Migratory connectivity analysis

by EURING Migration Atlas

Anas strepera (EURING code 01820)

1.1 Connectivity between individuals

The analysis evaluated 234 individuals (468 encounters) filtered from a total of 8358 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 01820-1; Figure 01820-1).

Table 01820-1. 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	234	0.711	0.001	0.611	0.779	5	0.478

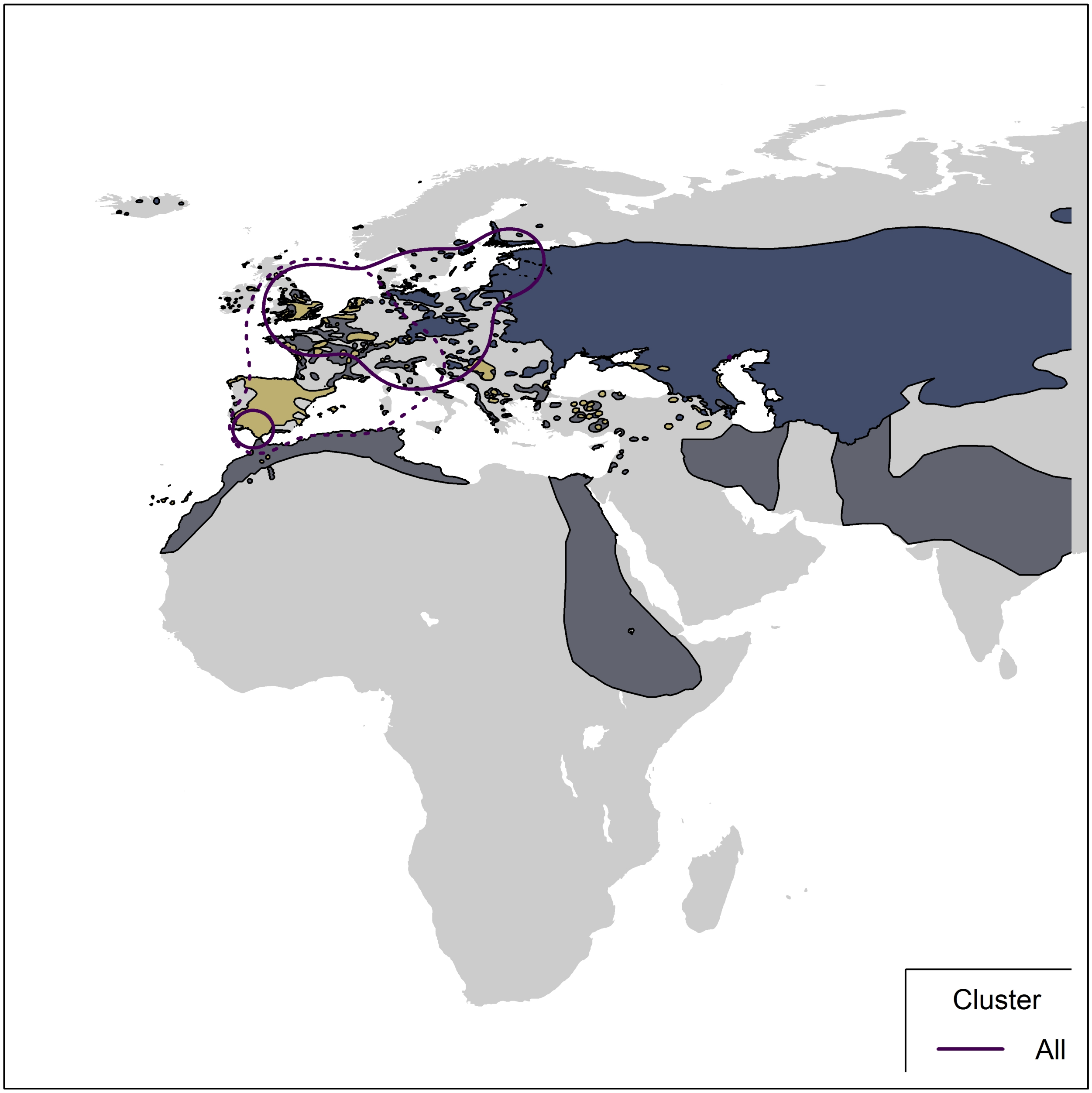

Figure 01820-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 01820-2) and stratified sampling of individuals within the breeding range (Figure 01820-3) and the non breeding range (Figure 01820-4). 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.

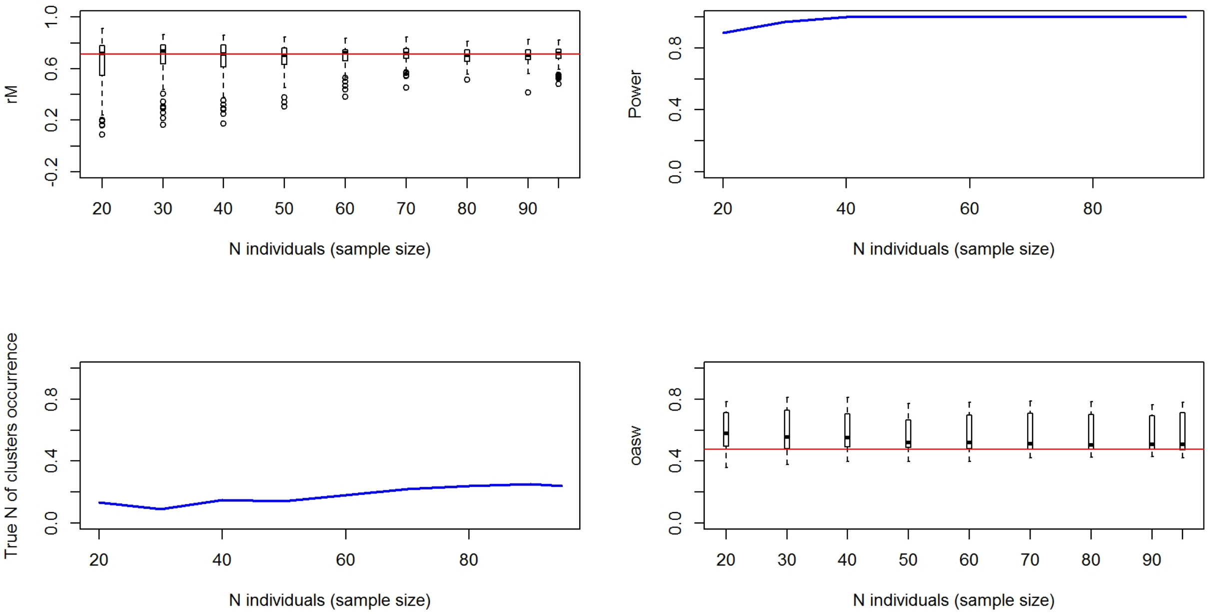

Figure 01820-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

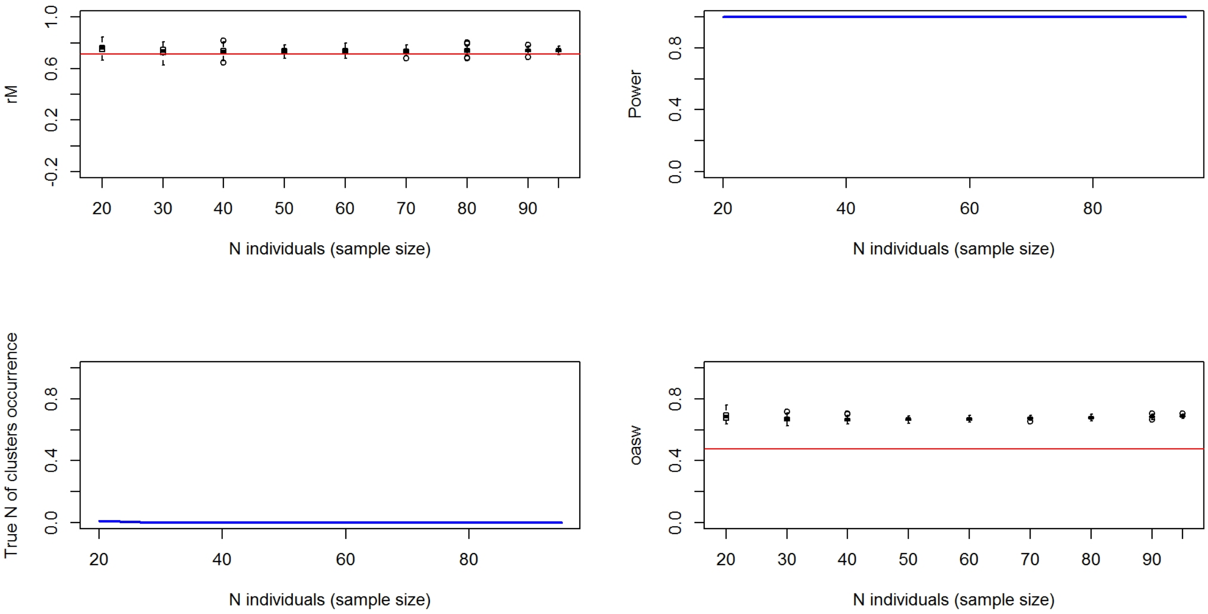

Figure 01820-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

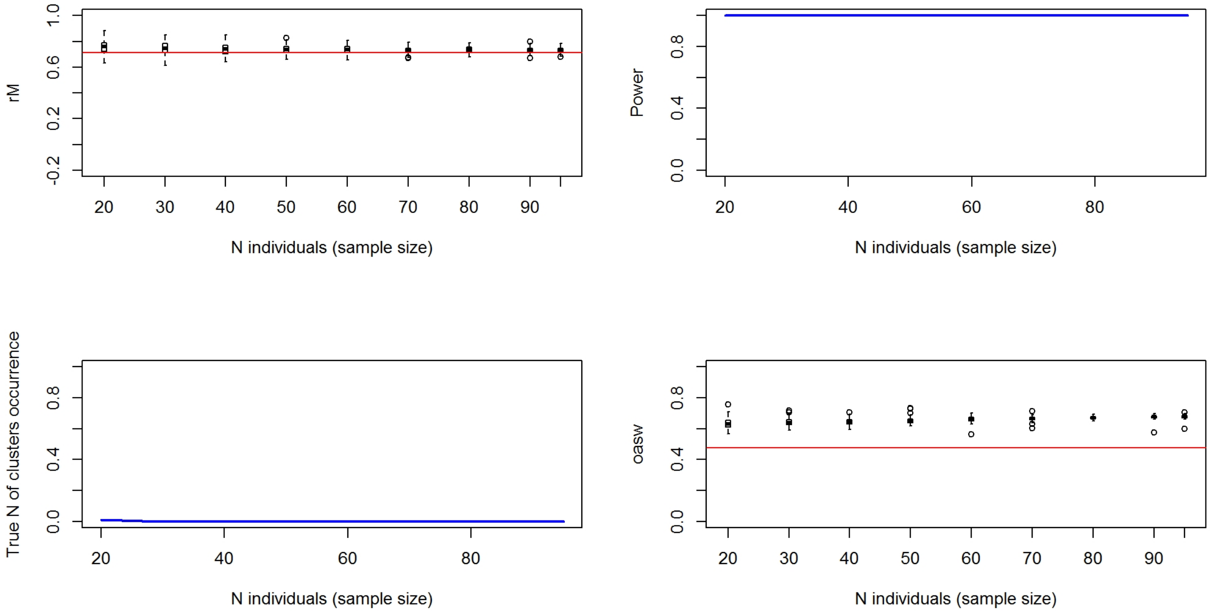

Figure 01820-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.05$); Figure 01820-5).

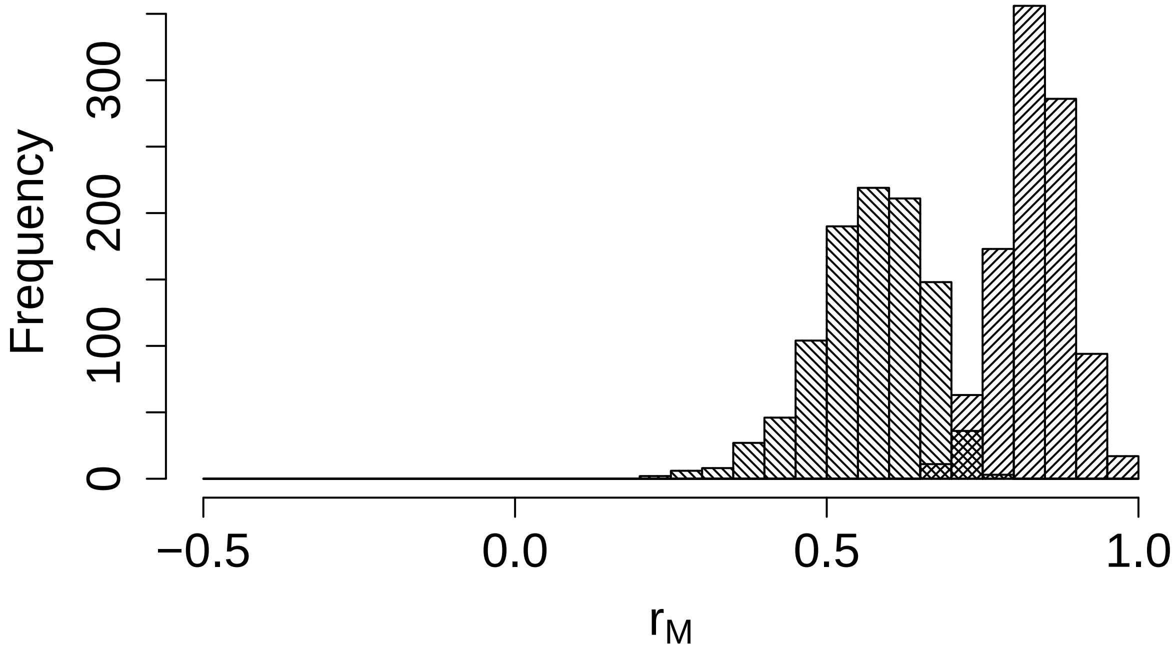

Figure 01820-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows no connectivity (MC = -0.005; MC = -0.01 when adjusted for absolute abundance) between 6 breeding regions and 9 non breeding regions (Table 01820-2; Figure 01820-6).

Table 01820-2. 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	28505	Central Europe	0.032
Central Europe	28505	North Africa	0.008
Central Europe	28505	North-west Europe	0.032
Central Europe	28505	South-central Europe	0.128
Central Europe	28505	South-west Europe	0.424
Central Europe	28505	West Europe	0.376
East Europe	95291	Arabian peninsula	0.121
East Europe	95291	East Europe	0.121
East Europe	95291	North Africa	0.030
East Europe	95291	North-west Europe	0.061
East Europe	95291	South-east Europe	0.091
East Europe	95291	South-west Europe	0.212
East Europe	95291	West Europe	0.364

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	6560	North-west Europe	0.125
North Europe	6560	South-west Europe	0.375
North Europe	6560	West Europe	0.500
North-west Europe	3357	North-west Europe	0.791
North-west Europe	3357	South-west Europe	0.070
North-west Europe	3357	West Europe	0.140
South-west Europe	17035	North Africa	0.154
South-west Europe	17035	North-west Europe	0.077
South-west Europe	17035	South-west Europe	0.692
South-west Europe	17035	West Europe	0.077
West Europe	38093	North-west Europe	0.250
West Europe	38093	South-west Europe	0.250
West Europe	38093	West Europe	0.500

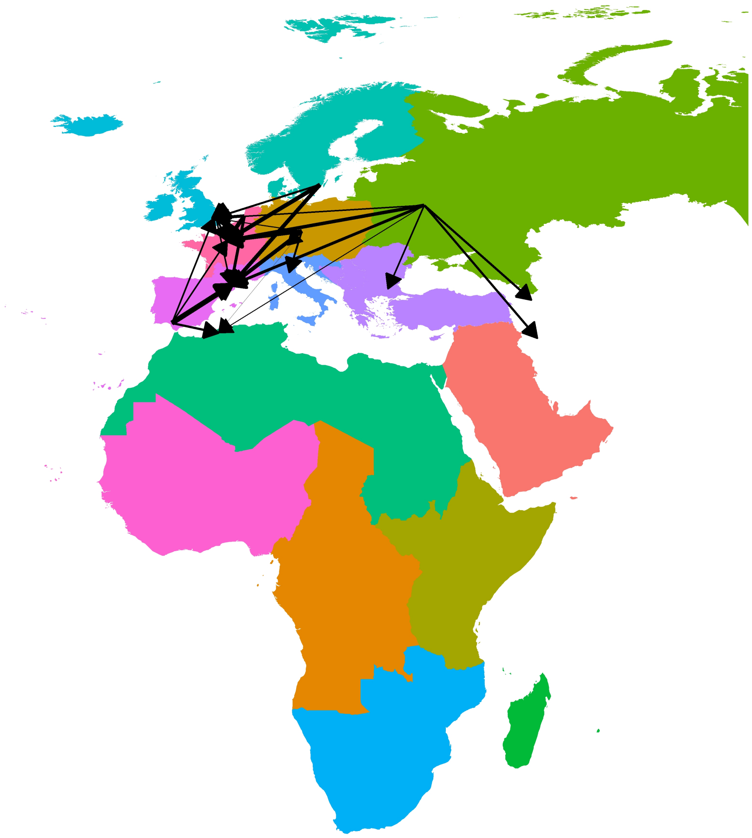

Figure 01820-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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.