

Migratory connectivity analysis

by EURING Migration Atlas

Turdus iliacus (EURING code 12010)

1.1 Connectivity between individuals

The analysis evaluated 683 individuals (1366 encounters) filtered from a total of 41281 records in the EURING databank which were considered for the Atlas. The species does not show a significant connectivity (Table 12010-1; Figure 12010-1).

Table 12010-1. 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	683	0.029	0.129	-0.015	0.08	-	-

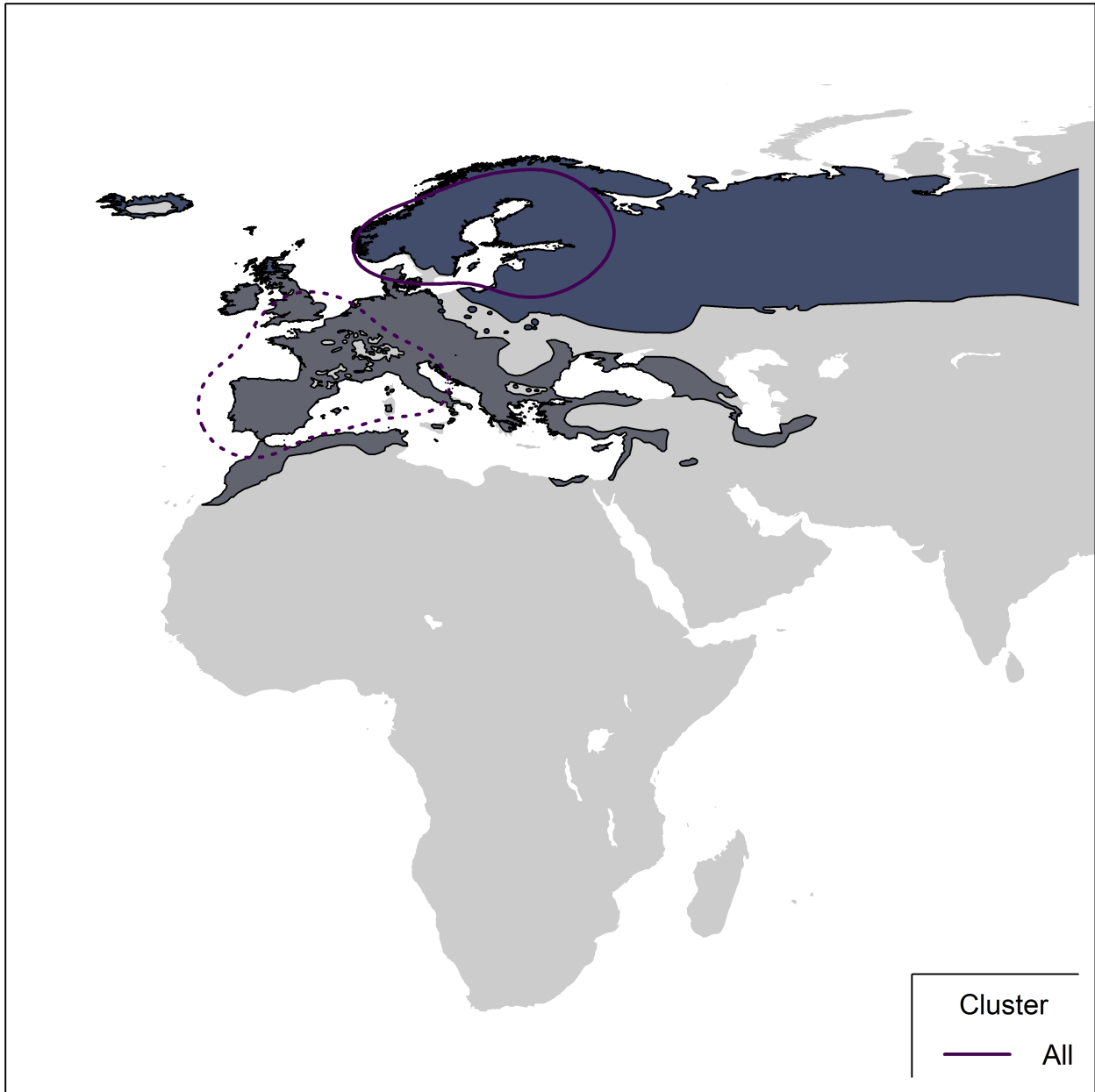


Figure 12010-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 12010-2) and stratified sampling of individuals within the breeding range (Figure 12010-3) and the non breeding range (Figure 12010-4). 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.

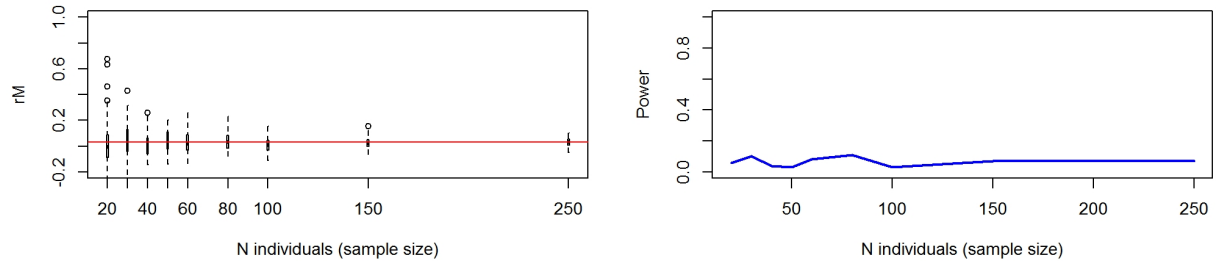


Figure 12010-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

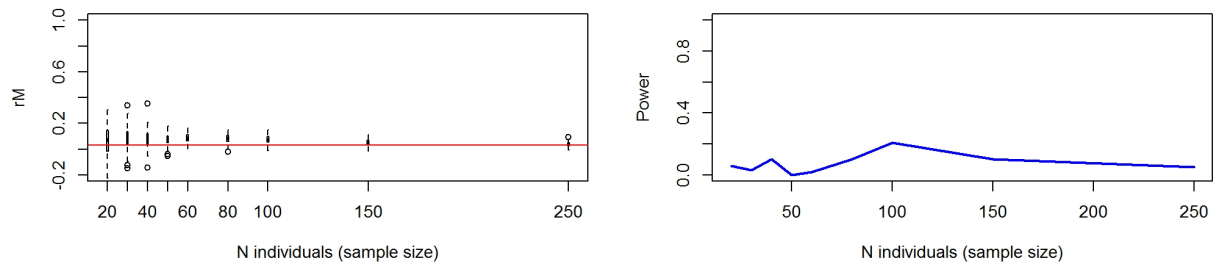


Figure 12010-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

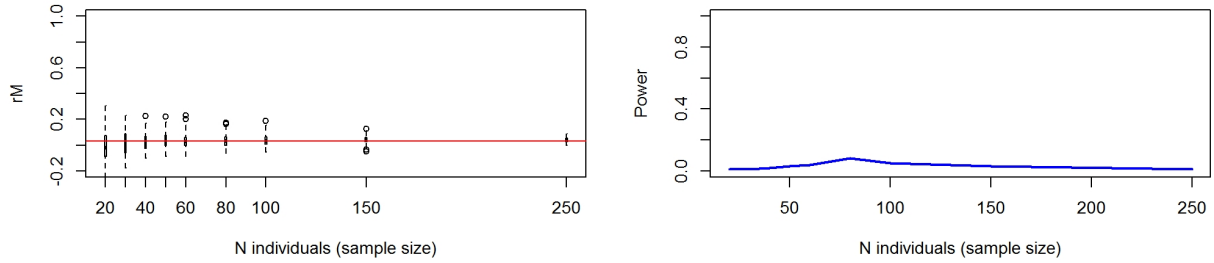


Figure 12010-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.352$); Figure 12010-5).

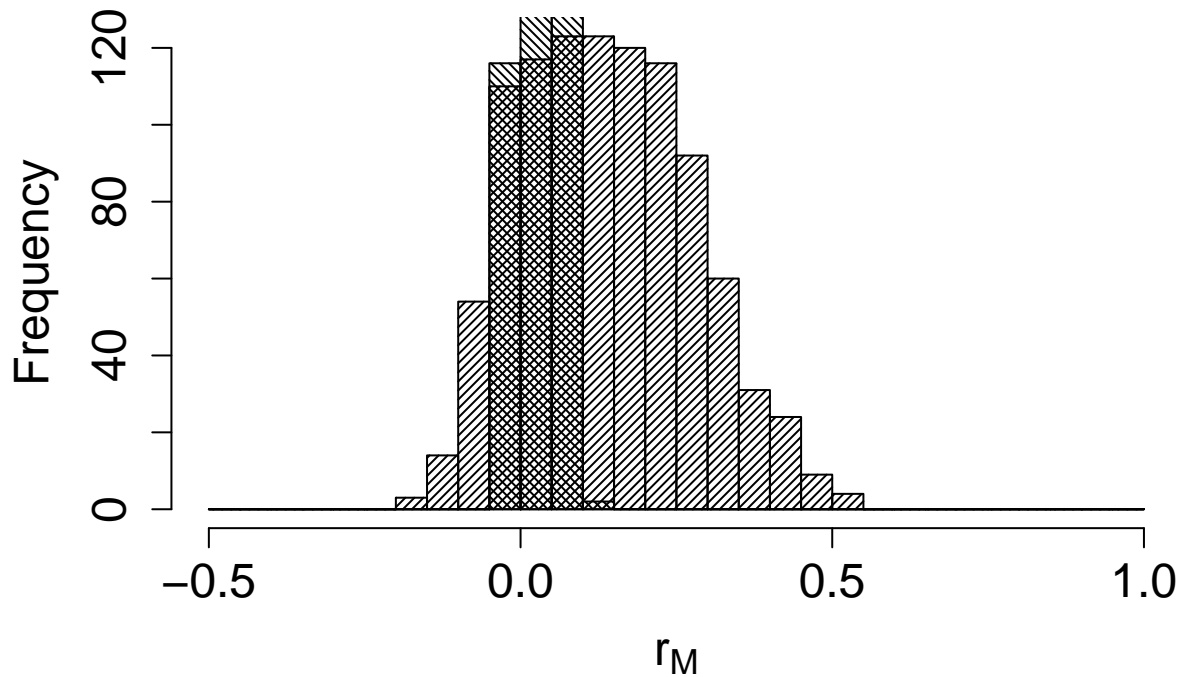


Figure 12010-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows no connectivity ($MC = -0.033$; $MC = -0.034$ when adjusted for absolute abundance) between 4 breeding regions and 9 non breeding regions (Table 12010-2; Figure 12010-6).

Table 12010-2. 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	410	South-west Europe	1.000
East Europe	25685740	Central Europe	0.014
East Europe	25685740	North-west Europe	0.041
East Europe	25685740	South-central Europe	0.137
East Europe	25685740	South-east Europe	0.027
East Europe	25685740	South-west Europe	0.562
East Europe	25685740	West Europe	0.219
North Europe	7300020	Arabian peninsula	0.007
North Europe	7300020	Central Europe	0.002
North Europe	7300020	East Europe	0.002
North Europe	7300020	North Africa	0.003
North Europe	7300020	North-west Europe	0.044
North Europe	7300020	South-central Europe	0.095

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	7300020	South-east Europe	0.020
North Europe	7300020	South-west Europe	0.516
North Europe	7300020	West Europe	0.311
North-west Europe	300020	South-west Europe	1.000

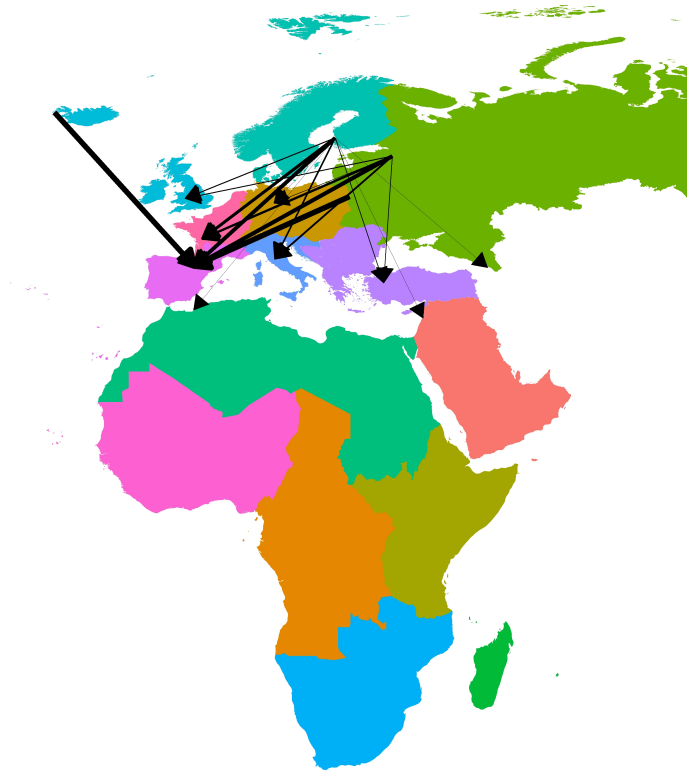


Figure 12010-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.