

# Migratory connectivity analysis

by EURING Migration Atlas

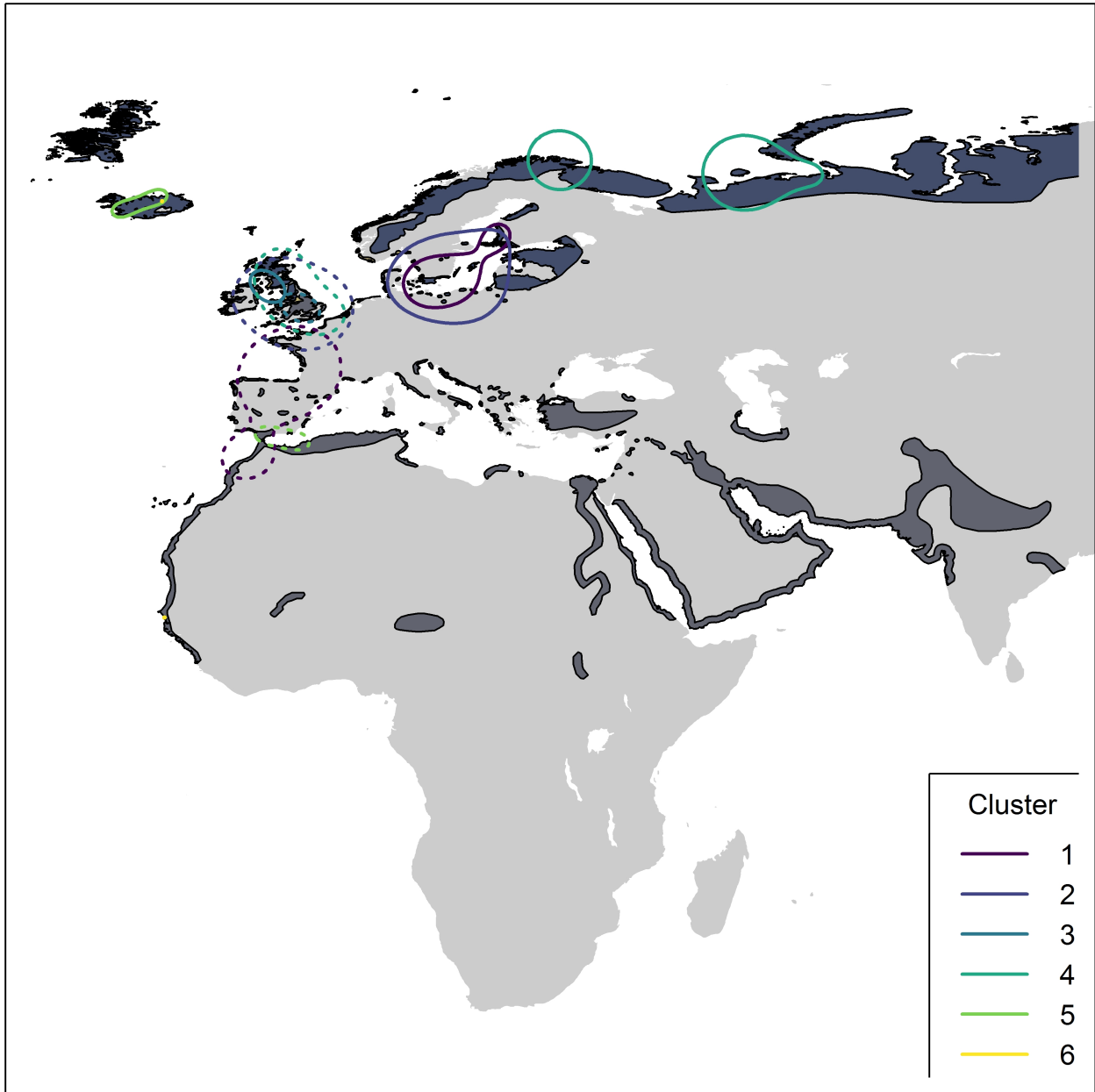
*Calidris alpina* (EURING code 05120)

## 1.1 Connectivity between individuals

The analysis evaluated 49 individuals (98 encounters) filtered from a total of 102840 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 = 6 (Table 05120-1; Figure 05120-1).

**Table 05120-1.** 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	49	0.225	0.042	-0.044	0.450	6	0.512
1	1	9	-	-	-	-	-	-
2	1	28	-0.151	0.904	-0.183	0.109	-	-
3	1	2	-	-	-	-	-	-
4	1	7	-	-	-	-	-	-
5	1	2	-	-	-	-	-	-
6	1	1	-	-	-	-	-	-

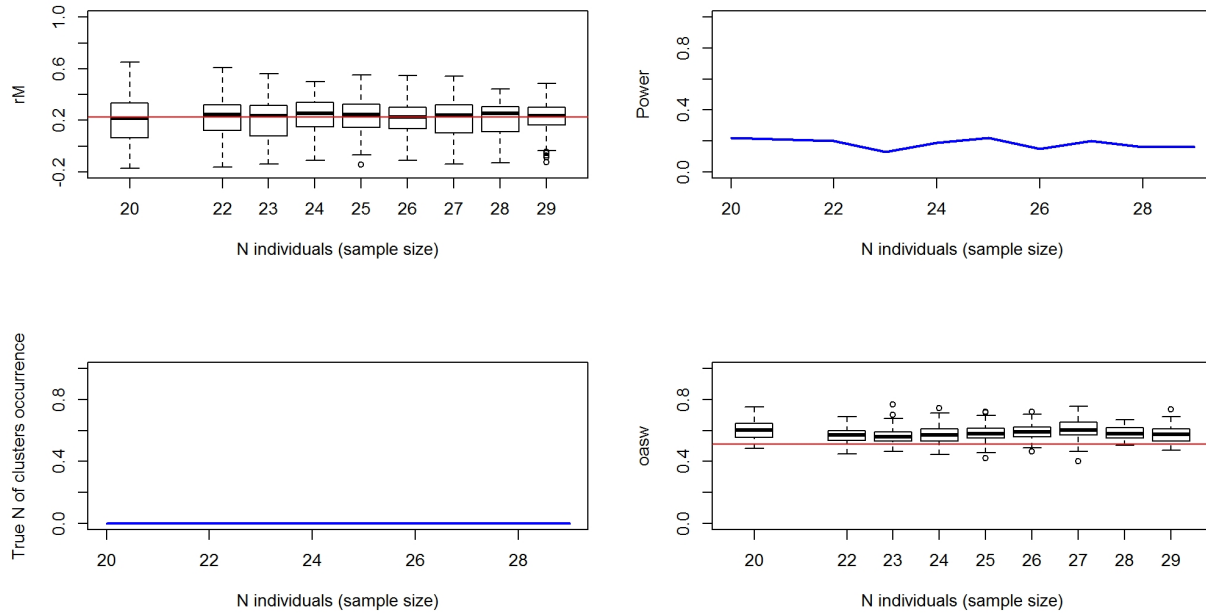


**Figure 05120-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

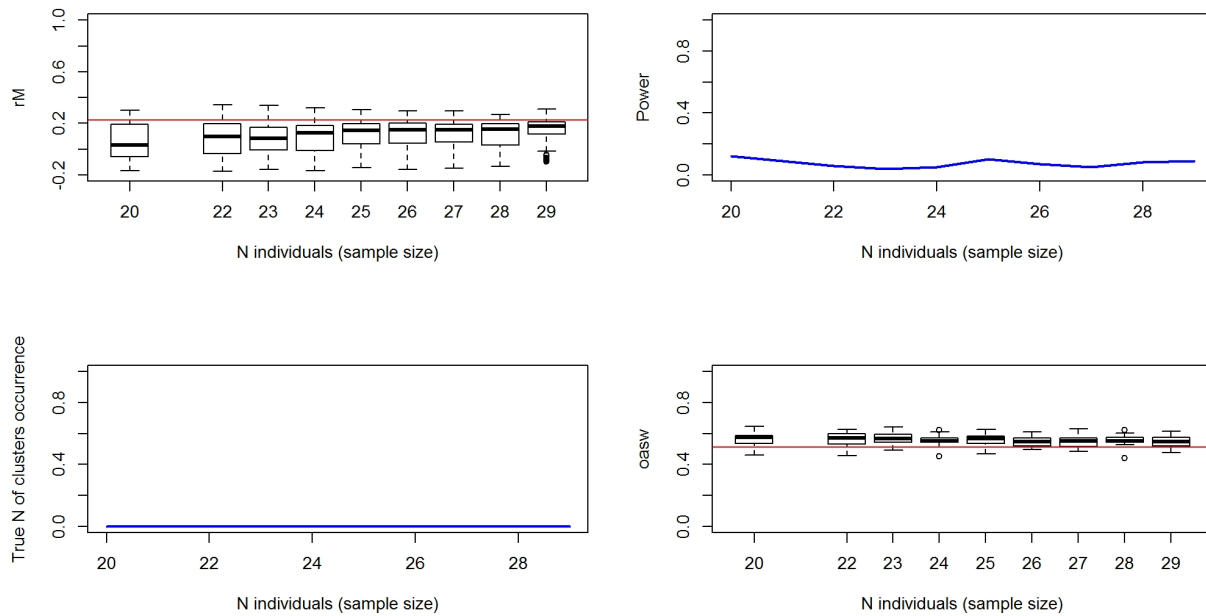
## 1.2 Sensitivity analysis

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 05120-2) and stratified sampling of individuals within the breeding range (Figure 05120-3) and the non breeding range (Figure 05120-4). 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.

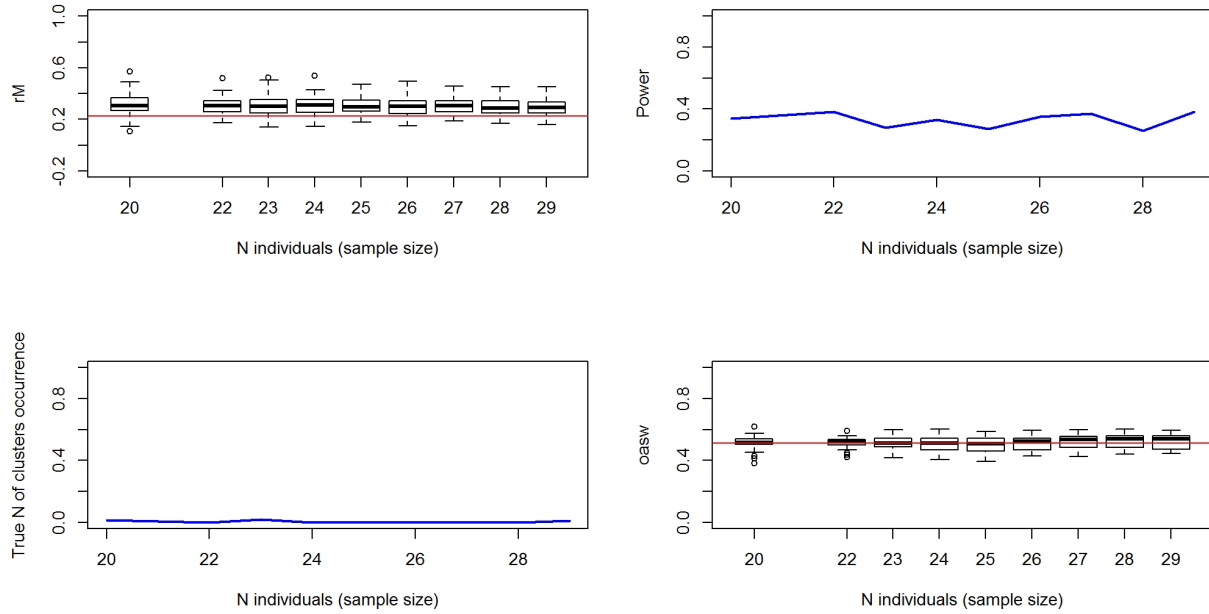


**Figure 05120-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



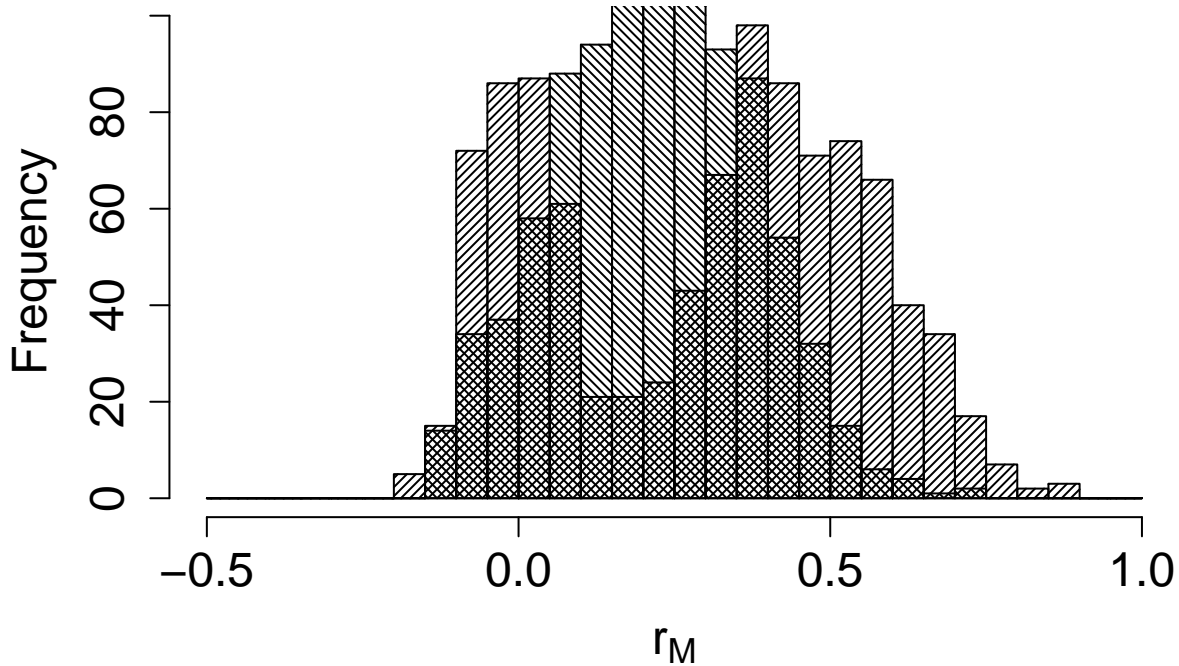
**Figure 05120-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 05120-4.** 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 ( $p = 0.581$ ); Figure 05120-5).



**Figure 05120-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

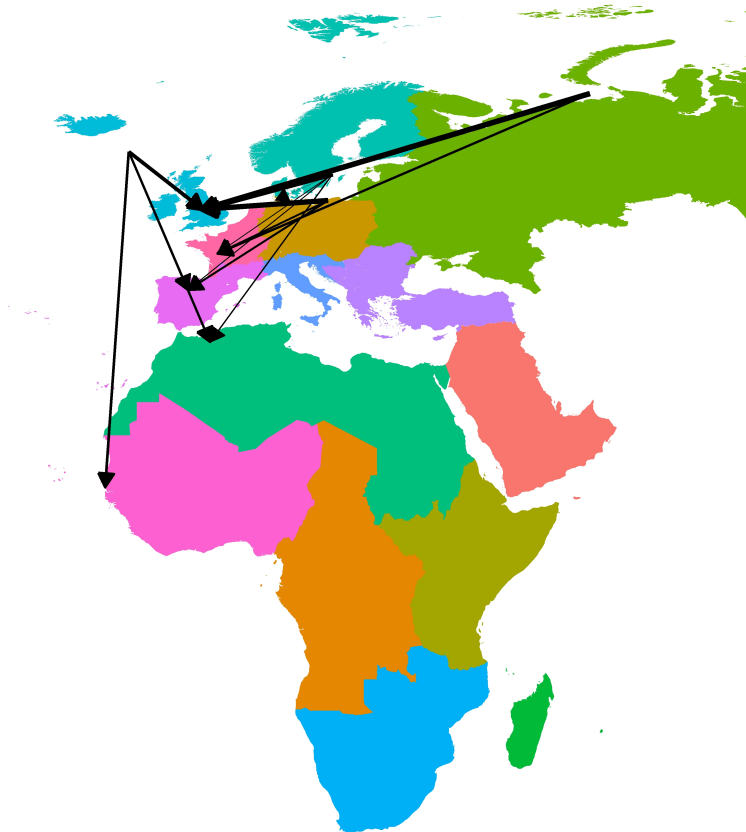
## 2. Connectivity between pre-defined regions

The species shows low connectivity ( $MC = 0.012$ ;  $MC = -0.008$  when adjusted for absolute abundance) between 4 breeding regions and 6 non breeding regions (Table 05120-2; Figure 05120-6).

**Table 05120-2.** 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	24	North-west Europe	0.714
Central Europe	24	South-west Europe	0.143
Central Europe	24	West Europe	0.143
East Europe	300461	North-west Europe	0.800
East Europe	300461	West Europe	0.200
North Europe	106110	Central Europe	0.031
North Europe	106110	North Africa	0.094
North Europe	106110	North-west Europe	0.750
North Europe	106110	South-west Europe	0.062
North Europe	106110	West Europe	0.062
North-west Europe	559500	North Africa	0.200
North-west Europe	559500	North-west Europe	0.400
North-west Europe	559500	South-west Europe	0.200

Breeding region	Abundance	Non breeding region	Transition probability
North-west Europe	559500	West Africa	0.200



**Figure 05120-6.** 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>.