

# Migratory connectivity analysis

by EURING Migration Atlas

*Parus caeruleus* (EURING code 14620)

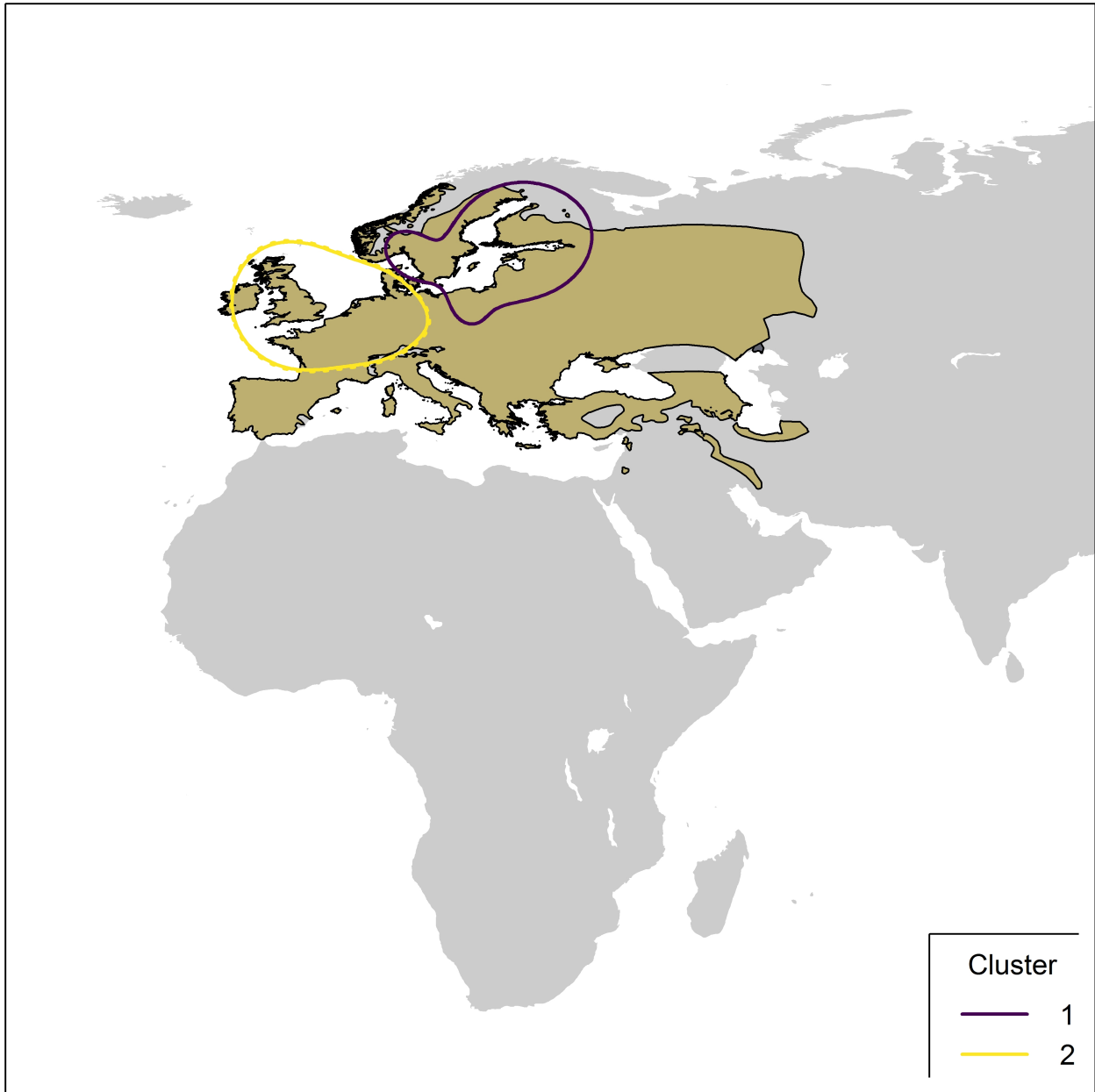
## 1.1 Connectivity between individuals

The analysis evaluated 28021 individuals (56042 encounters) filtered from a total of 2032708 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 14620-1; Figure 14620-1).

**Table 14620-1.** 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	28021	0.998	0.001	0.997	0.998	2	0.721
1	1	3436	0.996	0.001	0.993	0.998	3	0.765
2	1	24585	0.995	0.001	0.993	0.996	2	0.557
11	2	297	0.974	0.001	0.941	0.998	9	0.616
12	2	389	0.981	0.001	0.963	0.993	6	0.676
13	2	2750	0.976	0.001	0.959	0.990	9	0.663
21	2	6980	0.965	0.001	0.956	0.973	7	0.539
22	2	17605	0.999	0.001	0.998	1.000	2	0.453
111	3	21	0.980	0.001	0.877	0.999	2	0.804
112	3	60	0.823	0.001	0.581	0.999	9	0.855
113	3	19	-	-	-	-	-	-
114	3	13	-	-	-	-	-	-
115	3	69	0.985	0.001	0.980	1.000	6	0.785
116	3	18	-	-	-	-	-	-
117	3	25	0.999	0.001	0.995	1.000	9	0.828
118	3	43	1.000	0.001	1.000	1.000	9	0.853
119	3	29	0.603	0.001	0.291	0.998	5	0.931
121	3	48	0.771	0.001	0.502	0.989	3	0.651
122	3	185	0.891	0.001	0.751	0.998	9	0.519
123	3	19	-	-	-	-	-	-
124	3	40	0.998	0.001	0.988	1.000	4	0.776
125	3	25	0.867	0.001	0.700	0.986	7	0.507
126	3	72	0.778	0.001	0.592	0.974	2	0.758
131	3	220	0.993	0.001	0.965	1.000	9	0.772
132	3	820	0.924	0.001	0.830	0.972	2	0.509
133	3	229	0.975	0.001	0.916	0.993	6	0.755
134	3	506	0.814	0.001	0.724	0.899	9	0.835

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
135	3	175	0.909	0.001	0.844	0.969	7	0.705
136	3	622	0.829	0.001	0.602	0.998	2	0.957
137	3	74	0.994	0.001	0.985	1.000	5	0.910
138	3	60	0.843	0.001	0.737	0.974	7	0.744
139	3	44	0.944	0.001	0.834	1.000	5	0.810
211	3	2727	0.787	0.001	0.734	0.839	2	0.513
212	3	640	0.960	0.001	0.936	0.980	9	0.535
213	3	359	0.845	0.001	0.786	0.895	9	0.567
214	3	774	0.851	0.001	0.787	0.912	9	0.560
215	3	2248	0.931	0.001	0.872	0.970	9	0.615
216	3	98	0.822	0.001	0.643	0.999	2	0.787
217	3	134	0.993	0.001	0.985	0.998	8	0.787

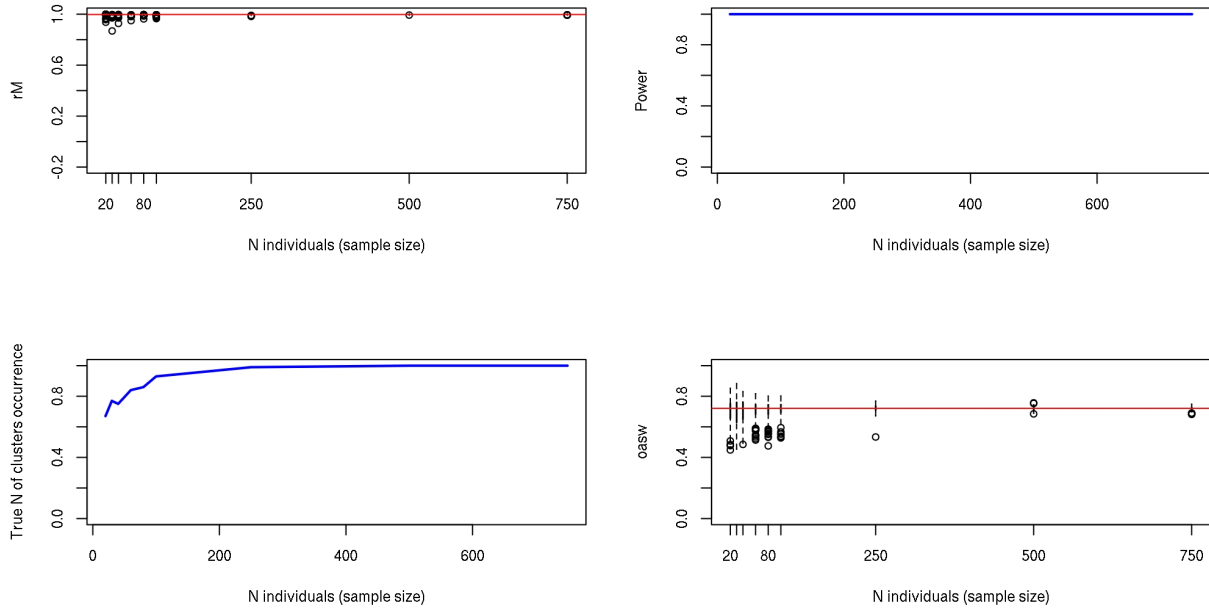


**Figure 14620-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

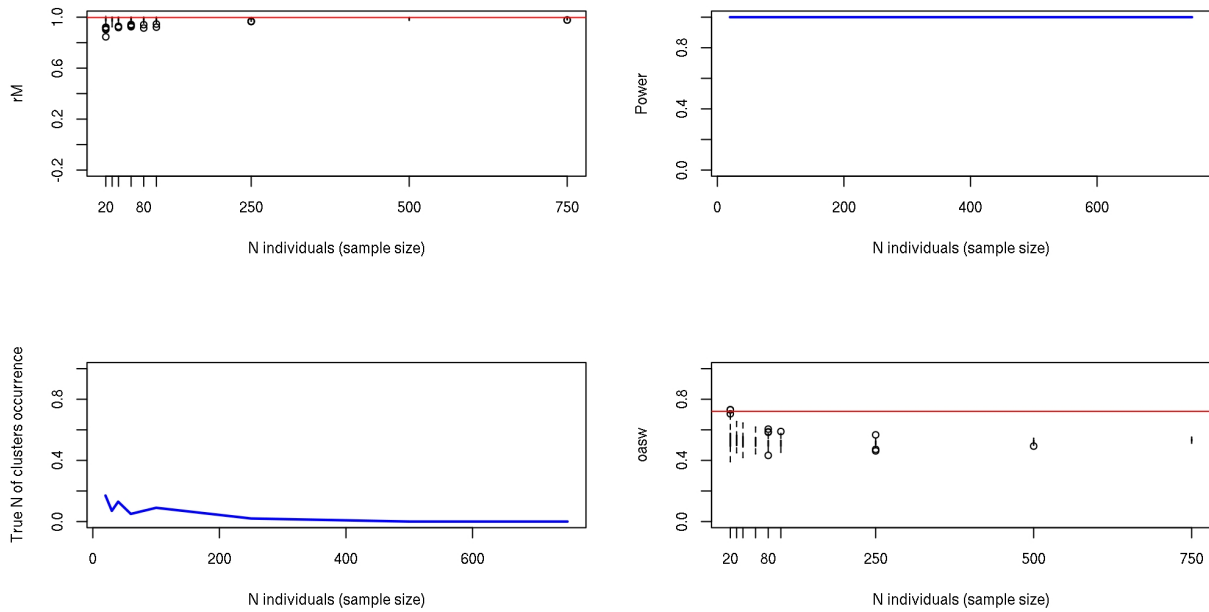
## 1.2 Sensitivity analysis

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 14620-2) and stratified sampling of individuals within the breeding range (Figure 14620-3) and the non breeding range (Figure 14620-4). 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.

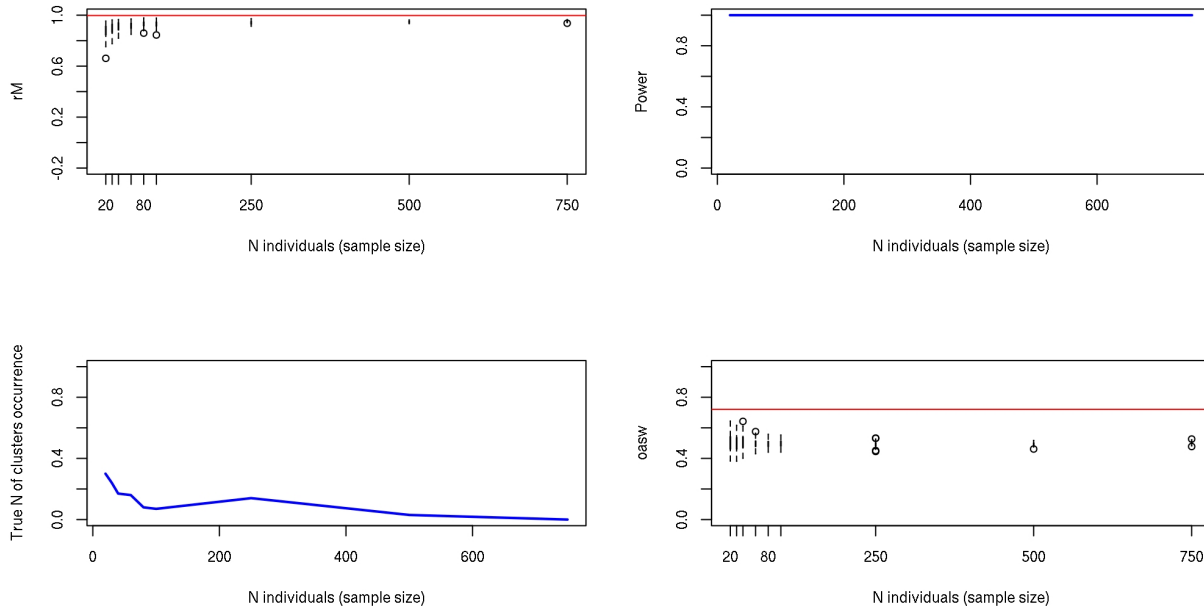


**Figure 14620-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



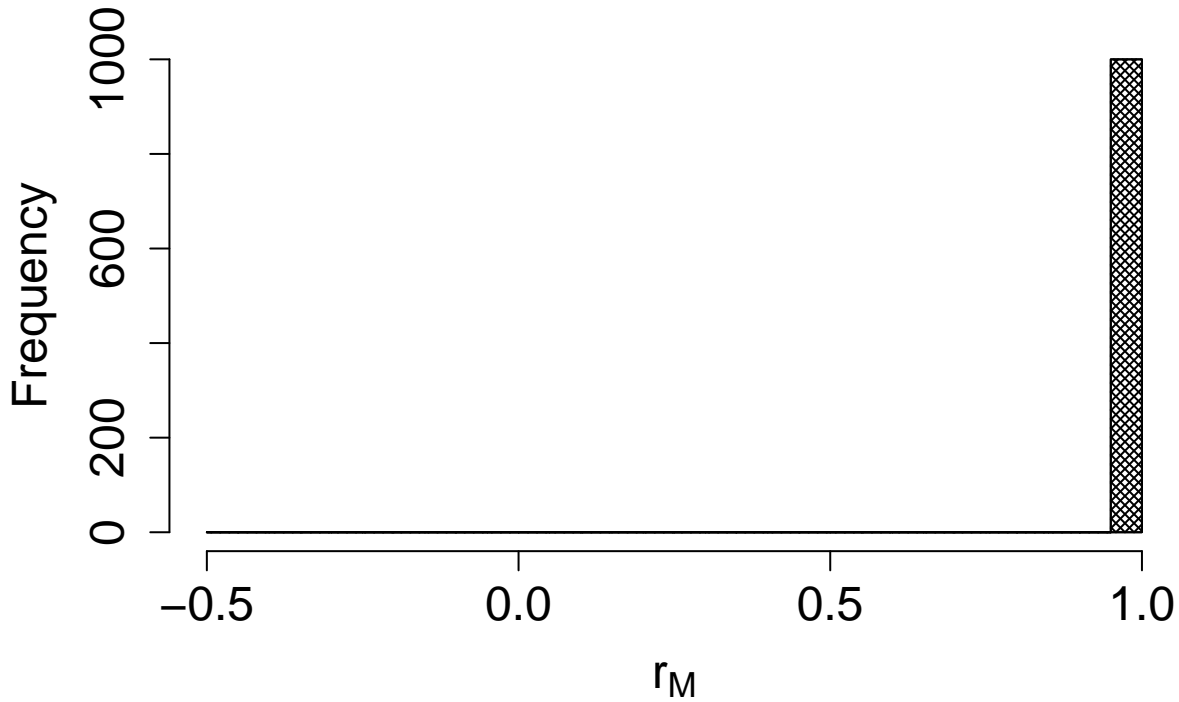
**Figure 14620-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 14620-4.** 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 14620-5).



**Figure 14620-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

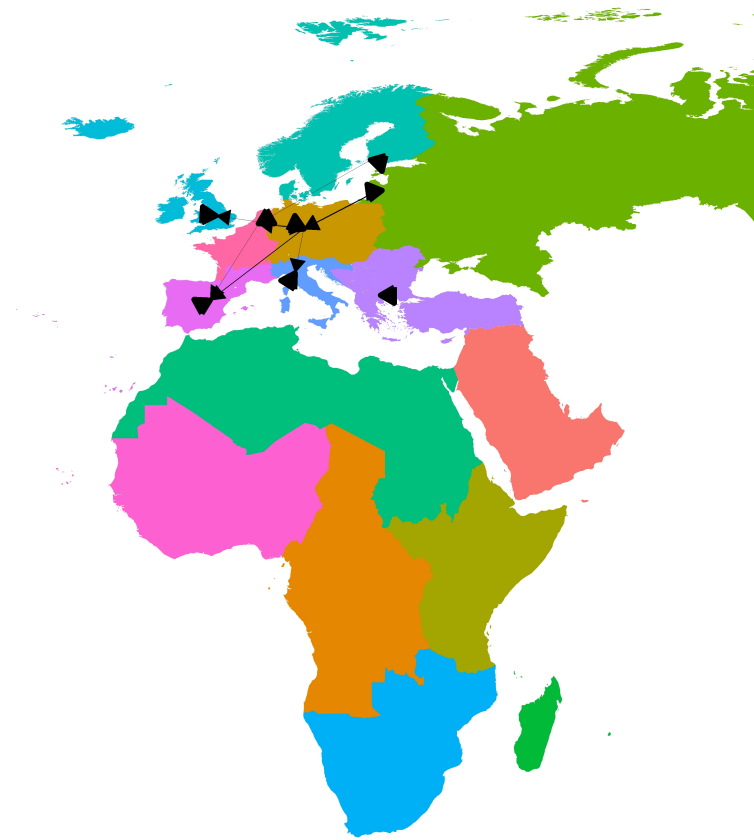
## 2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 0.984; MC = 0.984 when adjusted for absolute abundance) between 8 breeding regions and 8 non breeding regions (Table 14620-2; Figure 14620-6).

**Table 14620-2.** 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	16236100	Central Europe	0.955
Central Europe	16236100	North-west Europe	0.000
Central Europe	16236100	South-central Europe	0.003
Central Europe	16236100	South-west Europe	0.018
Central Europe	16236100	West Europe	0.025
East Europe	4767190	Central Europe	0.045
East Europe	4767190	East Europe	0.955
North Europe	3813000	North Europe	1.000
North Europe	3813000	West Europe	0.000
North-west Europe	10476470	North-west Europe	1.000
South-central Europe	3630692	South-central Europe	1.000
South-east Europe	9315000	South-east Europe	1.000
South-west Europe	22268397	South-west Europe	1.000

Breeding region	Abundance	Non breeding region	Transition probability
West Europe	8926632	Central Europe	0.000
West Europe	8926632	South-west Europe	0.000
West Europe	8926632	West Europe	0.999



**Figure 14620-6.** 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>.