

Migratory connectivity analysis

by EURING Migration Atlas

Emberiza schoeniclus (EURING code 18770)

1.1 Connectivity between individuals

The analysis evaluated 937 individuals (1874 encounters) filtered from a total of 330120 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 18770-1; Figure 18770-1).

Table 18770-1. 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	937	0.758	0.001	0.719	0.794	2	0.640
1	1	233	0.120	0.001	0.054	0.220	3	0.339
2	1	704	0.909	0.001	0.851	0.948	9	0.415

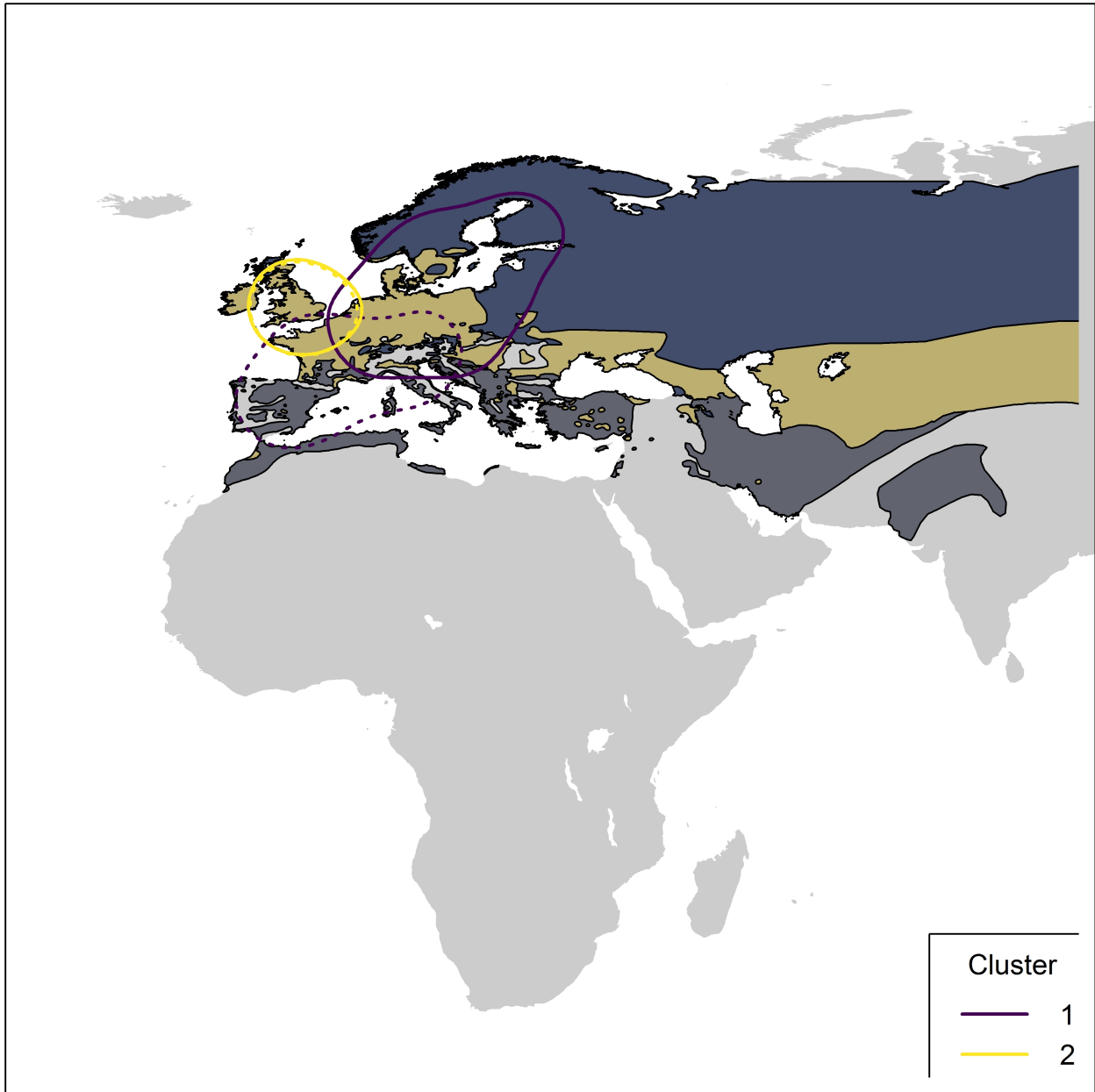


Figure 18770-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 18770-2) and stratified sampling of individuals within the breeding range (Figure 18770-3) and the non breeding range (Figure 18770-4). 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.

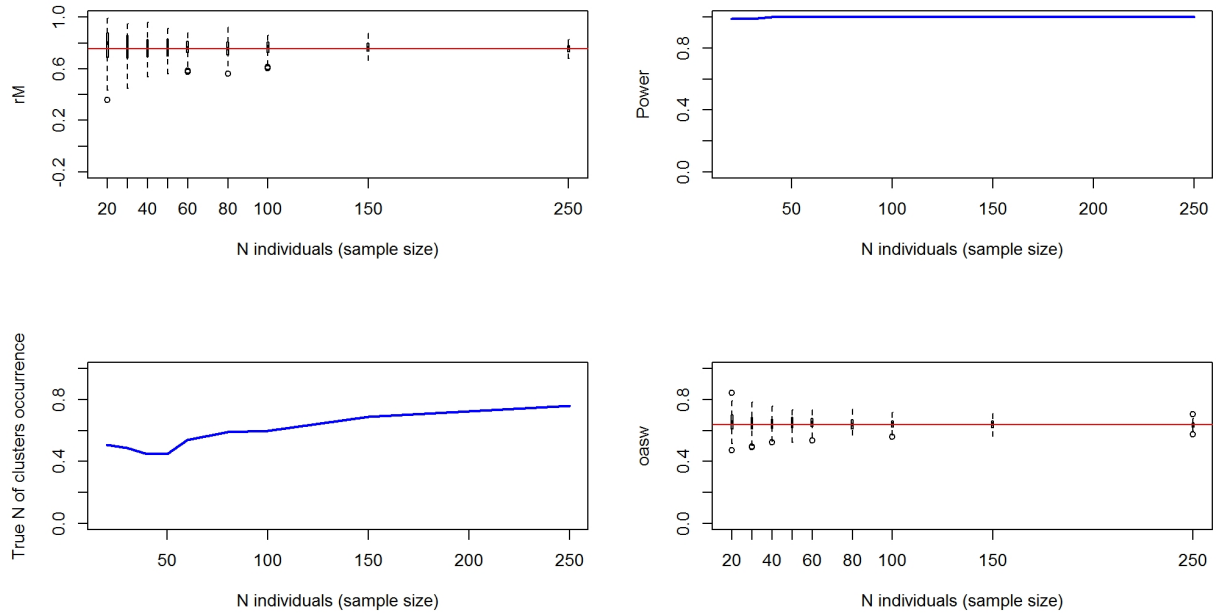


Figure 18770-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

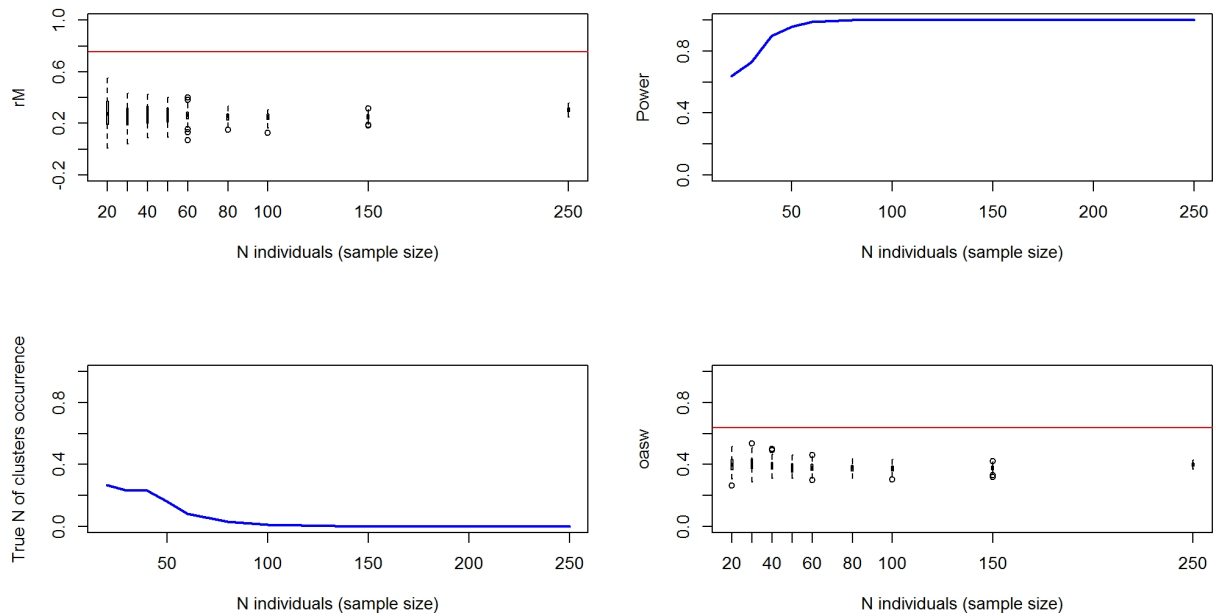


Figure 18770-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

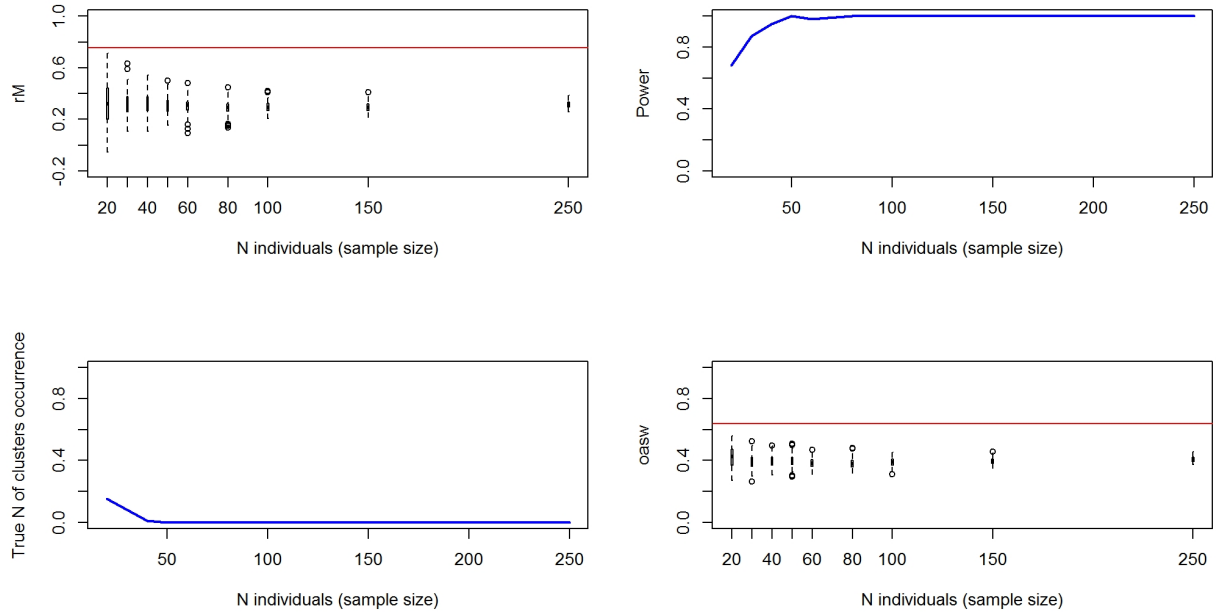


Figure 18770-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is significant ($p = 0.007$); Figure 18770-5).

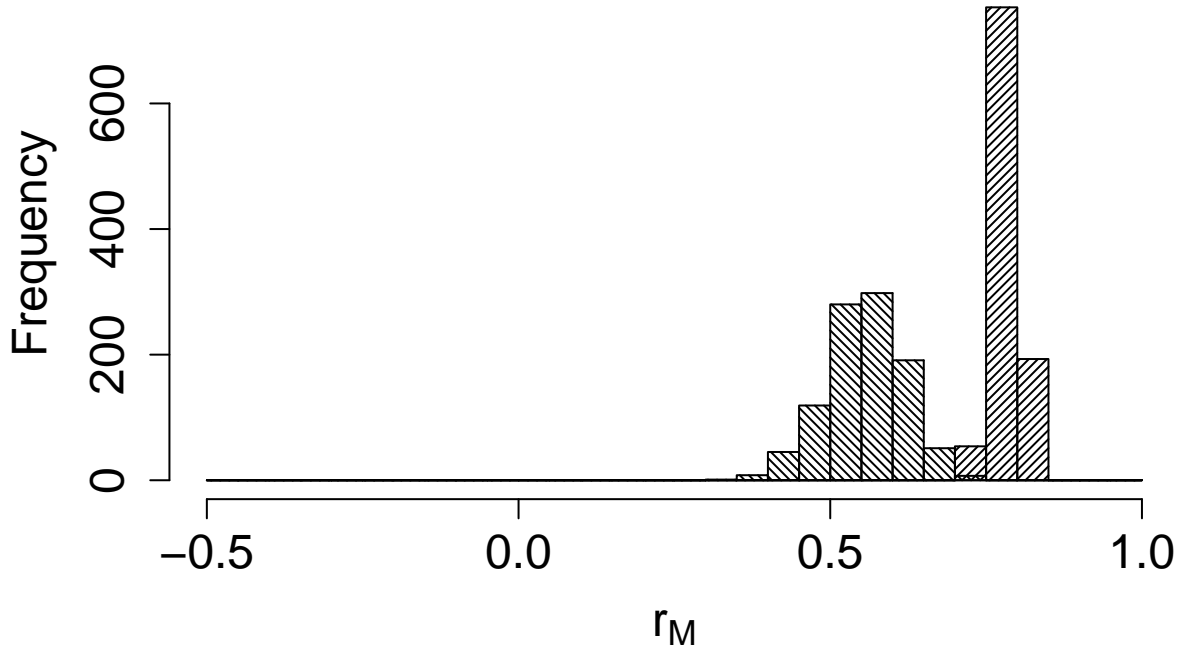


Figure 18770-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity ($MC = 0.393$; $MC = 0.392$ when adjusted for absolute abundance) between 8 breeding regions and 6 non breeding regions (Table 18770-2; Figure 18770-6).

Table 18770-2. 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	1868550	Central Europe	0.115
Central Europe	1868550	South-central Europe	0.270
Central Europe	1868550	South-east Europe	0.008
Central Europe	1868550	South-west Europe	0.525
Central Europe	1868550	West Europe	0.082
East Europe	5597543	South-central Europe	0.083
East Europe	5597543	South-west Europe	0.667
East Europe	5597543	West Europe	0.250
North Europe	1952000	Central Europe	0.103
North Europe	1952000	North-west Europe	0.034
North Europe	1952000	South-central Europe	0.138
North Europe	1952000	South-west Europe	0.414
North Europe	1952000	West Europe	0.310

Breeding region	Abundance	Non breeding region	Transition probability
North-west Europe	1109980	North-west Europe	1.000
South-central Europe	156300	South-central Europe	0.667
South-central Europe	156300	South-west Europe	0.333
South-east Europe	100538	South-east Europe	1.000
South-west Europe	7695	South-west Europe	1.000
West Europe	283614	North-west Europe	0.024
West Europe	283614	South-west Europe	0.207
West Europe	283614	West Europe	0.768



Figure 18770-6. 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>.