

Migratory connectivity analysis

by EURING Migration Atlas

Phalacrocorax carbo (EURING code 00720)

1.1 Connectivity between individuals

The analysis evaluated 2033 individuals (4066 encounters) filtered from a total of 89210 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 00720-1; Figure 00720-1).

Table 00720-1. 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	2033	0.507	0.001	0.461	0.551	2	0.488

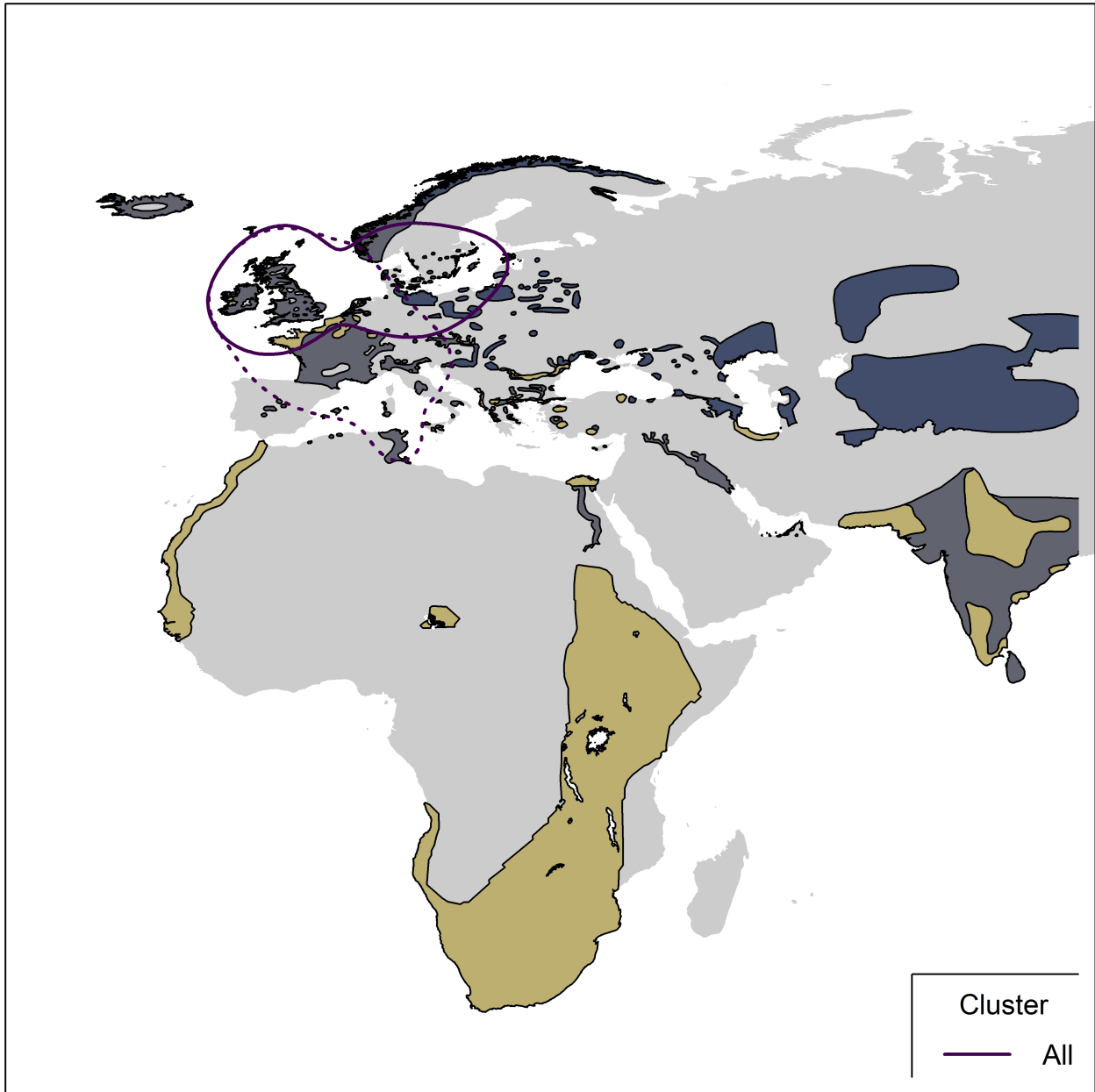


Figure 00720-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 00720-2) and stratified sampling of individuals within the breeding range (Figure 00720-3) and the non breeding range (Figure 00720-4). 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.

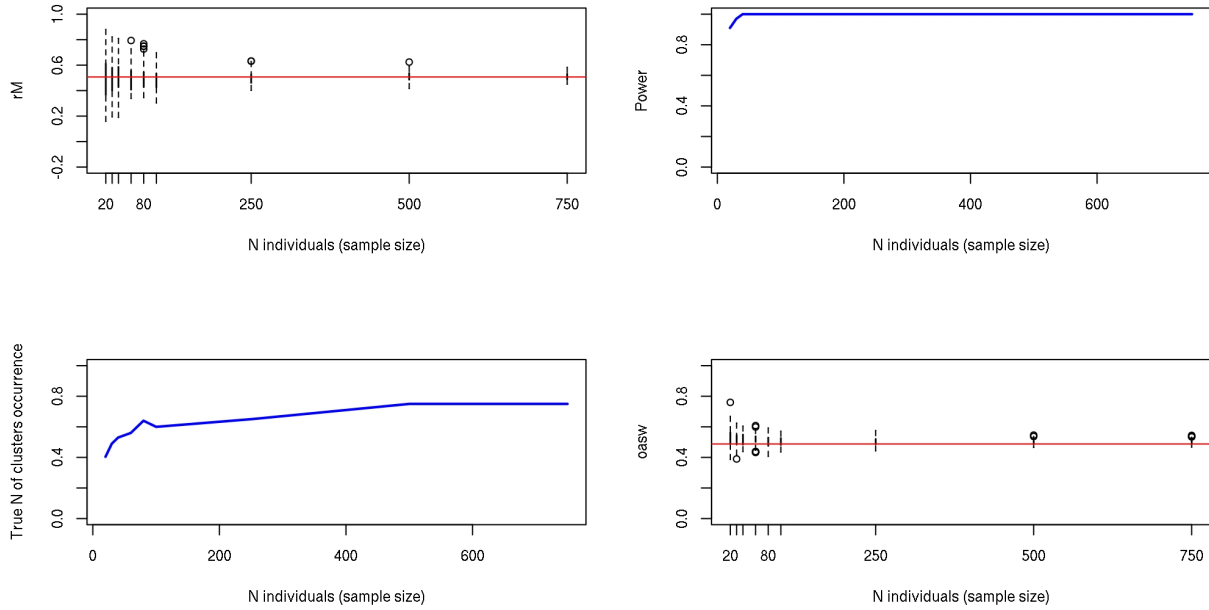


Figure 00720-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

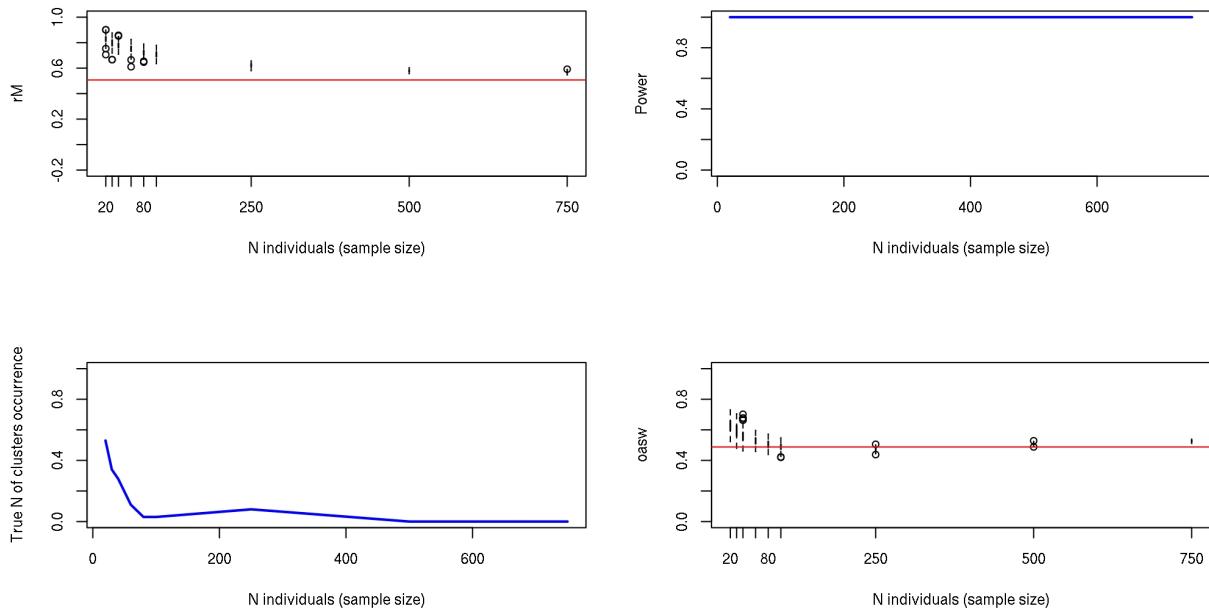


Figure 00720-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

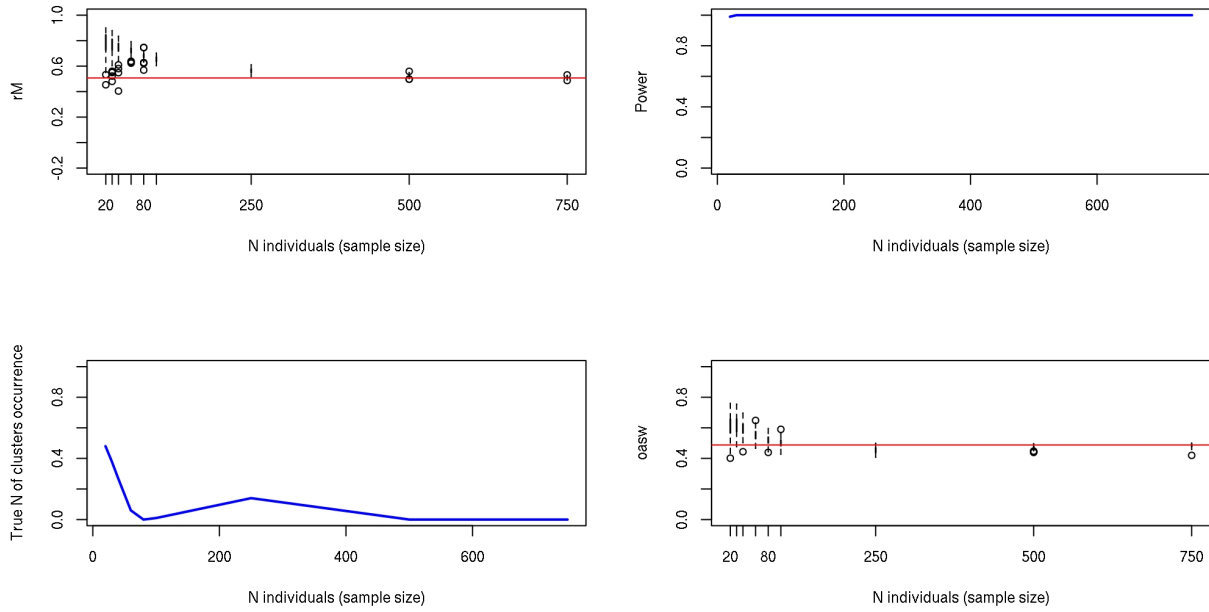


Figure 00720-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is significant ($p = 0.032$); Figure 00720-5).

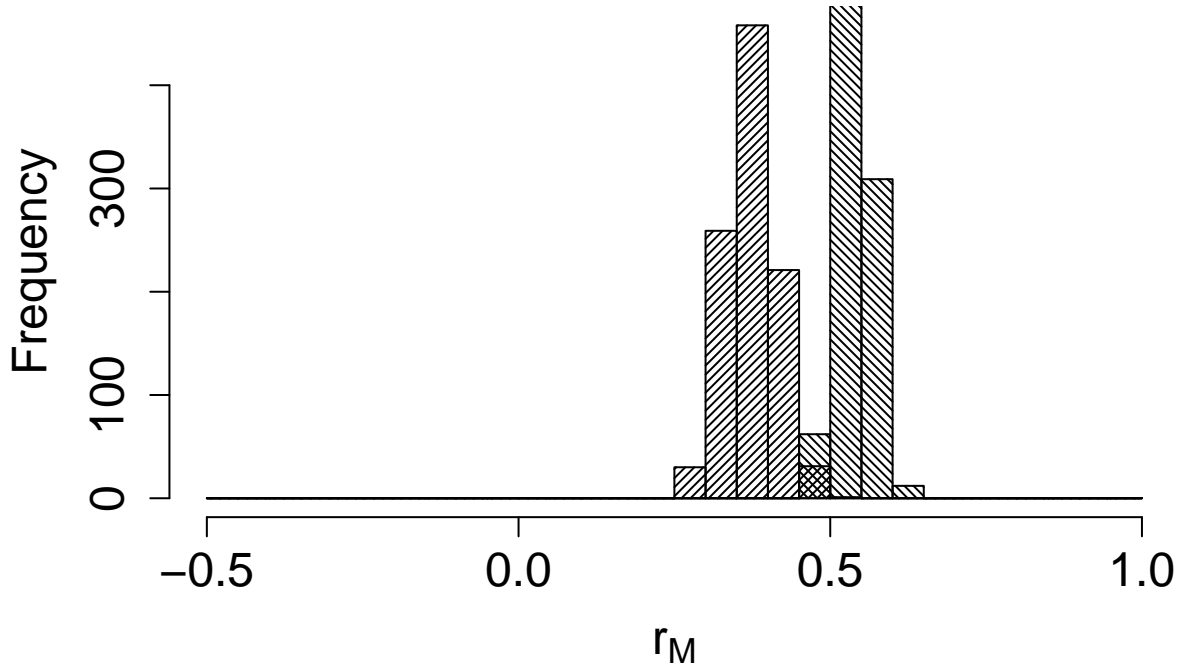


Figure 00720-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity ($MC = 0.103$; $MC = 0.102$ when adjusted for absolute abundance) between 6 breeding regions and 9 non breeding regions (Table 00720-2; Figure 00720-6).

Table 00720-2. 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	107701	Central Europe	0.261
Central Europe	107701	North Africa	0.101
Central Europe	107701	North-west Europe	0.014
Central Europe	107701	South-central Europe	0.304
Central Europe	107701	South-east Europe	0.072
Central Europe	107701	South-west Europe	0.043
Central Europe	107701	West Europe	0.203
East Europe	381240	Central Europe	0.125
East Europe	381240	East Europe	0.062
East Europe	381240	North Africa	0.083
East Europe	381240	North-west Europe	0.021
East Europe	381240	South-central Europe	0.271
East Europe	381240	South-east Europe	0.167

Breeding region	Abundance	Non breeding region	Transition probability
East Europe	381240	South-west Europe	0.125
East Europe	381240	West Europe	0.146
North Europe	216811	Central Europe	0.177
North Europe	216811	North Africa	0.068
North Europe	216811	North Europe	0.066
North Europe	216811	North-west Europe	0.017
North Europe	216811	South-central Europe	0.085
North Europe	216811	South-east Europe	0.008
North Europe	216811	South-west Europe	0.120
North Europe	216811	West Europe	0.459
North-west Europe	39654	North Europe	0.001
North-west Europe	39654	North-west Europe	0.832
North-west Europe	39654	South-west Europe	0.002
North-west Europe	39654	West Europe	0.164
South-central Europe	9369	North Africa	0.273
South-central Europe	9369	South-central Europe	0.727
West Europe	62848	Central Europe	0.016
West Europe	62848	North Africa	0.016
West Europe	62848	North-west Europe	0.095
West Europe	62848	South-central Europe	0.016
West Europe	62848	South-west Europe	0.127
West Europe	62848	West Europe	0.730

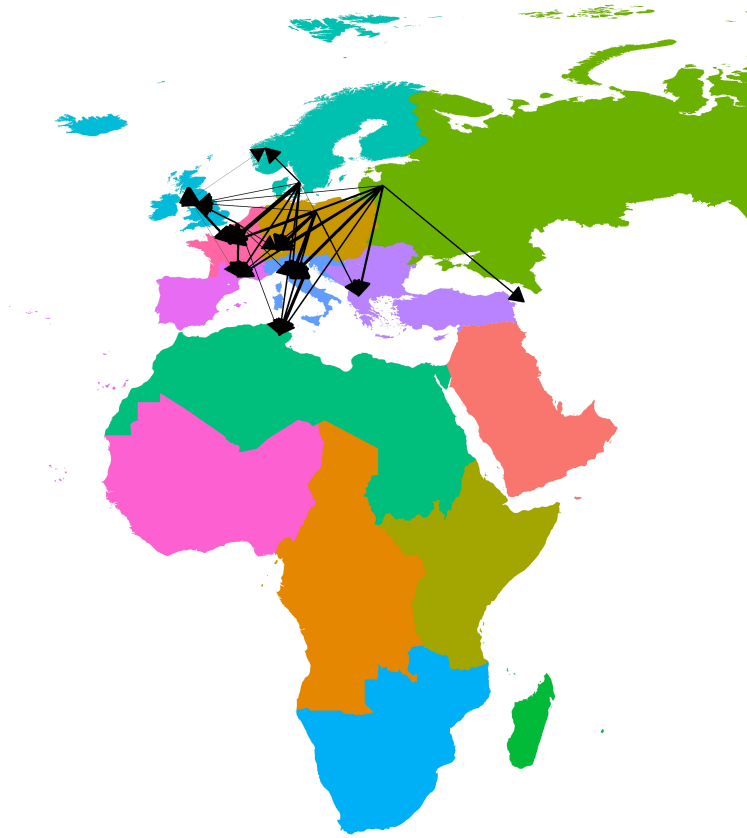


Figure 00720-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.