Migratory connectivity analysis

by EURING Migration Atlas

***Corvus corone* (EURING code 15670)**

1.1 Connectivity between individuals

The analysis evaluated 1264 individuals (2528 encounters) filtered from a total of 52736 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 15670-1; Figure 15670-1).

Table 15670-1. 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	1264	0.724	0.001	0.695	0.752	2	0.473
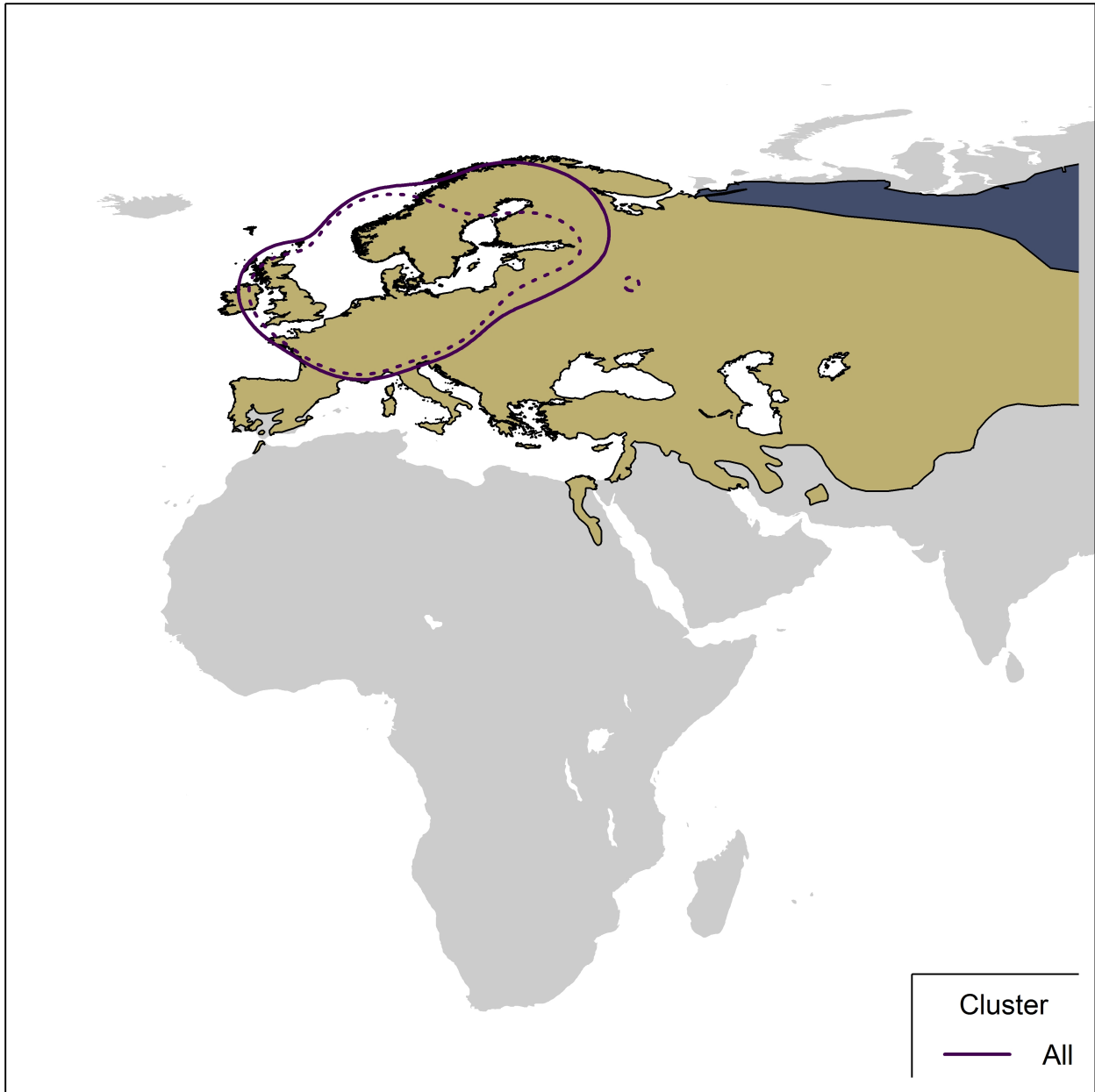
Figure 15670-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 15670-2) and stratified sampling of individuals within the breeding range (Figure 15670-3) and the non breeding range (Figure 15670-4). 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.
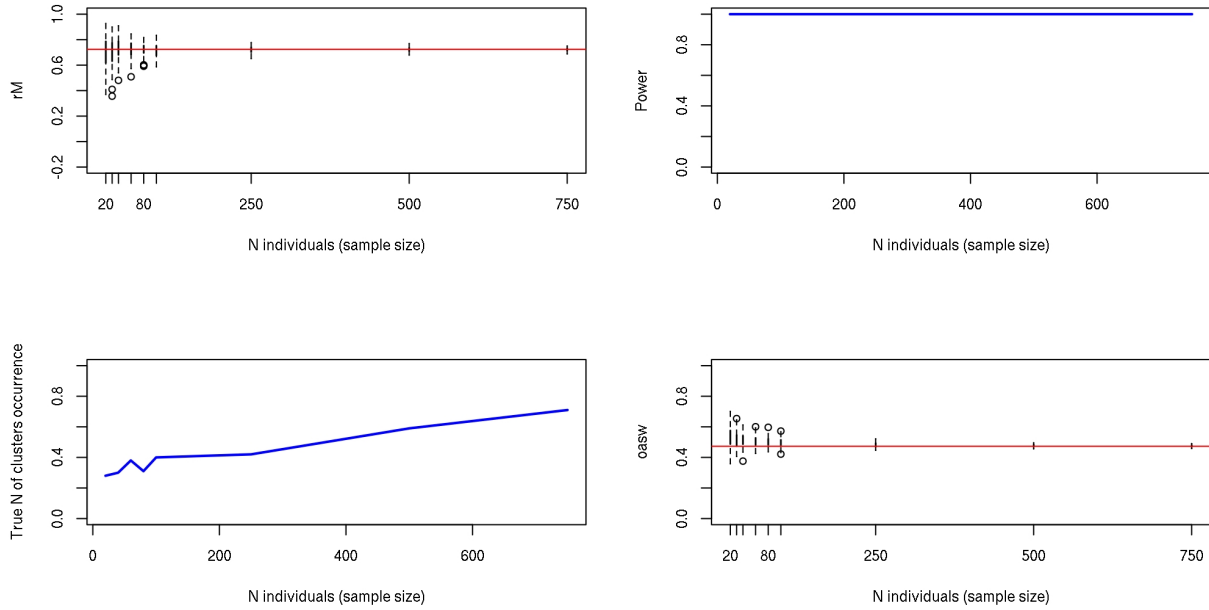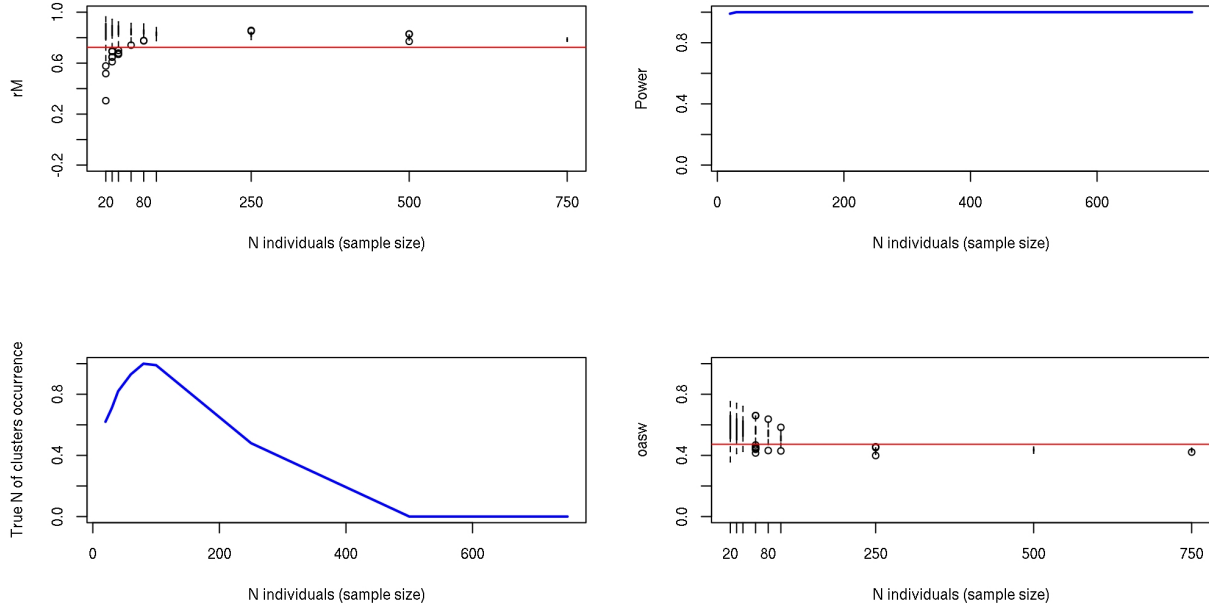

Figure 15670-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
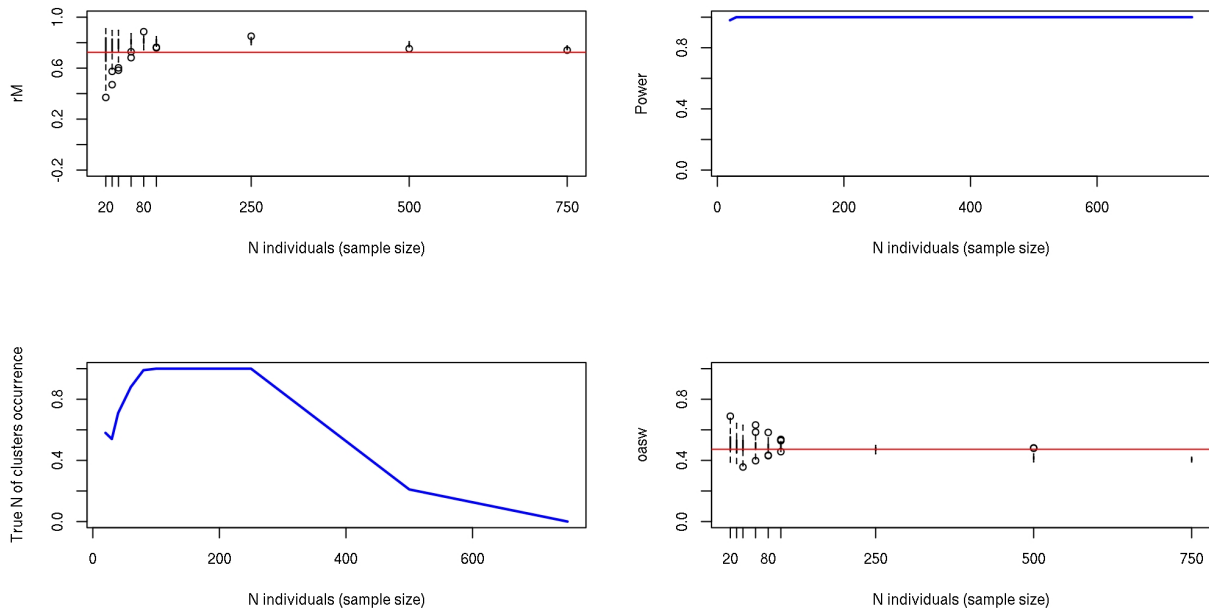
Figure 15670-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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


Figure 15670-4. 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 ($p < 0.001$; Figure 15670-5).
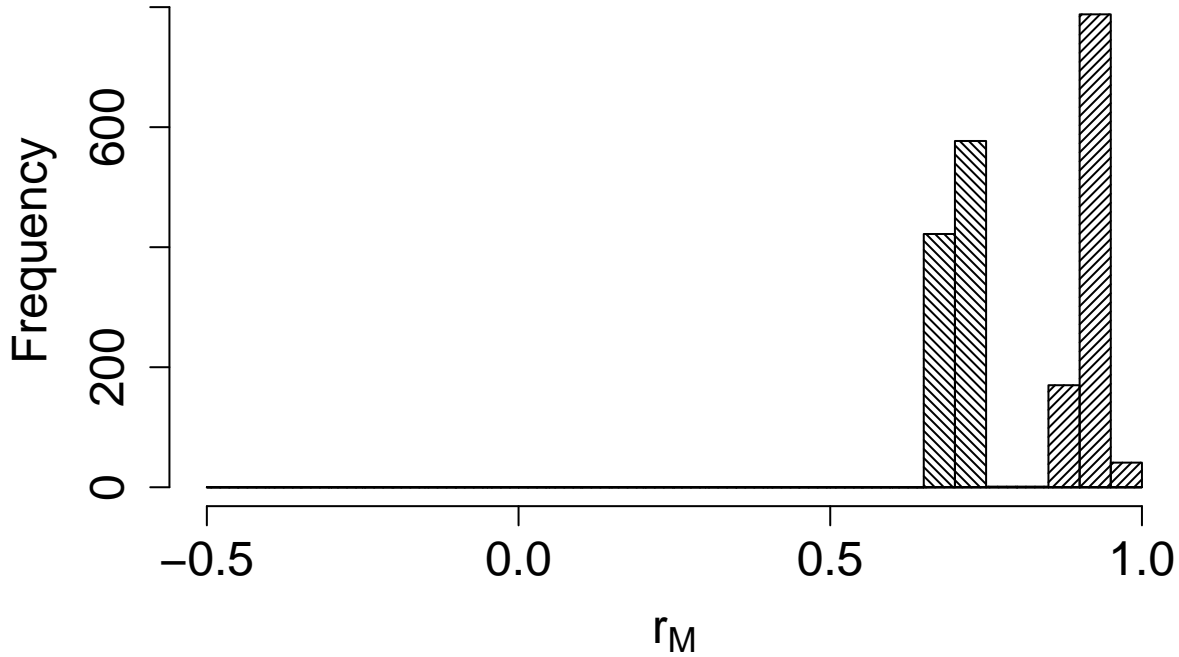
Figure 15670-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 0.912; MC = 0.912 when adjusted for absolute abundance) between 7 breeding regions and 7 non breeding regions (Table 15670-2; Figure 15670-6).

Table 15670-2. 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	2776220	Central Europe	0.987
Central Europe	2776220	West Europe	0.013
East Europe	6951148	Central Europe	0.073
East Europe	6951148	East Europe	0.866
East Europe	6951148	North Europe	0.061
North Europe	1260000	Central Europe	0.021
North Europe	1260000	East Europe	0.012
North Europe	1260000	North Europe	0.933
North Europe	1260000	North-west Europe	0.003
North Europe	1260000	West Europe	0.031
North-west Europe	3088243	North-west Europe	1.000
South-central Europe	1756141	South-central Europe	1.000
South-west Europe	3564443	South-west Europe	1.000

Breeding region	Abundance	Non breeding region	Transition probability
West Europe	2370367	West Europe	1.000
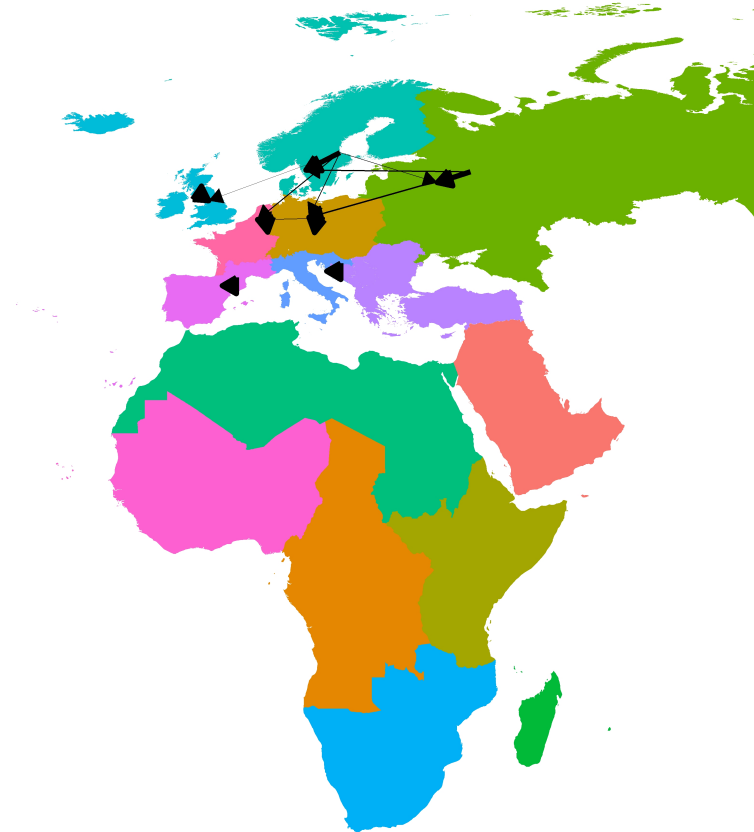
Figure 15670-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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.