

Migratory connectivity analysis

by EURING Migration Atlas

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1.1 Connectivity between individuals

The analysis evaluated 305 individuals (610 encounters) filtered from a total of 101782 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 01840-1; Figure 01840-1).

Table 01840-1. 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	305	0.204	0.001	0.088	0.318	2	0.389

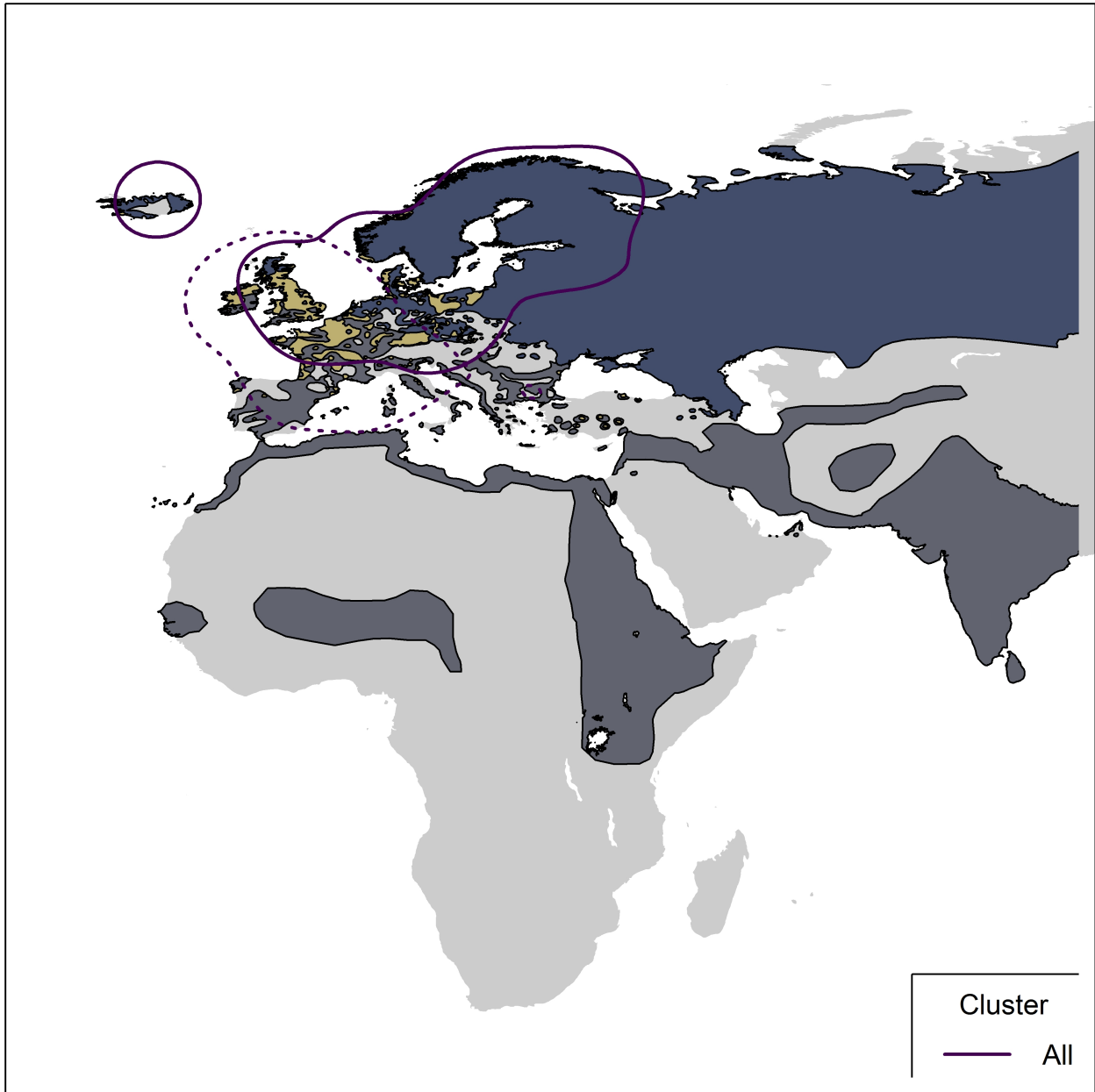


Figure 01840-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 01840-2) and stratified sampling of individuals within the breeding range (Figure 01840-3) and the non breeding range (Figure 01840-4). 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.

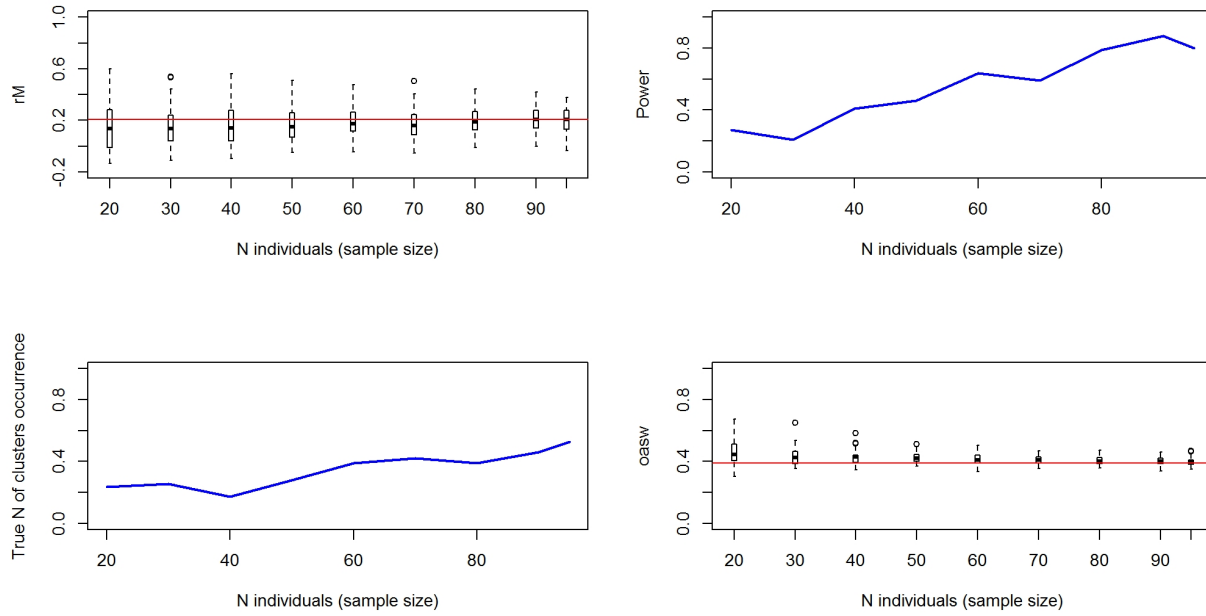


Figure 01840-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

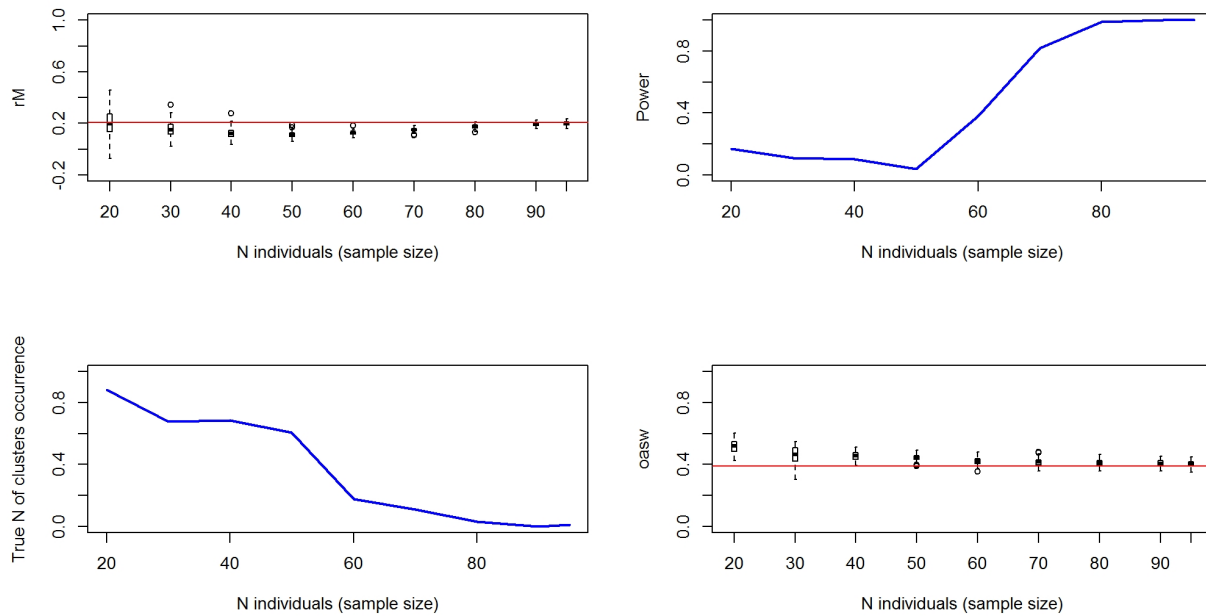


Figure 01840-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

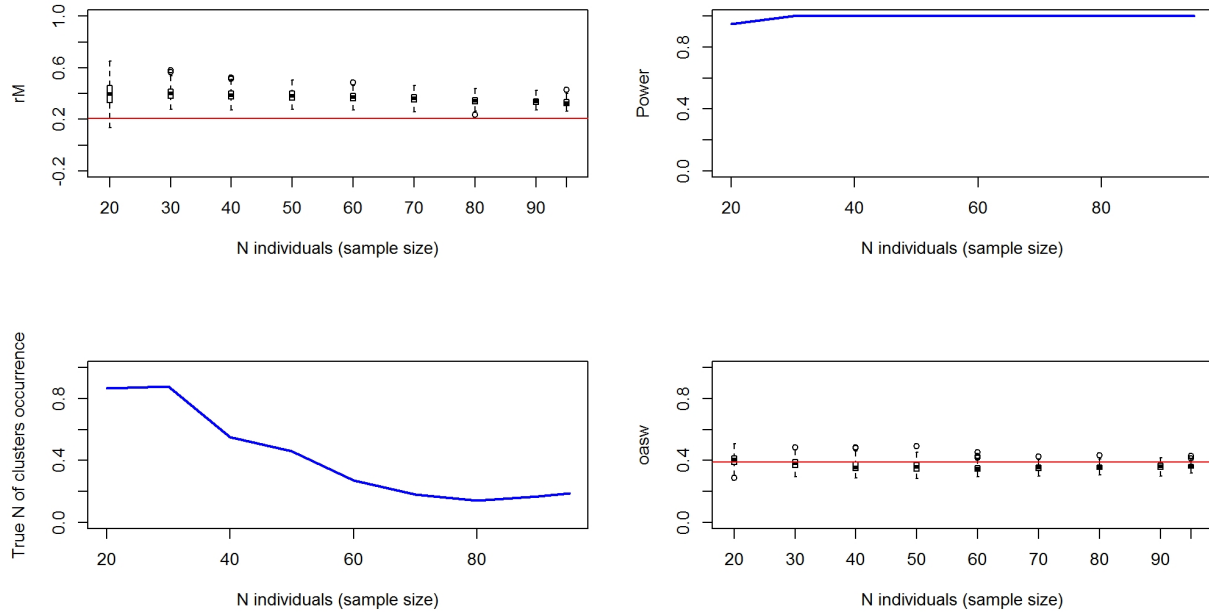


Figure 01840-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.075$); Figure 01840-5).

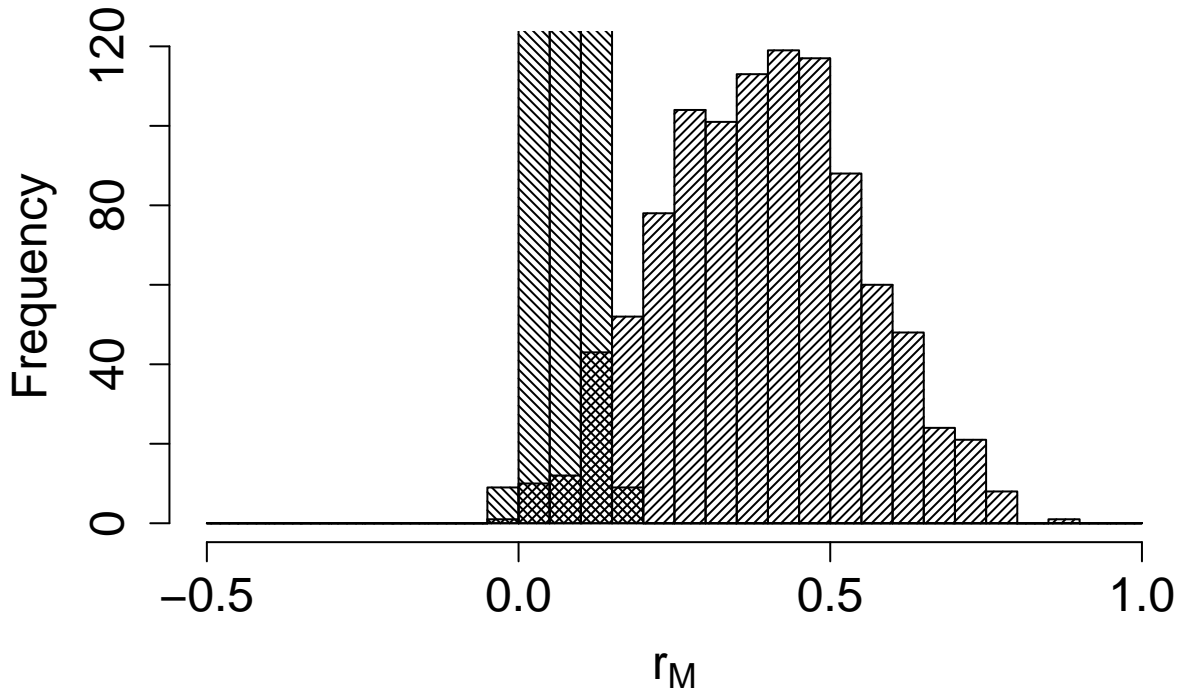


Figure 01840-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows no connectivity (MC = -0.002; MC = -0.005 when adjusted for absolute abundance) between 6 breeding regions and 9 non breeding regions (Table 01840-2; Figure 01840-6).

Table 01840-2. 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	14032	North-west Europe	0.367
Central Europe	14032	South-central Europe	0.025
Central Europe	14032	South-west Europe	0.241
Central Europe	14032	West Europe	0.367
East Europe	784000	Arabian peninsula	0.024
East Europe	784000	East Europe	0.024
East Europe	784000	North Africa	0.098
East Europe	784000	North-west Europe	0.415
East Europe	784000	South-central Europe	0.098
East Europe	784000	South-east Europe	0.098
East Europe	784000	South-west Europe	0.024
East Europe	784000	West Europe	0.220
North Europe	654108	Central Europe	0.025

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	654108	North-west Europe	0.512
North Europe	654108	South-central Europe	0.050
North Europe	654108	South-east Europe	0.025
North Europe	654108	South-west Europe	0.074
North Europe	654108	West Europe	0.314
North-west Europe	13816	North-west Europe	0.872
North-west Europe	13816	South-central Europe	0.021
North-west Europe	13816	South-west Europe	0.021
North-west Europe	13816	West Europe	0.085
South-central Europe	80	South-west Europe	1.000
West Europe	5376	Central Europe	0.062
West Europe	5376	North-west Europe	0.500
West Europe	5376	West Europe	0.438

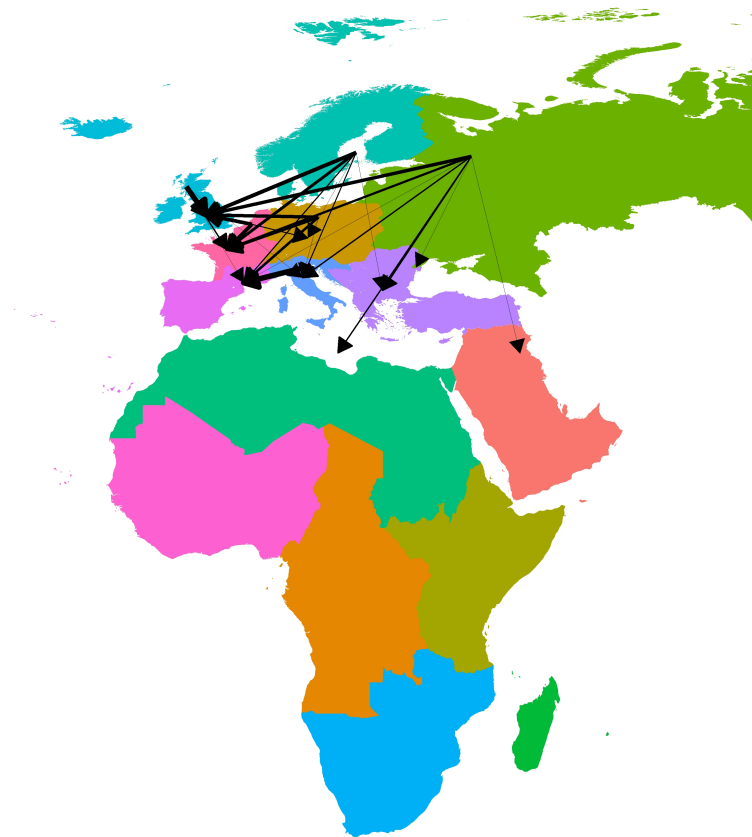


Figure 01840-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.