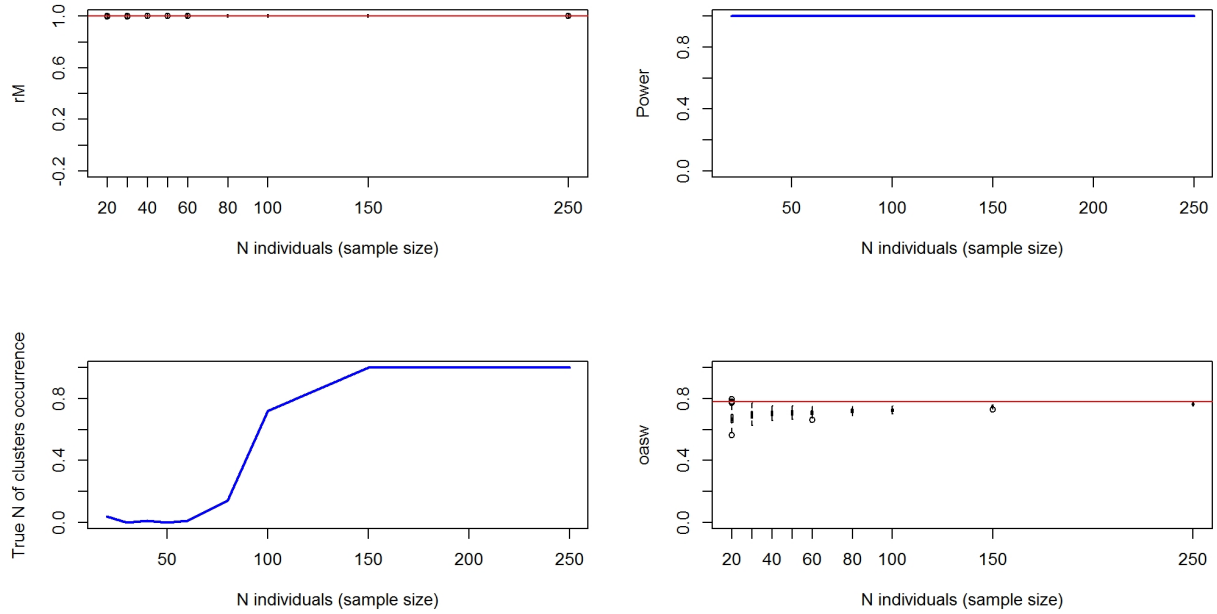


**Figure 14860-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



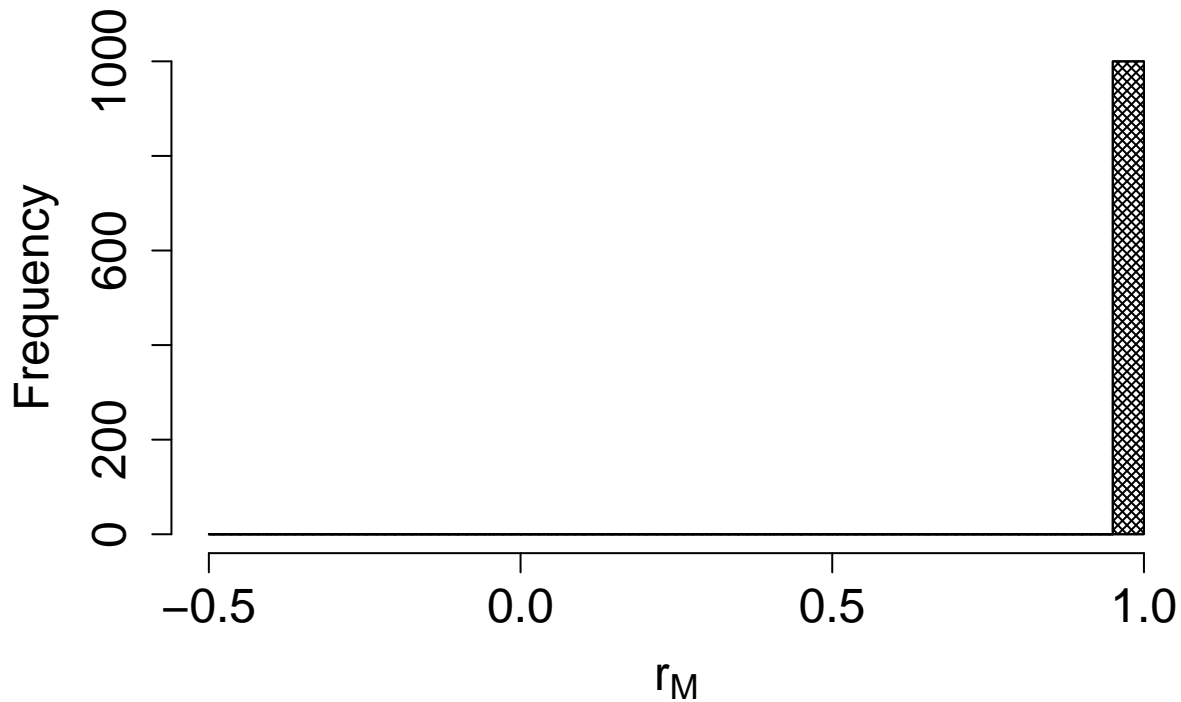
**Figure 14860-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 14860-4.** 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 14860-5).



**Figure 14860-5.** 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 3 breeding regions and 3 non breeding regions (Table 14860-2; Figure 14860-6).

**Table 14860-2.** 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	3129000	Central Europe	1
North Europe	2365000	North Europe	1
North-west Europe	678120	North-west Europe	1



**Figure 14860-6.** 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>.