Migratory connectivity analysis

by EURING Migration Atlas

***Turdus pilaris* (EURING code 11980)**

1.1 Connectivity between individuals

The analysis evaluated 1572 individuals (3144 encounters) filtered from a total of 30007 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 11980-1; Figure 11980-1).

Table 11980-1. 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	1572	0.025	0.024	-0.001	0.061	2	0.411

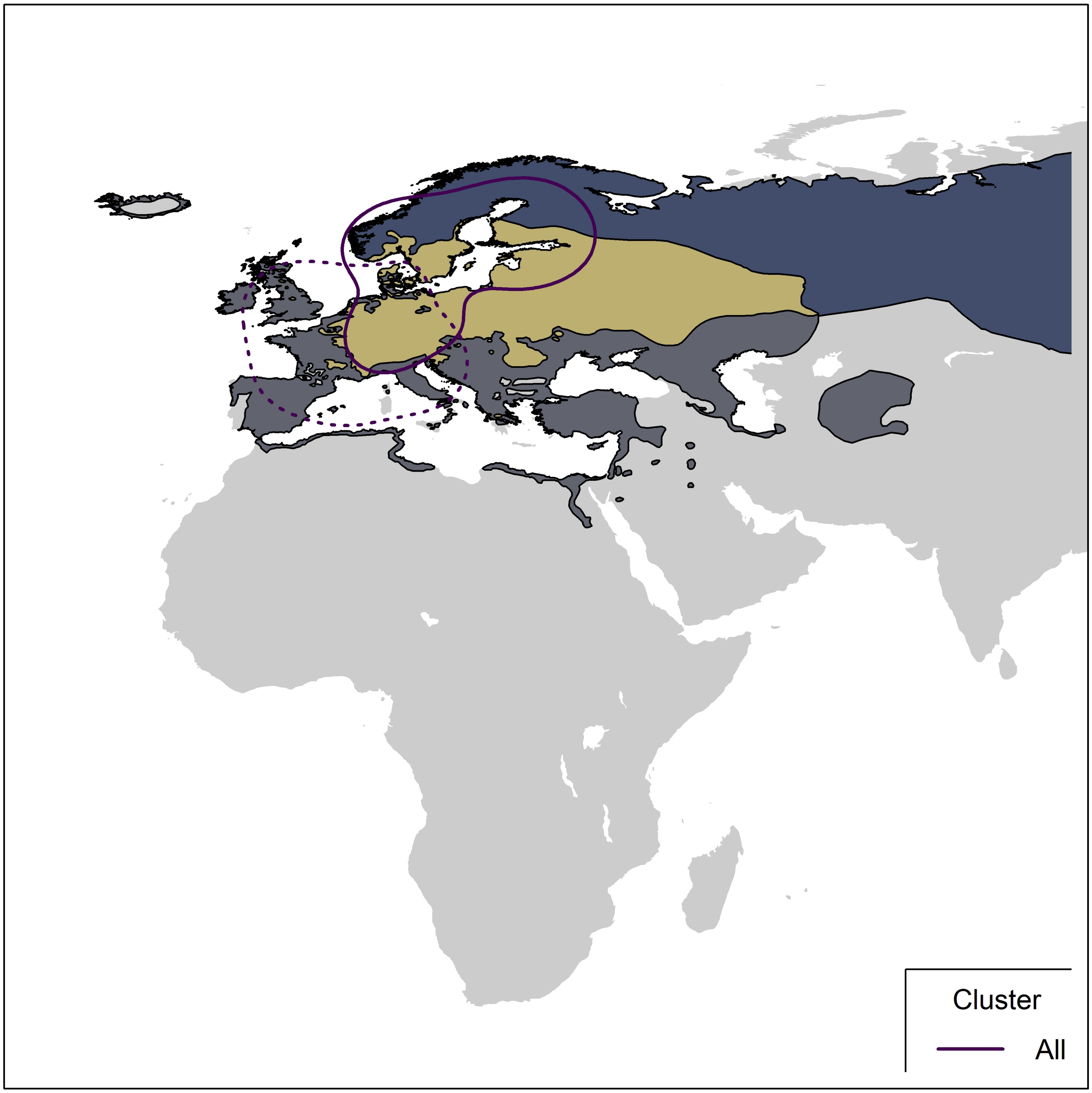

Figure 11980-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 11980-2) and stratified sampling of individuals within the breeding range (Figure 11980-3) and the non breeding range (Figure 11980-4). 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.

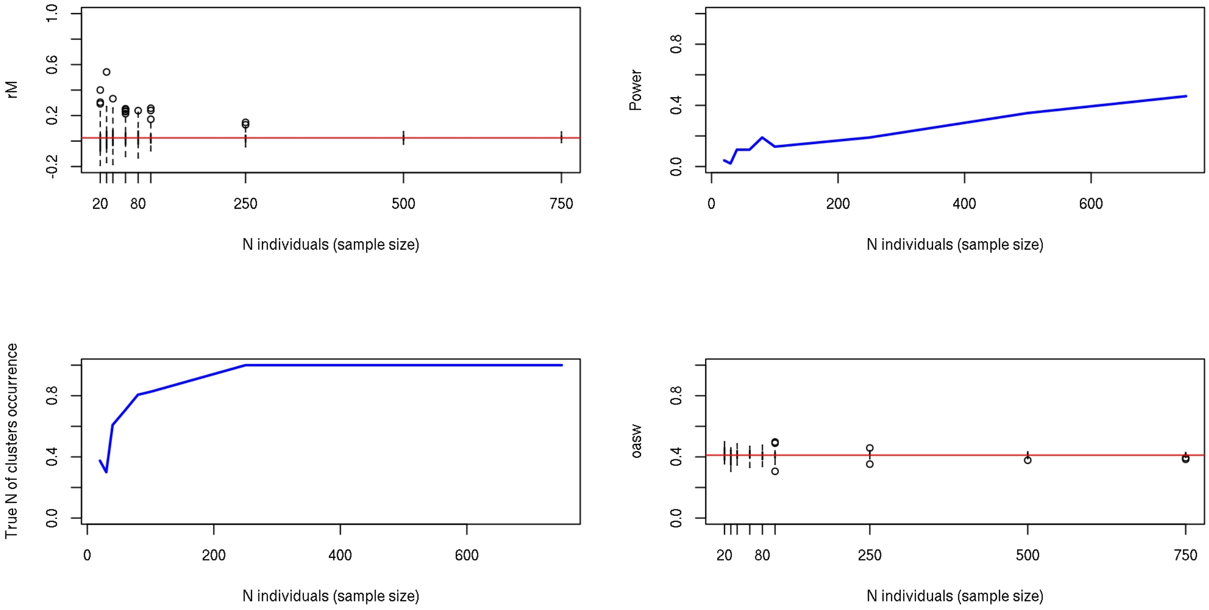

Figure 11980-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

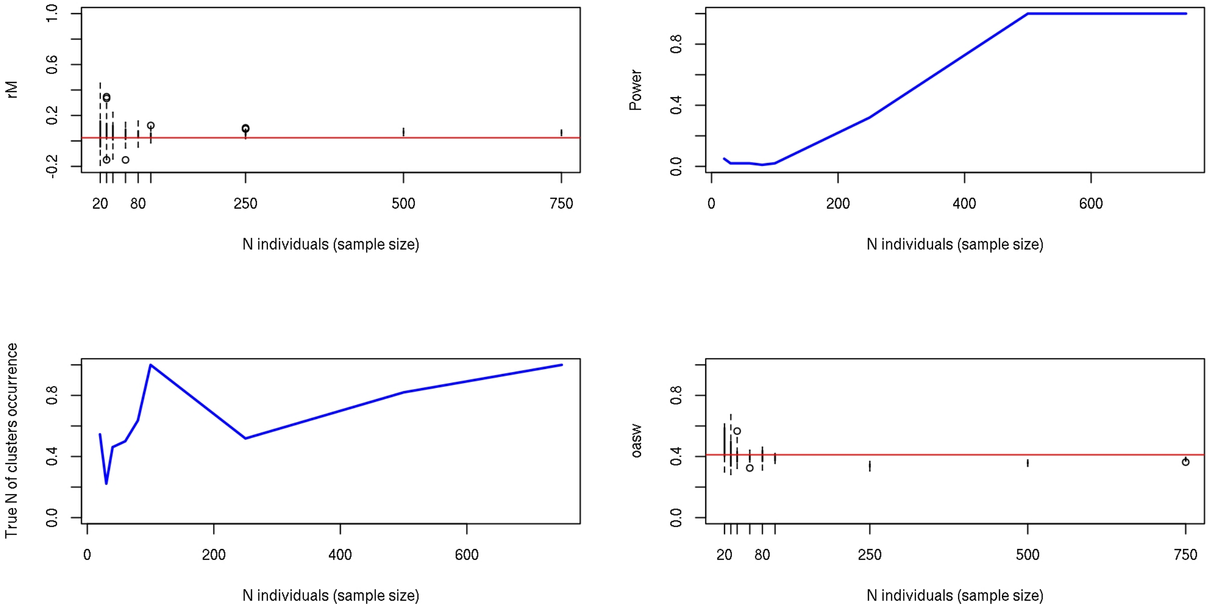

Figure 11980-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

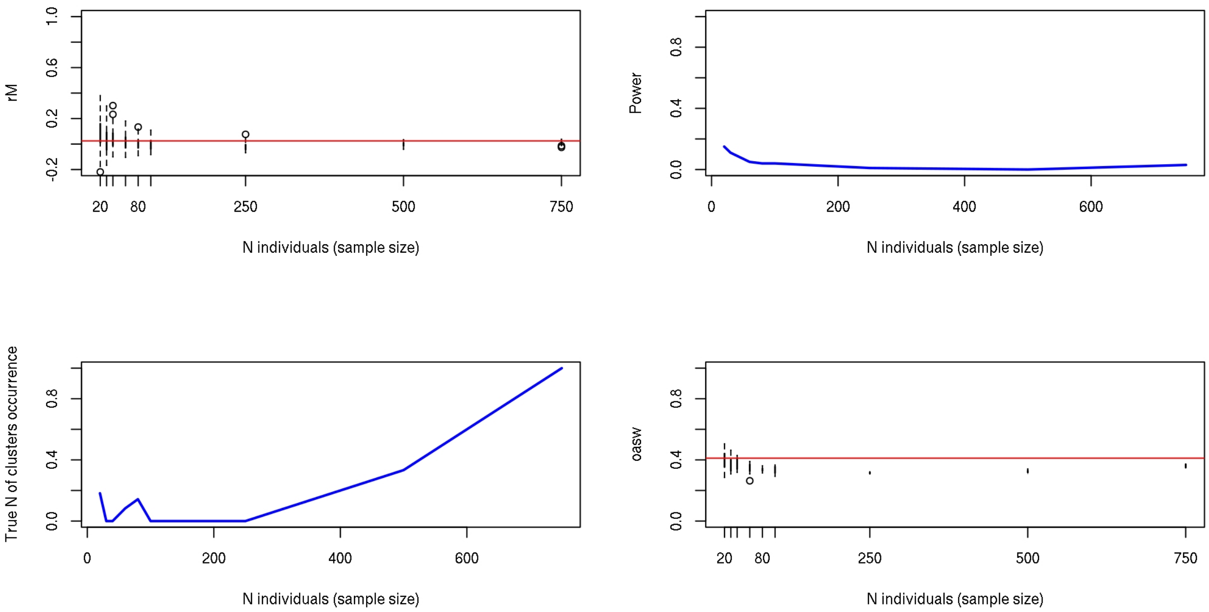

Figure 11980-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is significant ($p = 0.038$); Figure 11980-5).

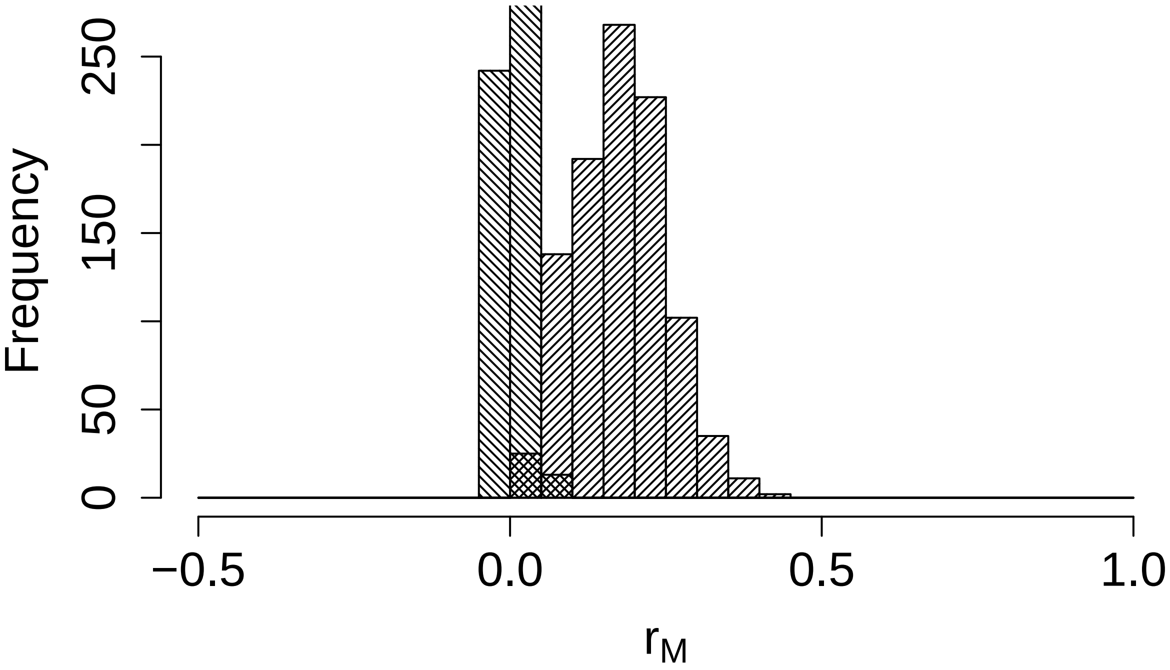

Figure 11980-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity (MC = 0.013; MC = 0.012 when adjusted for absolute abundance) between 4 breeding regions and 9 non breeding regions (Table 11980-2; Figure 11980-6).

Table 11980-2. 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	2580730	Central Europe	0.076
Central Europe	2580730	South-central Europe	0.219
Central Europe	2580730	South-east Europe	0.010
Central Europe	2580730	South-west Europe	0.540
Central Europe	2580730	West Europe	0.156
East Europe	31227982	Central Europe	0.101
East Europe	31227982	East Europe	0.039
East Europe	31227982	North Europe	0.023
East Europe	31227982	North-west Europe	0.031
East Europe	31227982	South-central Europe	0.403
East Europe	31227982	South-east Europe	0.031
East Europe	31227982	South-west Europe	0.233
East Europe	31227982	West Europe	0.140

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	8701000	Arabian peninsula	0.001
North Europe	8701000	Central Europe	0.043
North Europe	8701000	East Europe	0.004
North Europe	8701000	North Europe	0.048
North Europe	8701000	North-west Europe	0.185
North Europe	8701000	South-central Europe	0.126
North Europe	8701000	South-east Europe	0.007
North Europe	8701000	South-west Europe	0.218
North Europe	8701000	West Europe	0.369
West Europe	51203	Central Europe	0.120
West Europe	51203	North-west Europe	0.040
West Europe	51203	South-central Europe	0.080
West Europe	51203	South-west Europe	0.240
West Europe	51203	West Europe	0.520

Figure 11980-6. 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.