

# Migratory connectivity analysis

by EURING Migration Atlas

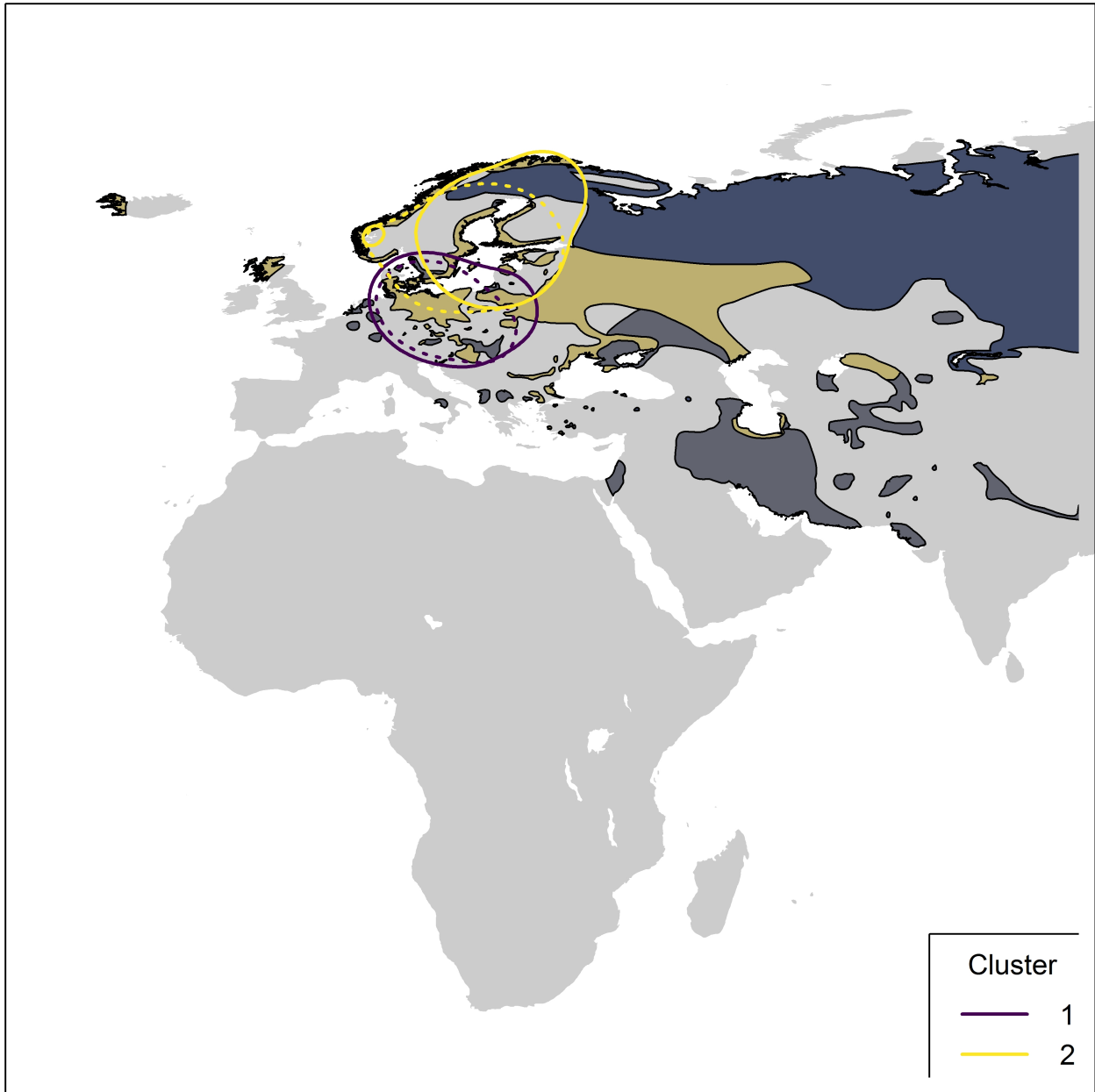
*Haliaeetus albicilla* (EURING code 02430)

## 1.1 Connectivity between individuals

The analysis evaluated 2629 individuals (5258 encounters) filtered from a total of 84410 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 02430-1; Figure 02430-1).

**Table 02430-1.** 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	2629	0.690	0.001	0.664	0.714	2	0.640
1	1	358	0.760	0.001	0.701	0.818	2	0.558
2	1	2271	0.421	0.001	0.385	0.457	5	0.452
11	2	268	0.540	0.001	0.406	0.709	3	0.497
12	2	90	0.124	0.010	0.009	0.296	5	0.550
121	3	5	-	-	-	-	-	-
122	3	21	0.035	0.283	-0.070	0.397	-	-
123	3	13	-	-	-	-	-	-
124	3	30	-0.007	0.482	-0.119	0.353	-	-
125	3	21	0.245	0.063	-0.059	0.649	4	0.563

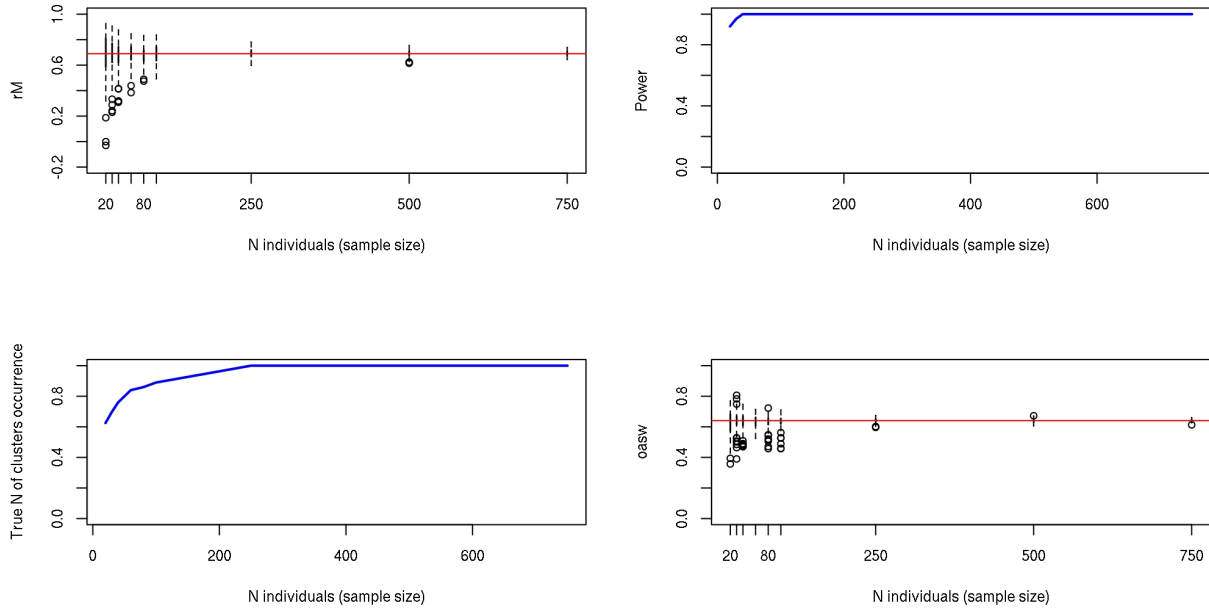


**Figure 02430-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

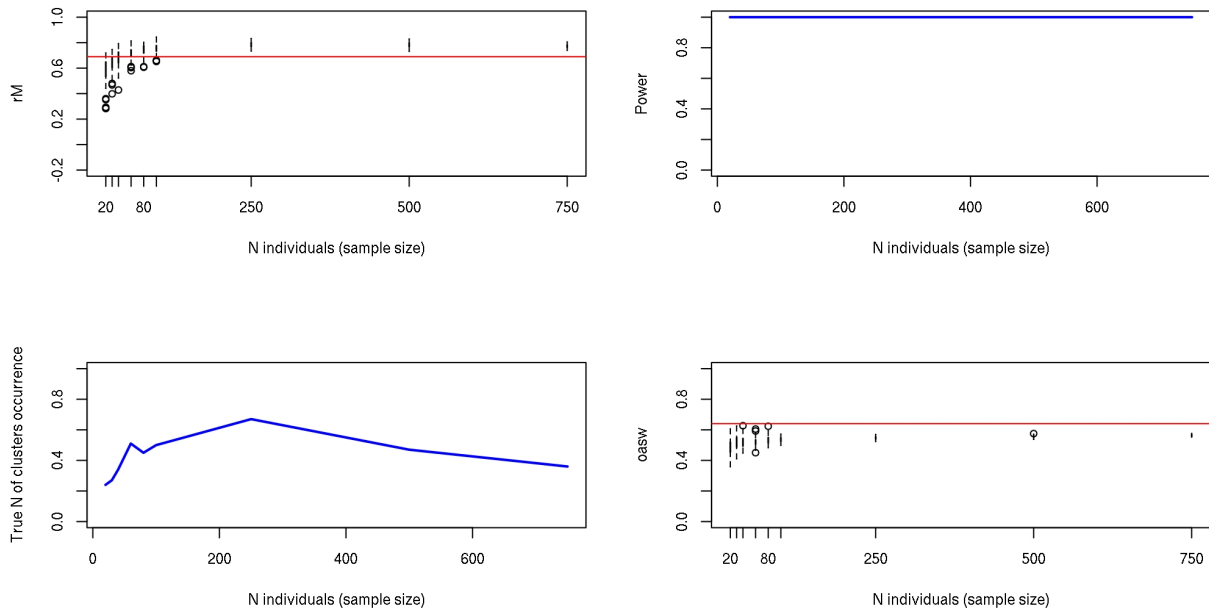
## 1.2 Sensitivity analysis

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 02430-2) and stratified sampling of individuals within the breeding range (Figure 02430-3) and the non breeding range (Figure 02430-4). 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.

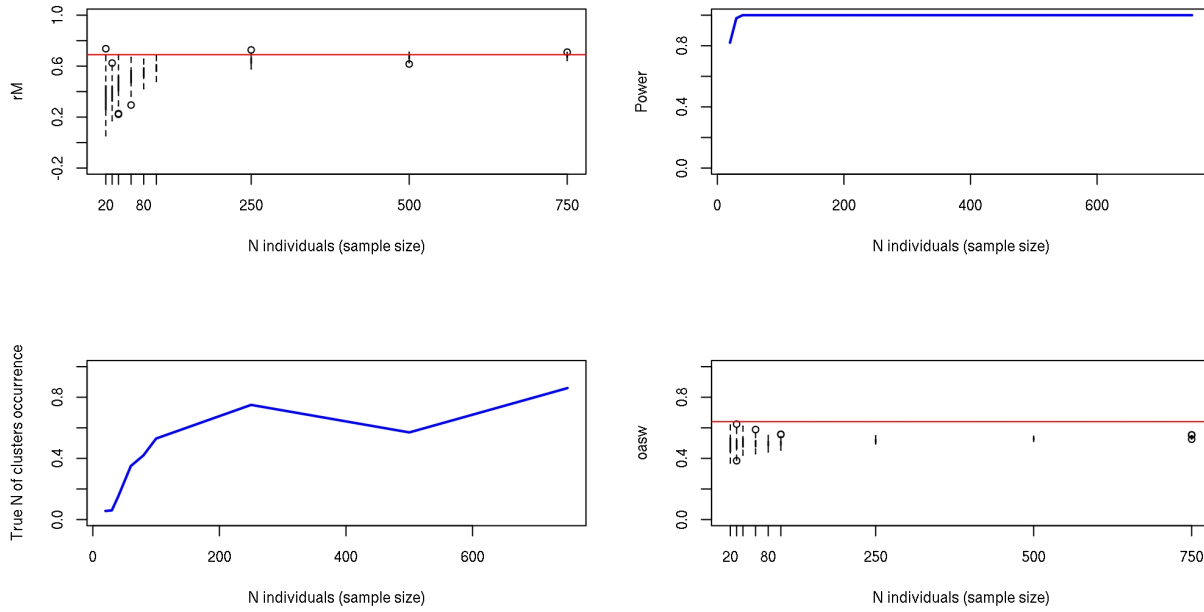


**Figure 02430-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



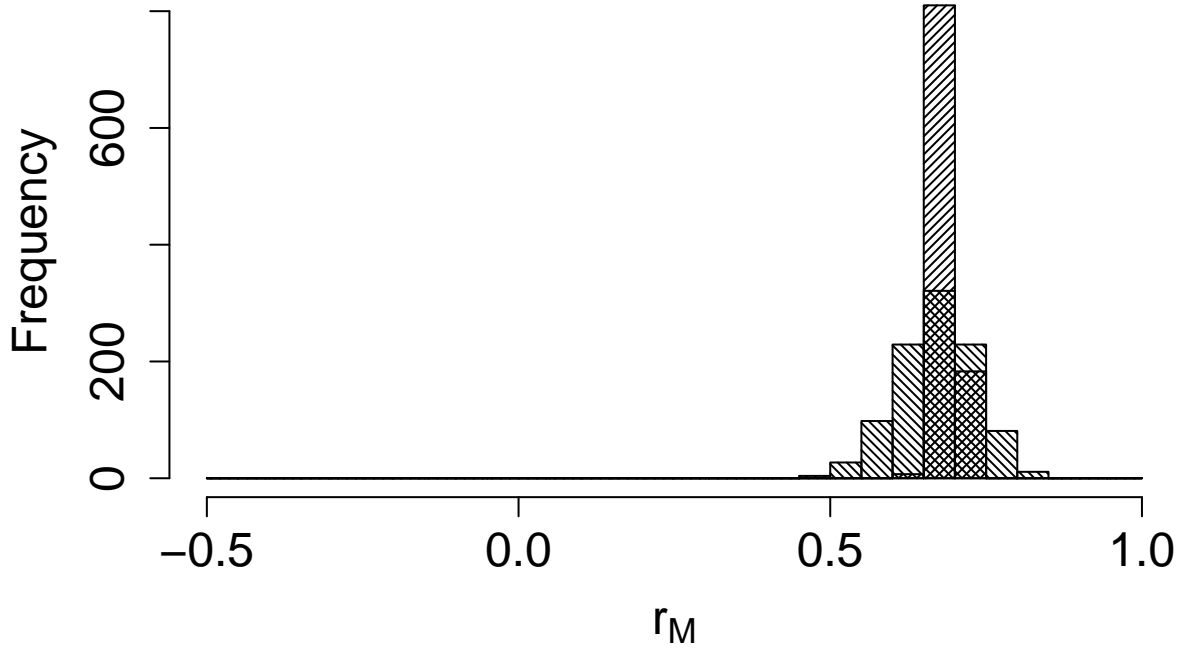
**Figure 02430-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 02430-4.** 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 ( $p = 0.511$ ); Figure 02430-5).



**Figure 02430-5.** 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 ( $MC = 0.835$ ;  $MC = 0.835$  when adjusted for absolute abundance) between 4 breeding regions and 5 non breeding regions (Table 02430-2; Figure 02430-6).

**Table 02430-2.** 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	4274	Central Europe	0.985
Central Europe	4274	North Europe	0.003
Central Europe	4274	South-east Europe	0.006
Central Europe	4274	West Europe	0.006
East Europe	6300	Central Europe	0.116
East Europe	6300	East Europe	0.528
East Europe	6300	North Europe	0.357
North Europe	9226	Central Europe	0.007
North Europe	9226	East Europe	0.026
North Europe	9226	North Europe	0.967
North Europe	9226	South-east Europe	0.001
South-central Europe	319	South-east Europe	1.000



**Figure 02430-6.** 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>.