Migratory connectivity analysis

by EURING Migration Atlas

Turdus viscivorus **(EURING code 12020)**

1.1 Connectivity between individuals

The analysis evaluated 542 individuals (1084 encounters) filtered from a total of 7678 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 12020-1; Figure 12020-1).

Table 12020-1. 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	542	0.671	0.001	0.577	0.762	4	0.381
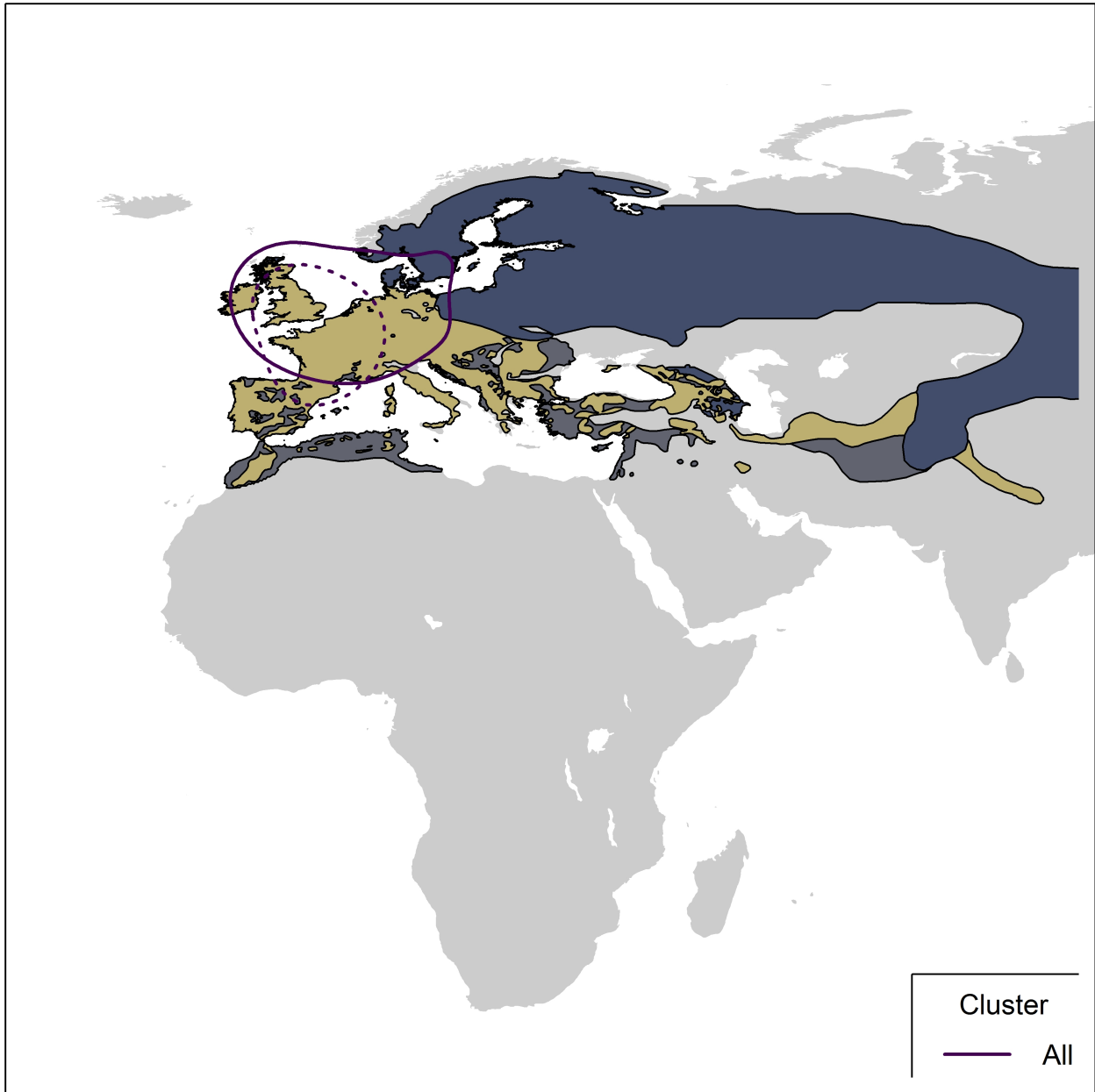
Figure 12020-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 12020-2) and stratified sampling of individuals within the breeding range (Figure 12020-3) and the non breeding range (Figure 12020-4). 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.
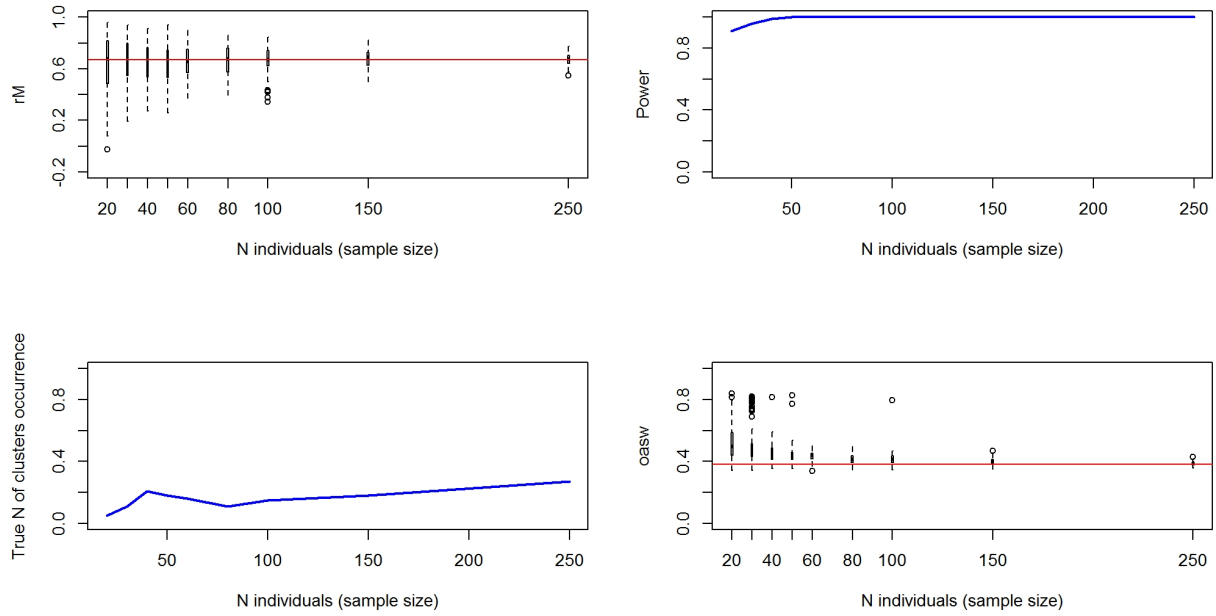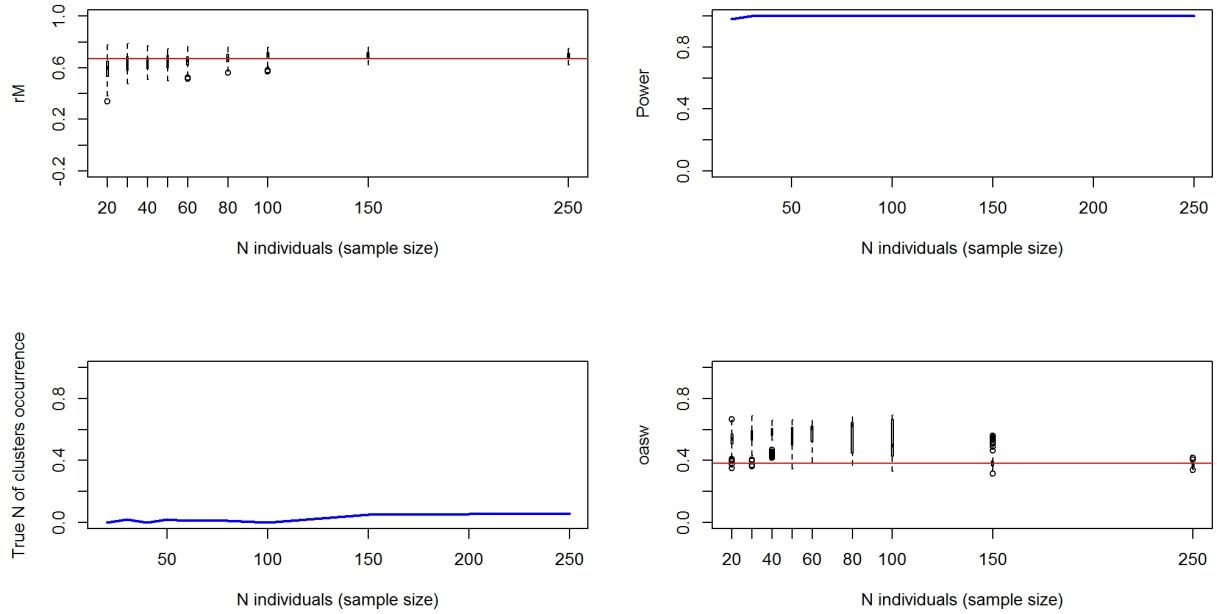

Figure 12020-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
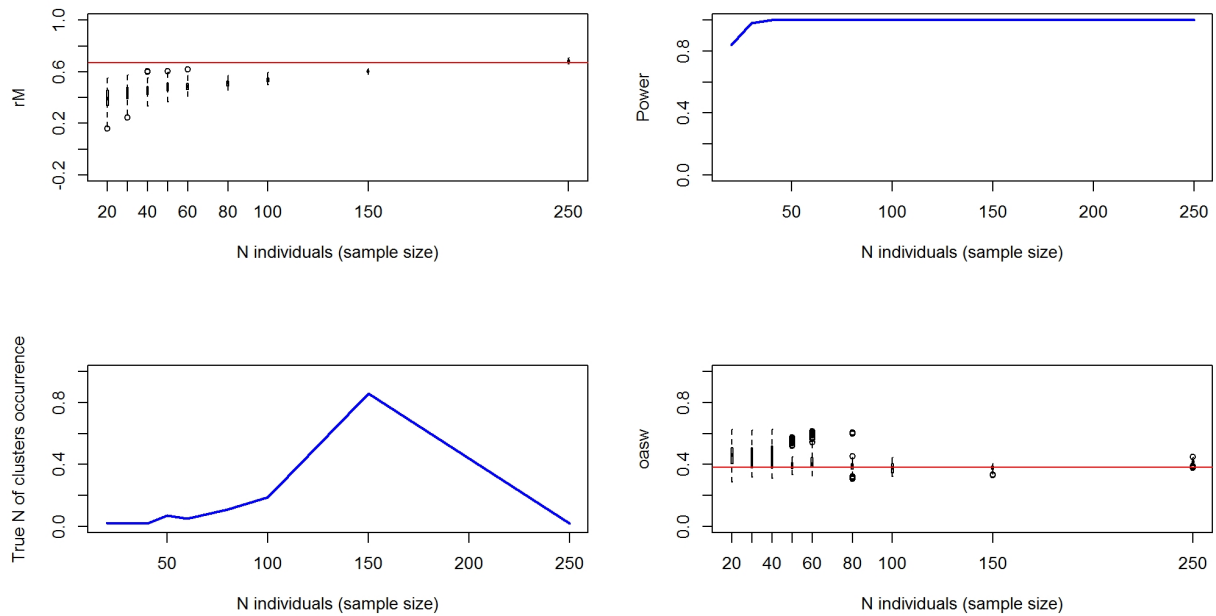
Figure 12020-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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


Figure 12020-4. 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 = 0.633); Figure 12020-5).
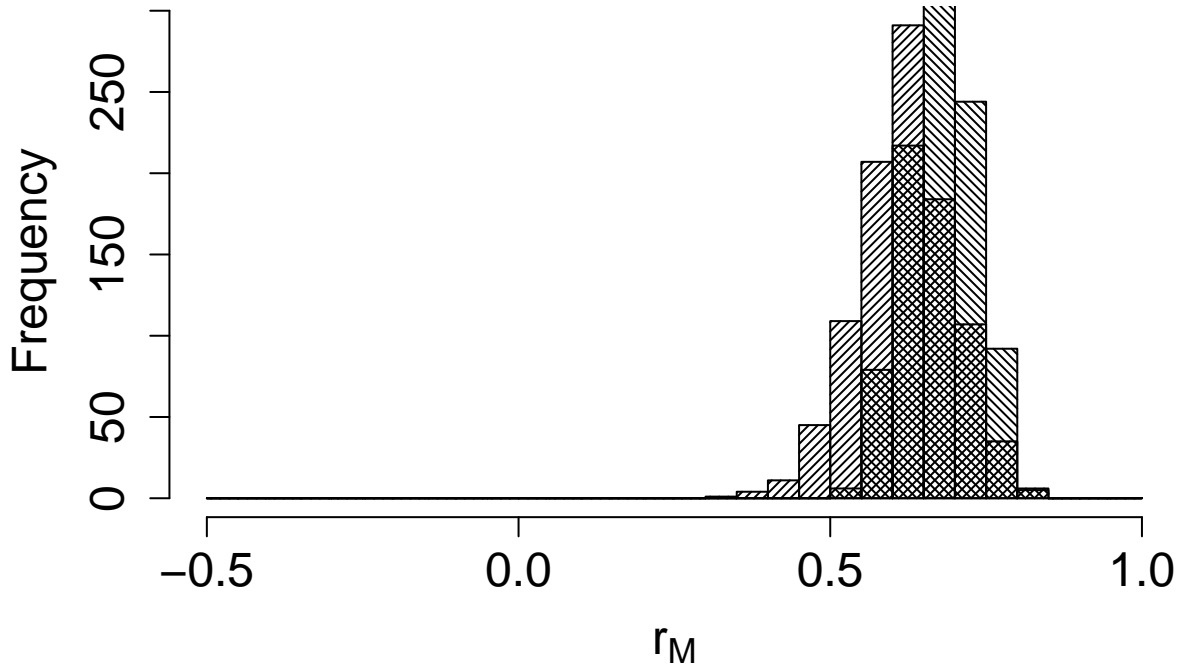
Figure 12020-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity (MC = 0.011; MC = 0.008 when adjusted for absolute abundance) between 7 breeding regions and 8 non breeding regions (Table 12020-2; Figure 12020-6).

Table 12020-2. 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	1397150	Central Europe	0.078
Central Europe	1397150	South-central Europe	0.020
Central Europe	1397150	South-west Europe	0.353
Central Europe	1397150	West Europe	0.549
East Europe	4712761	East Europe	0.167
East Europe	4712761	North Africa	0.167
East Europe	4712761	North-west Europe	0.167
East Europe	4712761	South-central Europe	0.167
East Europe	4712761	South-west Europe	0.167
East Europe	4712761	West Europe	0.167
North Europe	1286000	South-central Europe	0.083
North Europe	1286000	South-east Europe	0.167
North Europe	1286000	South-west Europe	0.417

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	1286000	West Europe	0.333
North-west Europe	690843	North-west Europe	0.942
North-west Europe	690843	South-west Europe	0.005
North-west Europe	690843	West Europe	0.053
South-central Europe	862738	South-central Europe	1.000
South-west Europe	1233447	South-west Europe	1.000
West Europe	1123949	Central Europe	0.004
West Europe	1123949	North-west Europe	0.004
West Europe	1123949	South-central Europe	0.004
West Europe	1123949	South-west Europe	0.100
West Europe	1123949	West Europe	0.888
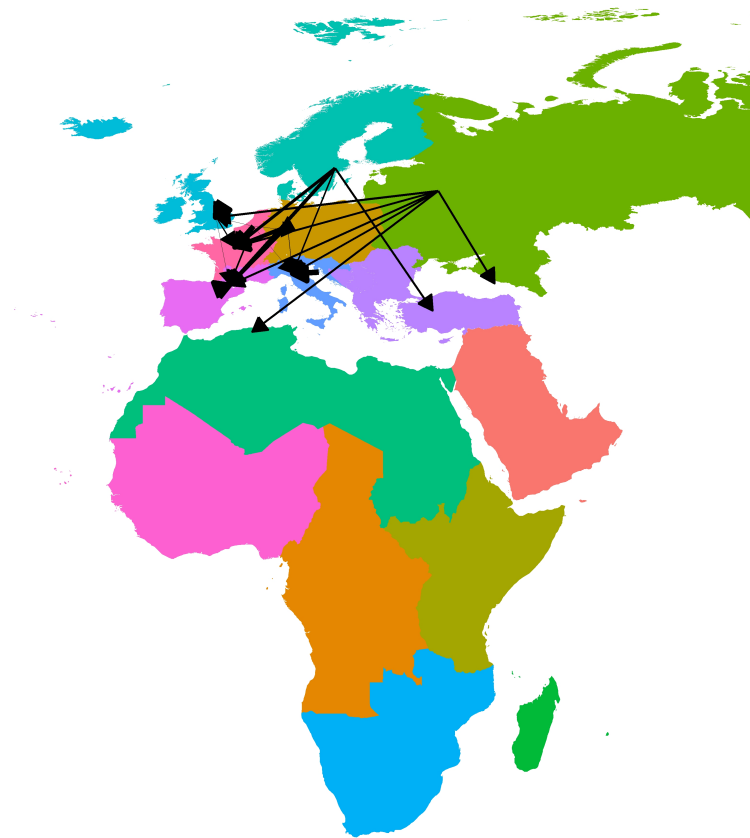
Figure 12020-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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.