

Migratory connectivity analysis

by EURING Migration Atlas

Scolopax rusticola (EURING code 05290)

1.1 Connectivity between individuals

The analysis evaluated 518 individuals (1036 encounters) filtered from a total of 26505 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 05290-1; Figure 05290-1).

Table 05290-1. 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	518	0.231	0.001	0.169	0.305	2	0.486

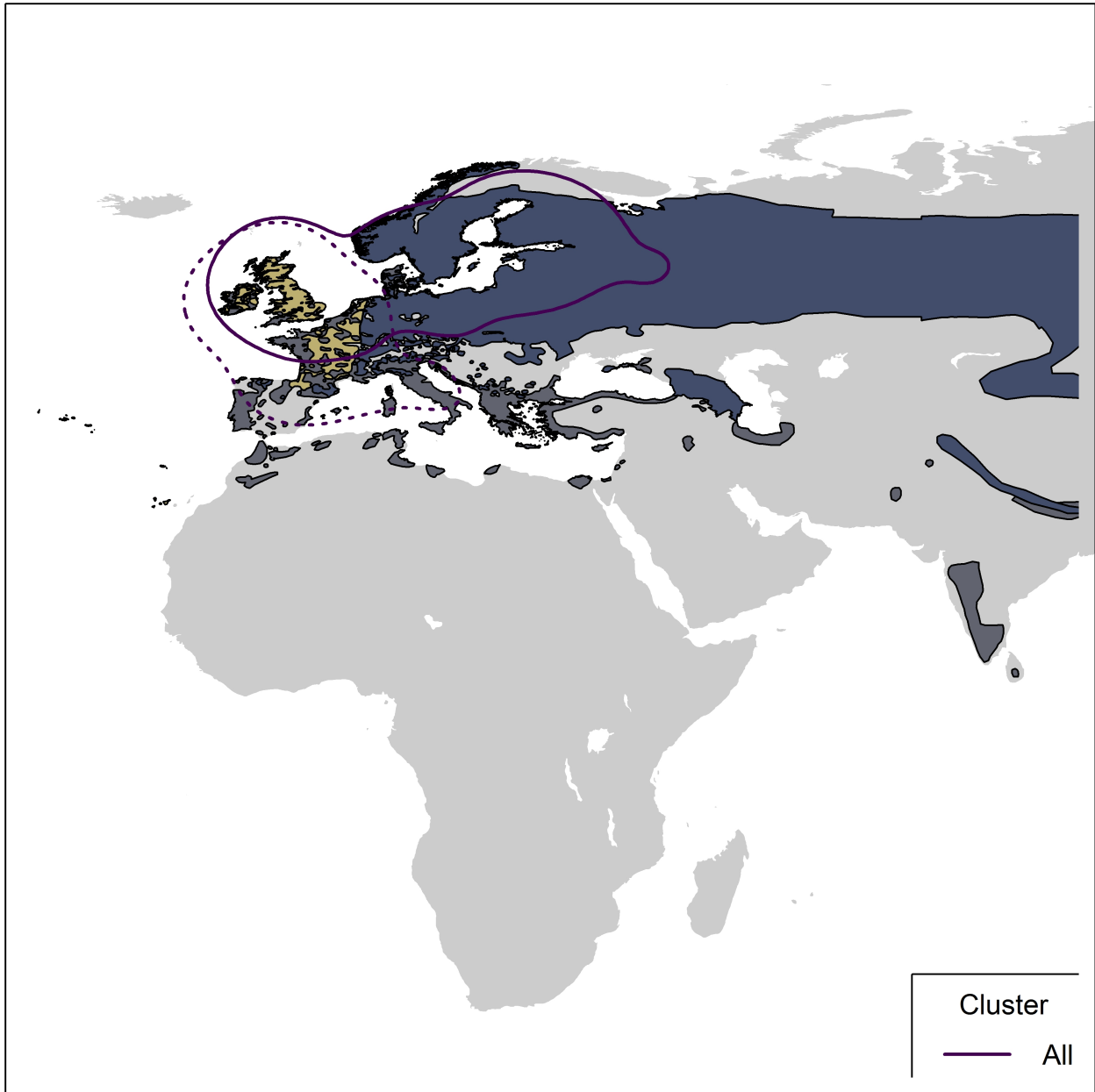


Figure 05290-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 05290-2) and stratified sampling of individuals within the breeding range (Figure 05290-3) and the non breeding range (Figure 05290-4). 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.

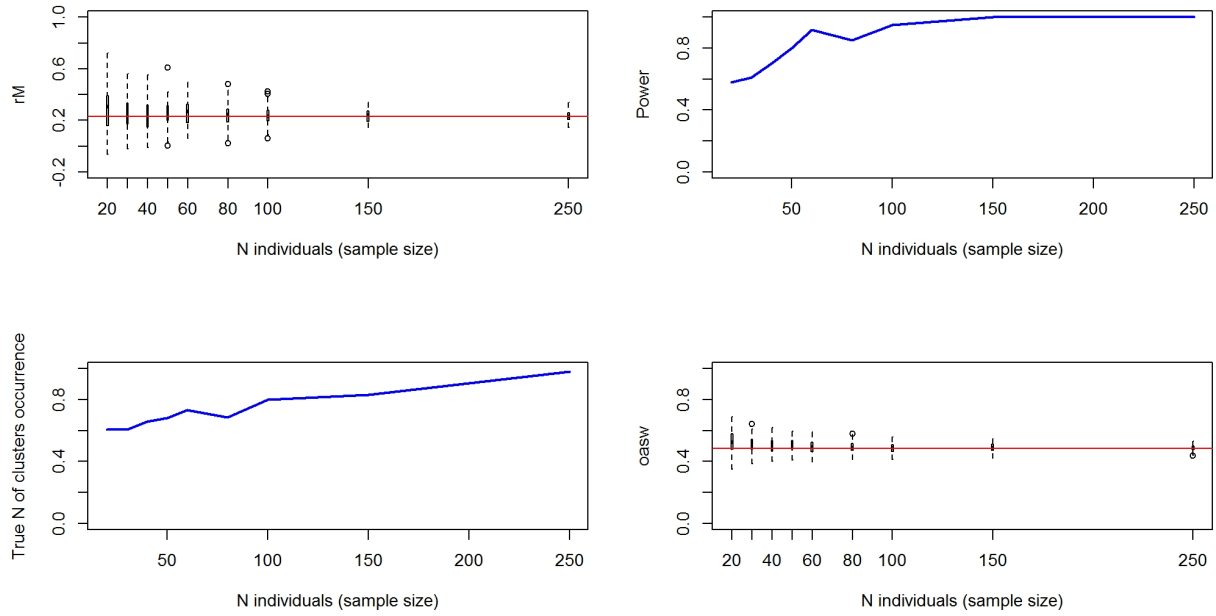


Figure 05290-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

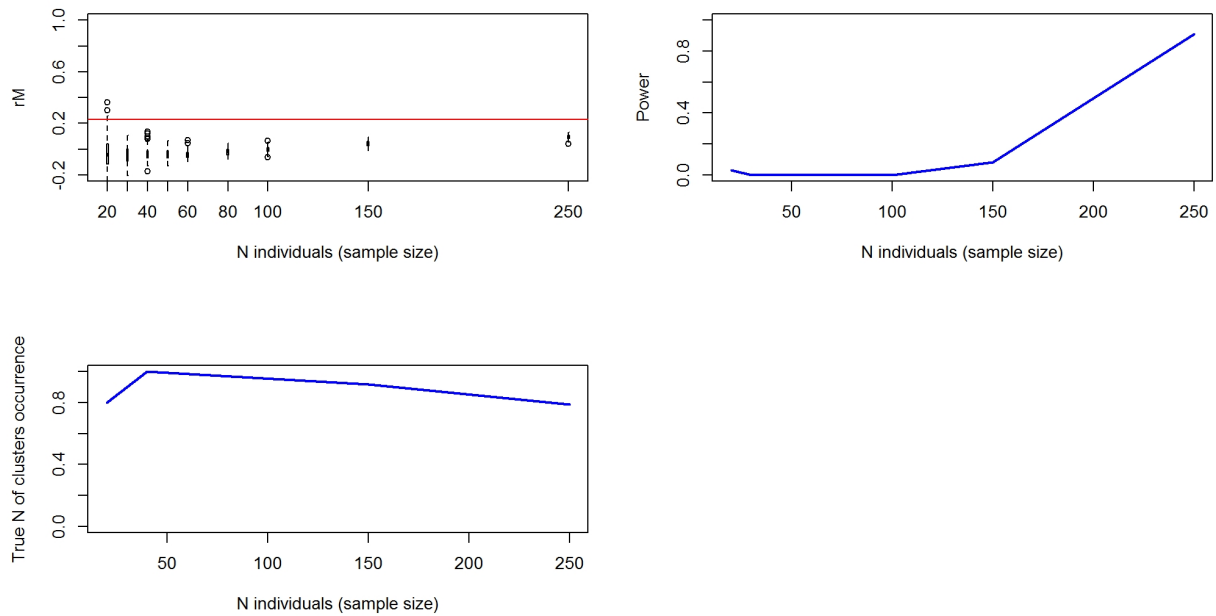


Figure 05290-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

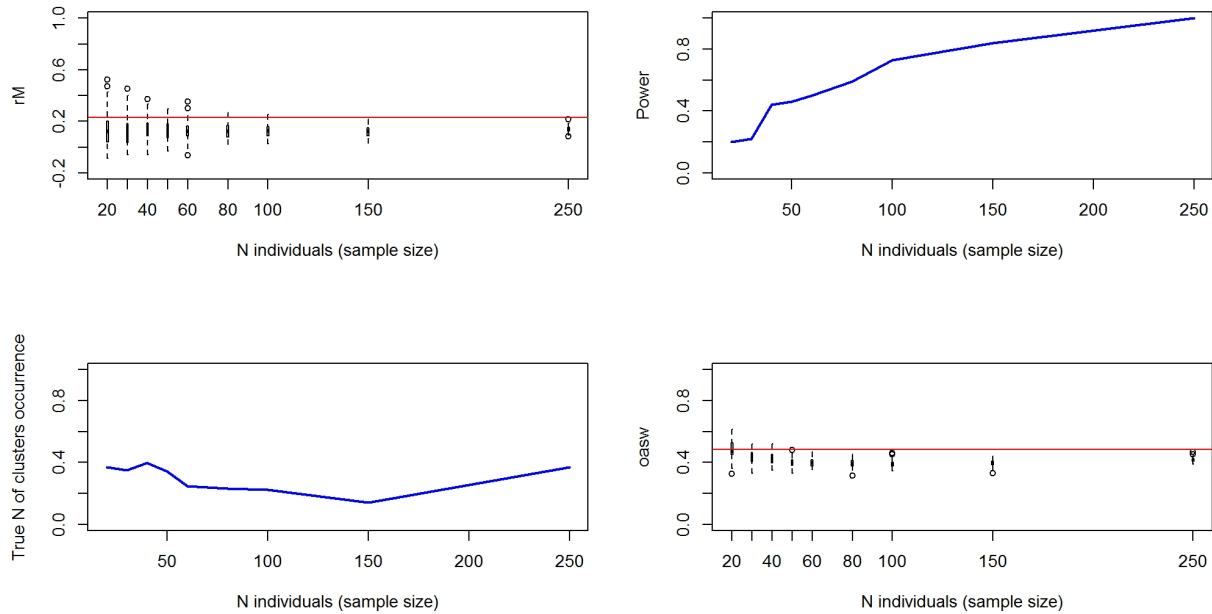


Figure 05290-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

2. Connectivity between pre-defined regions

The species shows low connectivity ($MC = 0.001$; $MC = 0$ when adjusted for absolute abundance) between 6 breeding regions and 6 non breeding regions (Table 05290-2; Figure 05290-6).

Table 05290-2. 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	223952	North-west Europe	0.071
Central Europe	223952	South-central Europe	0.214
Central Europe	223952	South-west Europe	0.429
Central Europe	223952	West Europe	0.286
East Europe	14823256	North Europe	0.016
East Europe	14823256	North-west Europe	0.131
East Europe	14823256	South-central Europe	0.164
East Europe	14823256	South-east Europe	0.066
East Europe	14823256	South-west Europe	0.197
East Europe	14823256	West Europe	0.426
North Europe	1863400	North Europe	0.013
North Europe	1863400	North-west Europe	0.319
North Europe	1863400	South-central Europe	0.043
North Europe	1863400	South-east Europe	0.039

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	1863400	South-west Europe	0.138
North Europe	1863400	West Europe	0.448
North-west Europe	180400	North-west Europe	0.964
North-west Europe	180400	South-west Europe	0.005
North-west Europe	180400	West Europe	0.031
South-west Europe	23932	South-west Europe	1.000
West Europe	30153	North-west Europe	0.062
West Europe	30153	South-west Europe	0.125
West Europe	30153	West Europe	0.812

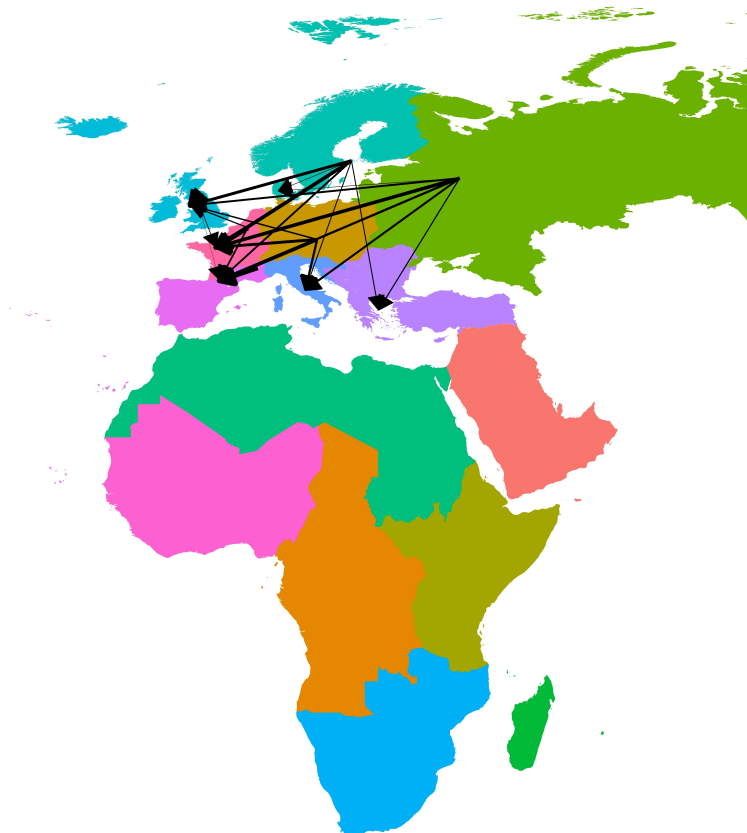


Figure 05290-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.