

# Migratory connectivity analysis

by EURING Migration Atlas

*Dendrocopos major* (EURING code 08760)

## 1.1 Connectivity between individuals

The analysis evaluated 3180 individuals (6360 encounters) filtered from a total of 86173 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 08760-1; Figure 08760-1).

**Table 08760-1.** 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	3180	0.998	0.001	0.996	1.000	3	0.636
1	1	862	0.998	0.001	0.996	1.000	2	0.589
2	1	1907	0.998	0.001	0.996	1.000	2	0.518
3	1	411	0.969	0.001	0.920	0.998	3	0.603
11	2	125	0.999	0.001	0.996	1.000	9	0.648
12	2	737	0.996	0.001	0.991	0.999	9	0.548
21	2	366	0.990	0.001	0.977	0.999	9	0.576
22	2	1541	0.999	0.001	0.999	1.000	9	0.492
31	2	40	0.735	0.001	0.532	1.000	2	0.557
32	2	256	0.975	0.001	0.922	1.000	9	0.585
33	2	115	0.998	0.001	0.993	1.000	2	0.737
111	3	1	-	-	-	-	-	-
112	3	11	-	-	-	-	-	-
113	3	7	-	-	-	-	-	-
114	3	16	-	-	-	-	-	-
115	3	44	1.000	0.001	1.000	1.000	8	0.884
116	3	20	1.000	0.001	1.000	1.000	5	0.929
117	3	10	-	-	-	-	-	-
118	3	12	-	-	-	-	-	-
119	3	4	-	-	-	-	-	-
121	3	188	0.999	0.001	0.997	1.000	2	0.753
122	3	92	1.000	0.001	1.000	1.000	6	0.717
123	3	120	0.954	0.001	0.882	0.999	4	0.712
124	3	77	0.985	0.001	0.962	1.000	8	0.789
125	3	58	0.999	0.001	0.999	0.999	6	0.899
126	3	84	1.000	0.001	0.999	1.000	9	0.856
127	3	33	0.897	0.001	0.739	0.998	7	0.626

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
128	3	33	0.903	0.001	0.731	1.000	5	0.685
129	3	52	1.000	0.001	0.999	1.000	4	0.894
211	3	61	0.994	0.001	0.719	0.999	2	0.944
212	3	125	0.964	0.001	0.904	0.998	5	0.750
213	3	22	0.838	0.001	0.713	1.000	8	0.776
214	3	21	0.997	0.001	0.992	1.000	6	0.811
215	3	5	-	-	-	-	-	-
216	3	60	0.965	0.001	0.931	0.993	9	0.628
217	3	37	0.990	0.001	0.969	1.000	8	0.814
218	3	28	0.891	0.001	0.748	0.997	9	0.745
219	3	7	-	-	-	-	-	-
311	3	10	-	-	-	-	-	-
312	3	30	0.950	0.001	0.747	1.000	3	0.600
321	3	43	1.000	0.001	0.998	1.000	8	0.517
322	3	6	-	-	-	-	-	-
323	3	19	-	-	-	-	-	-
324	3	54	0.949	0.001	0.923	0.999	9	0.797
325	3	23	0.999	0.001	-0.008	1.000	2	0.956
326	3	12	-	-	-	-	-	-
327	3	24	0.992	0.001	0.985	1.000	5	0.868
328	3	69	0.999	0.001	0.969	1.000	2	0.943
329	3	6	-	-	-	-	-	-
331	3	91	0.995	0.001	0.987	1.000	7	0.697
332	3	24	0.860	0.001	0.624	1.000	9	0.754

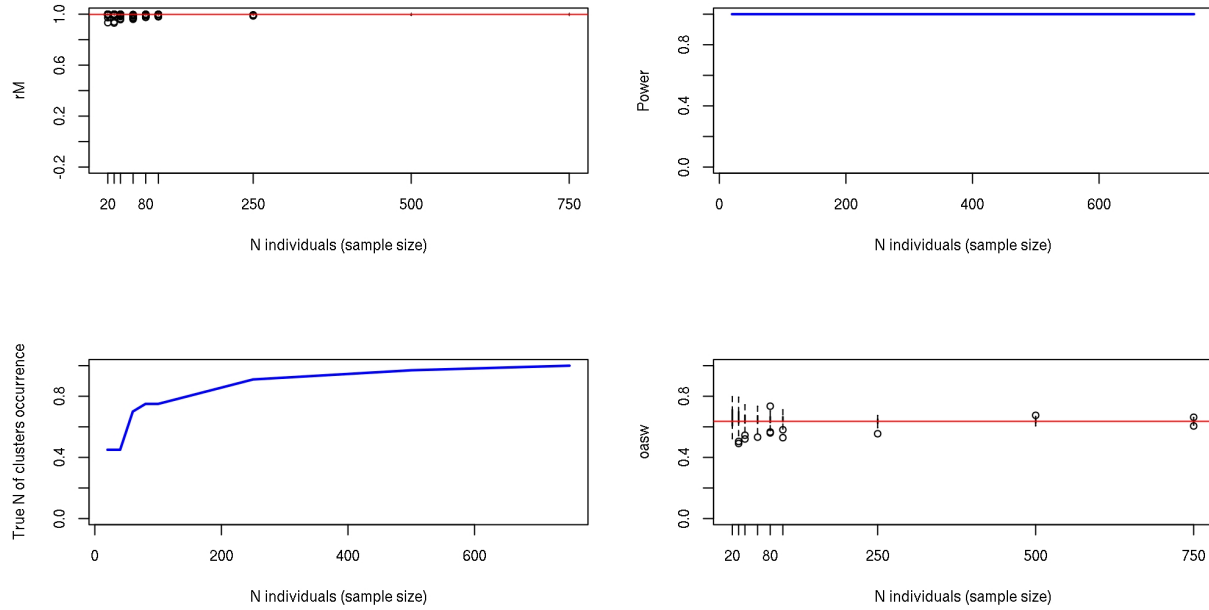


**Figure 08760-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

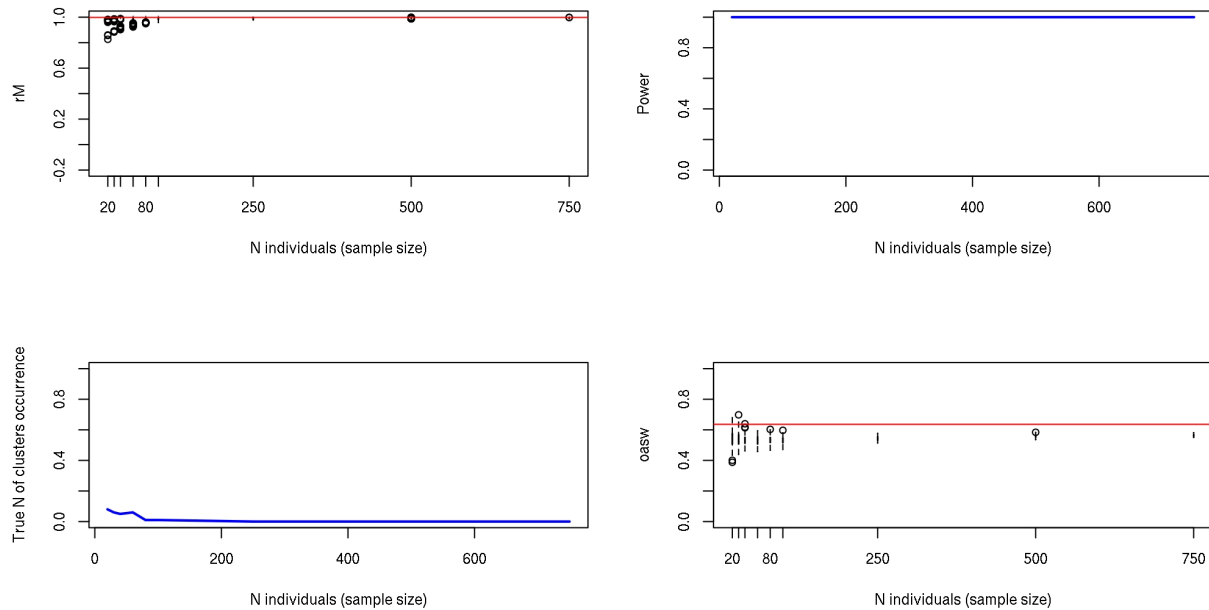
## 1.2 Sensitivity analysis

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 08760-2) and stratified sampling of individuals within the breeding range (Figure 08760-3) and the non breeding range (Figure 08760-4). 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.

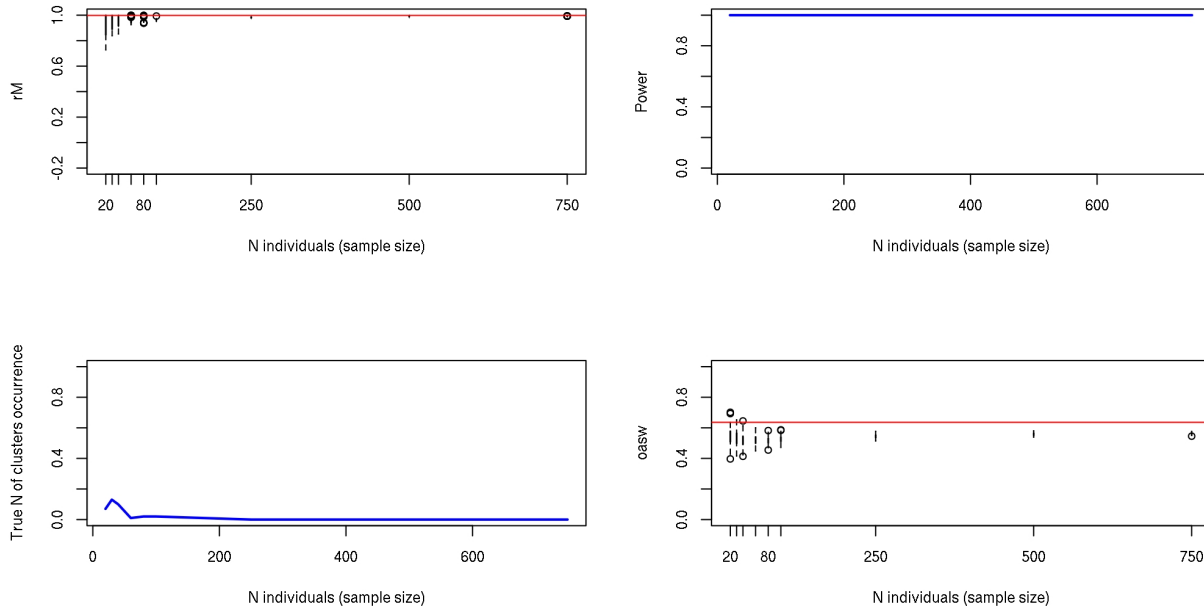


**Figure 08760-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



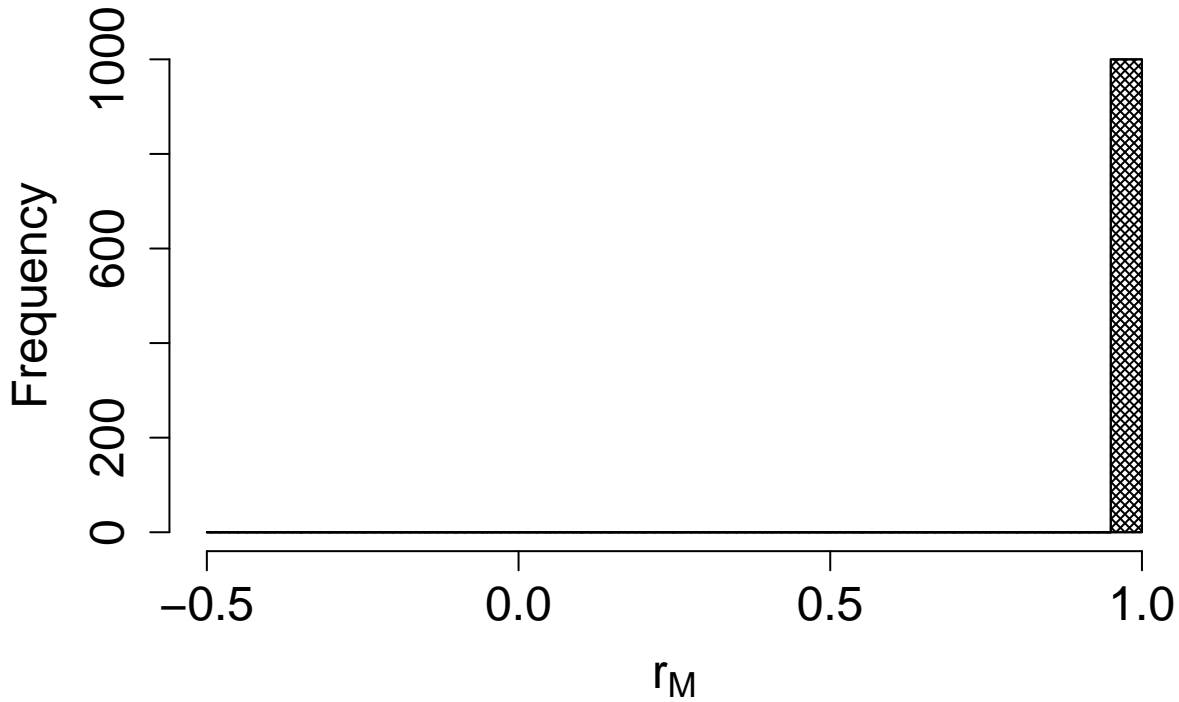
**Figure 08760-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 08760-4.** 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 08760-5).



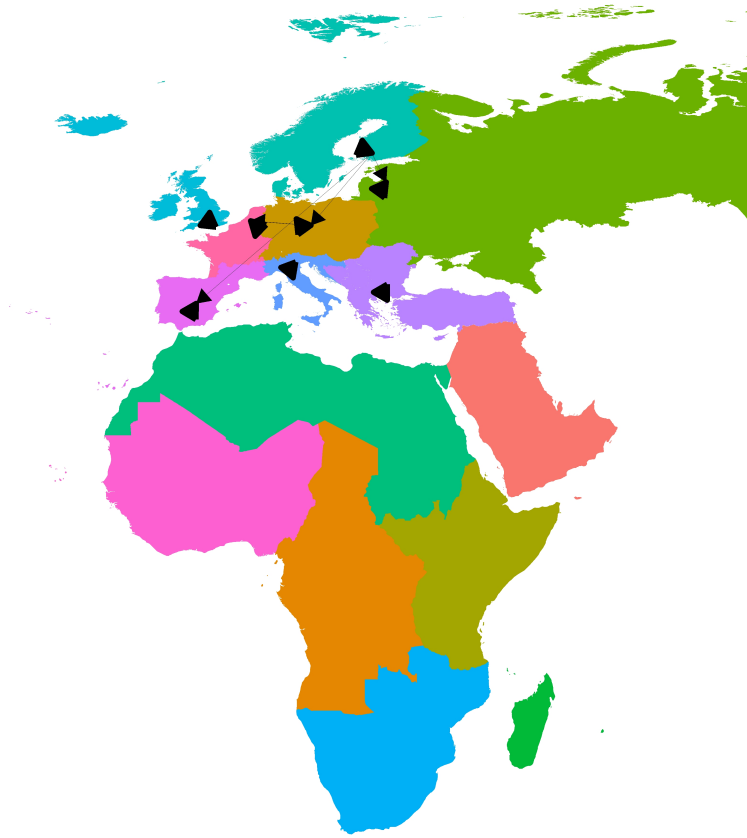
**Figure 08760-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

## 2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 0.999; MC = 0.999 when adjusted for absolute abundance) between 8 breeding regions and 8 non breeding regions (Table 08760-2; Figure 08760-6).

**Table 08760-2.** 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	5142580	Central Europe	0.997
Central Europe	5142580	West Europe	0.003
East Europe	20977551	East Europe	1.000
North Europe	1305000	Central Europe	0.002
North Europe	1305000	East Europe	0.002
North Europe	1305000	North Europe	0.993
North Europe	1305000	South-west Europe	0.002
North-west Europe	280053	North-west Europe	1.000
South-central Europe	537318	South-central Europe	1.000
South-east Europe	1733500	South-east Europe	1.000
South-west Europe	1520688	South-west Europe	1.000
West Europe	707543	Central Europe	0.003
West Europe	707543	West Europe	0.997



**Figure 08760-6.** 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>.