

Migratory connectivity analysis

by EURING Migration Atlas

Corvus frugilegus (EURING code 15630)

1.1 Connectivity between individuals

The analysis evaluated 517 individuals (1034 encounters) filtered from a total of 22882 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 15630-1; Figure 15630-1).

Table 15630-1. 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	517	0.58	0.001	0.537	0.622	2	0.483

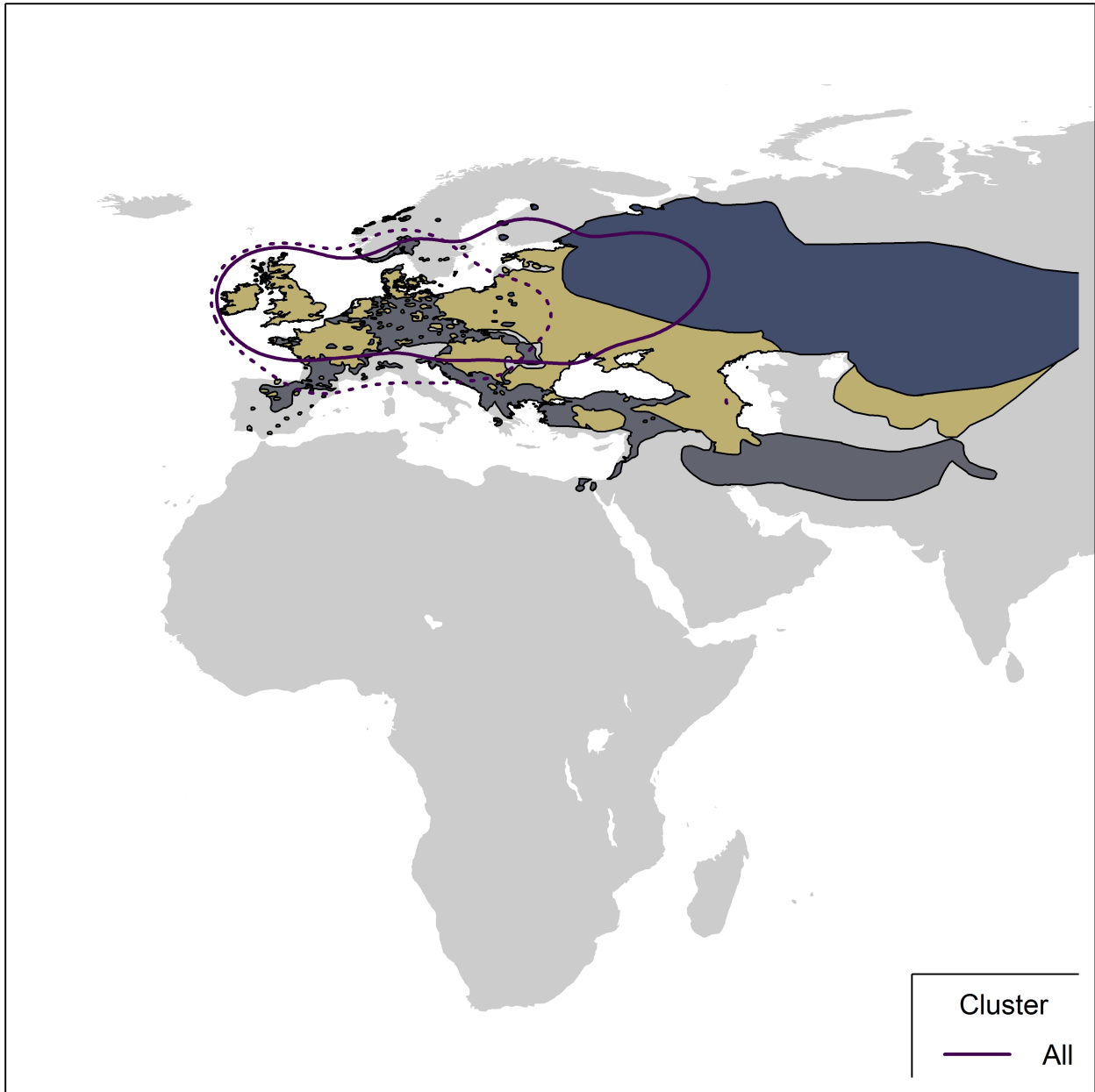


Figure 15630-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 15630-2) and stratified sampling of individuals within the breeding range (Figure 15630-3) and the non breeding range (Figure 15630-4). 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.

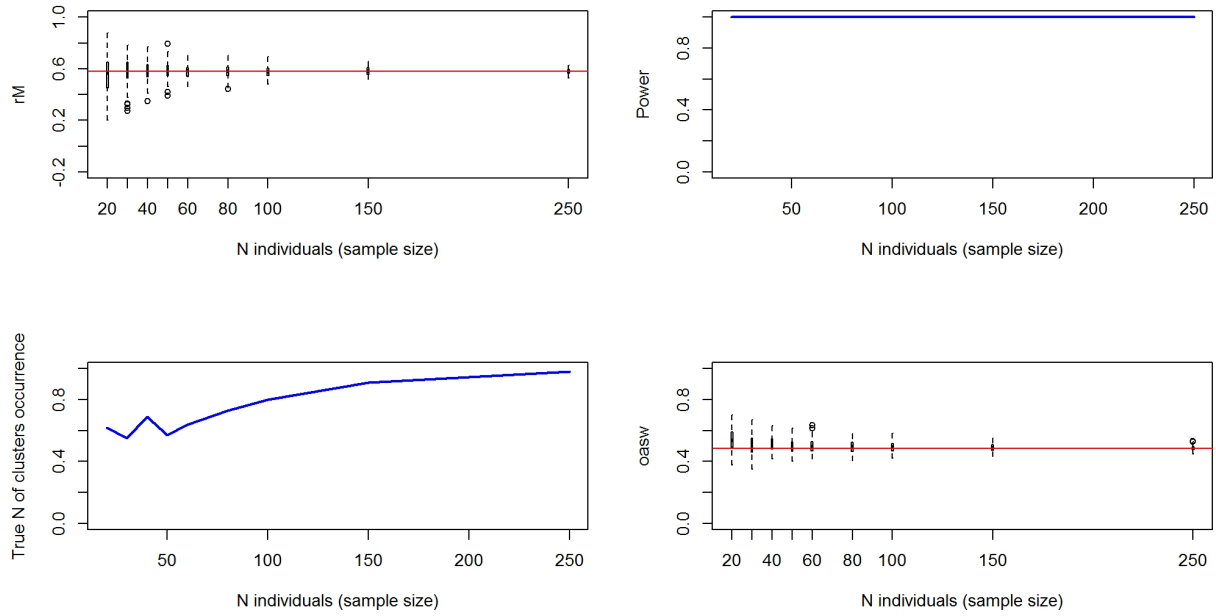


Figure 15630-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

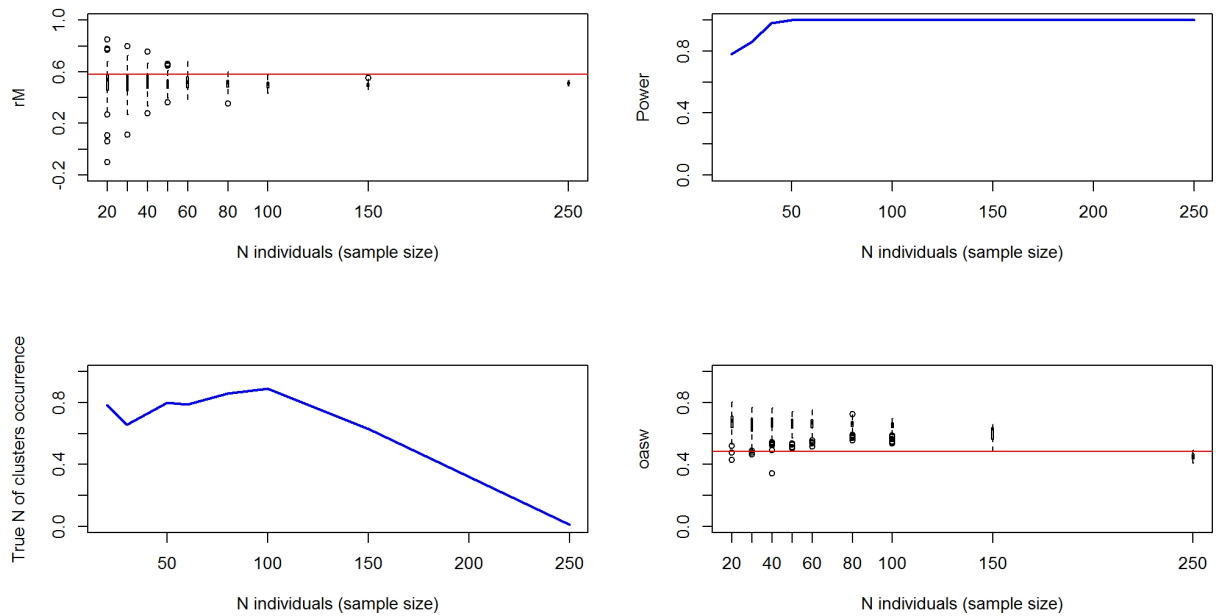


Figure 15630-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

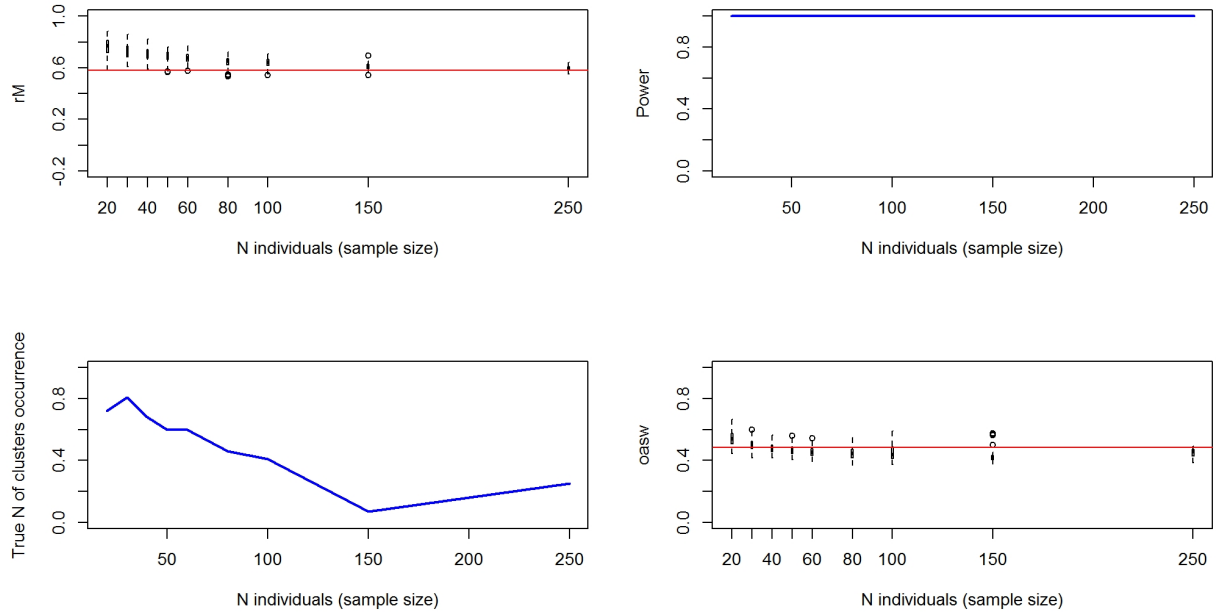


Figure 15630-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.774$); Figure 15630-5).

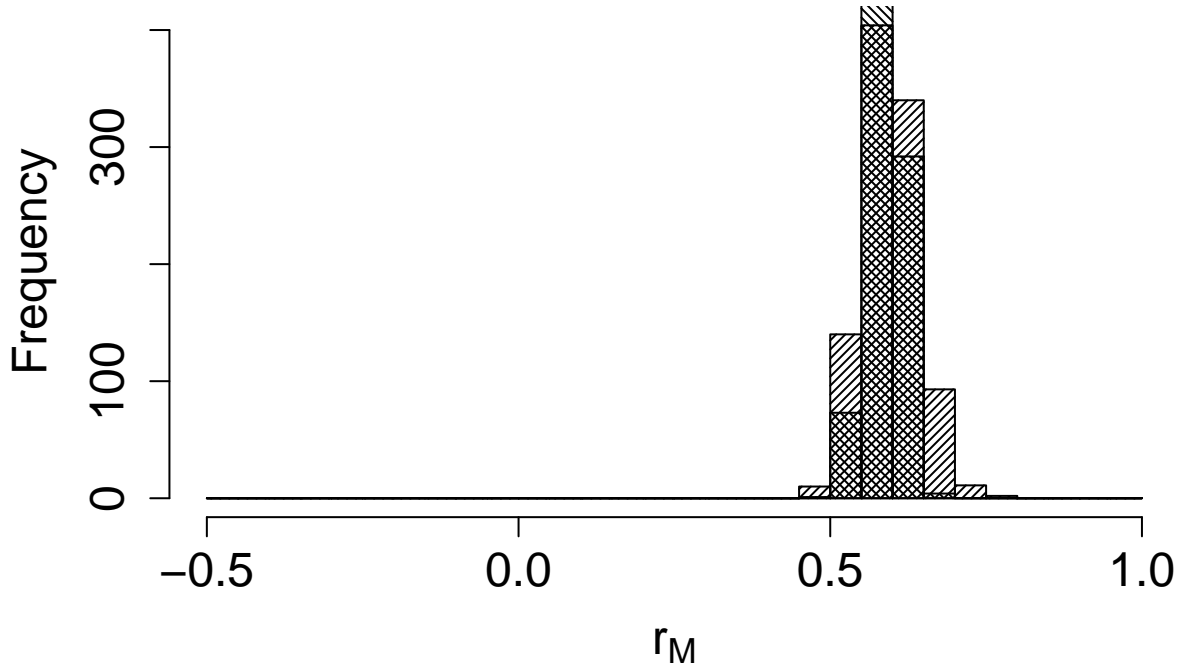


Figure 15630-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows moderate connectivity (MC = 0.453; MC = 0.452 when adjusted for absolute abundance) between 5 breeding regions and 9 non breeding regions (Table 15630-2; Figure 15630-6).

Table 15630-2. 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	2494252	Central Europe	0.675
Central Europe	2494252	North-west Europe	0.012
Central Europe	2494252	South-west Europe	0.012
Central Europe	2494252	West Europe	0.301
East Europe	11212604	Arabian peninsula	0.004
East Europe	11212604	Central Europe	0.706
East Europe	11212604	East Europe	0.105
East Europe	11212604	North Europe	0.032
East Europe	11212604	North-west Europe	0.008
East Europe	11212604	South-central Europe	0.008
East Europe	11212604	South-east Europe	0.020
East Europe	11212604	South-west Europe	0.008
East Europe	11212604	West Europe	0.109

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	249665	North Europe	0.946
North Europe	249665	North-west Europe	0.027
North Europe	249665	West Europe	0.027
North-west Europe	6456365	North-west Europe	1.000
West Europe	658645	Central Europe	0.026
West Europe	658645	North-west Europe	0.282
West Europe	658645	West Europe	0.692

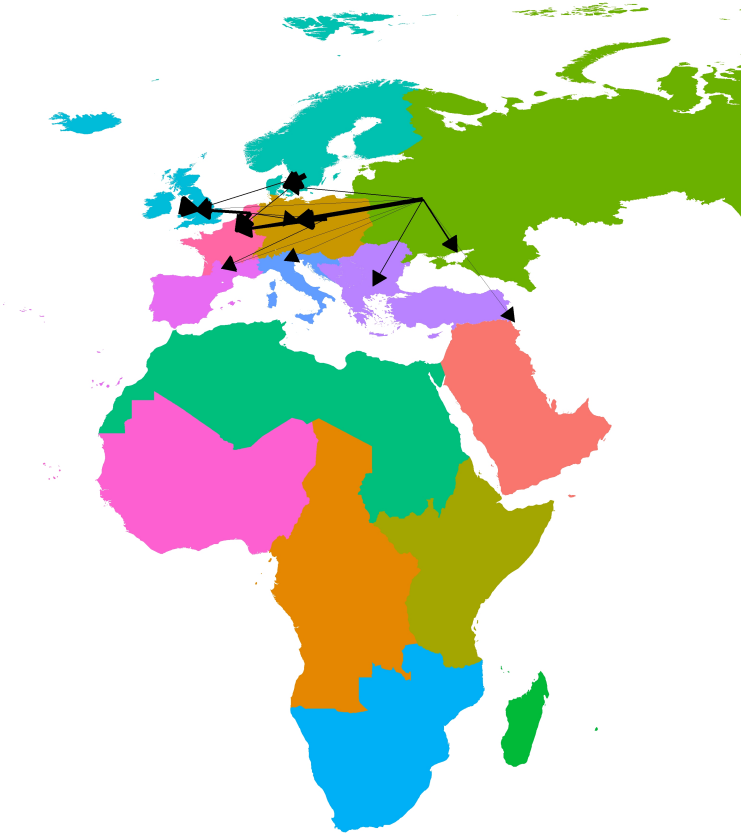


Figure 15630-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.