

Migratory connectivity analysis

by EURING Migration Atlas

Haematopus ostralegus (EURING code 04500)

1.1 Connectivity between individuals

The analysis evaluated 2349 individuals (4698 encounters) filtered from a total of 110854 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 04500-1; Figure 04500-1).

Table 04500-1. 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	2349	0.351	0.001	0.315	0.396	2	0.48

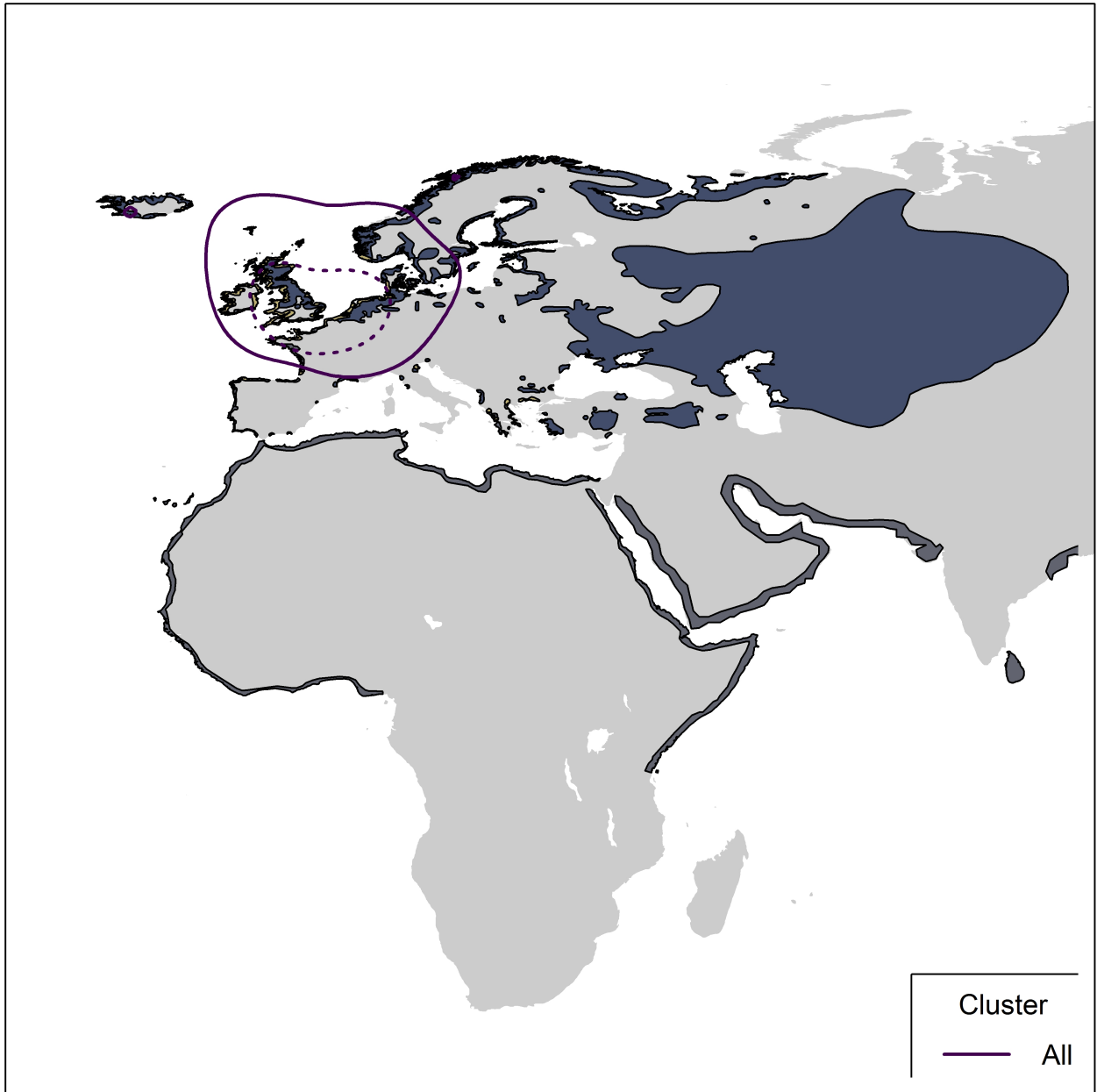


Figure 04500-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 04500-2) and stratified sampling of individuals within the breeding range (Figure 04500-3) and the non breeding range (Figure 04500-4). 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.

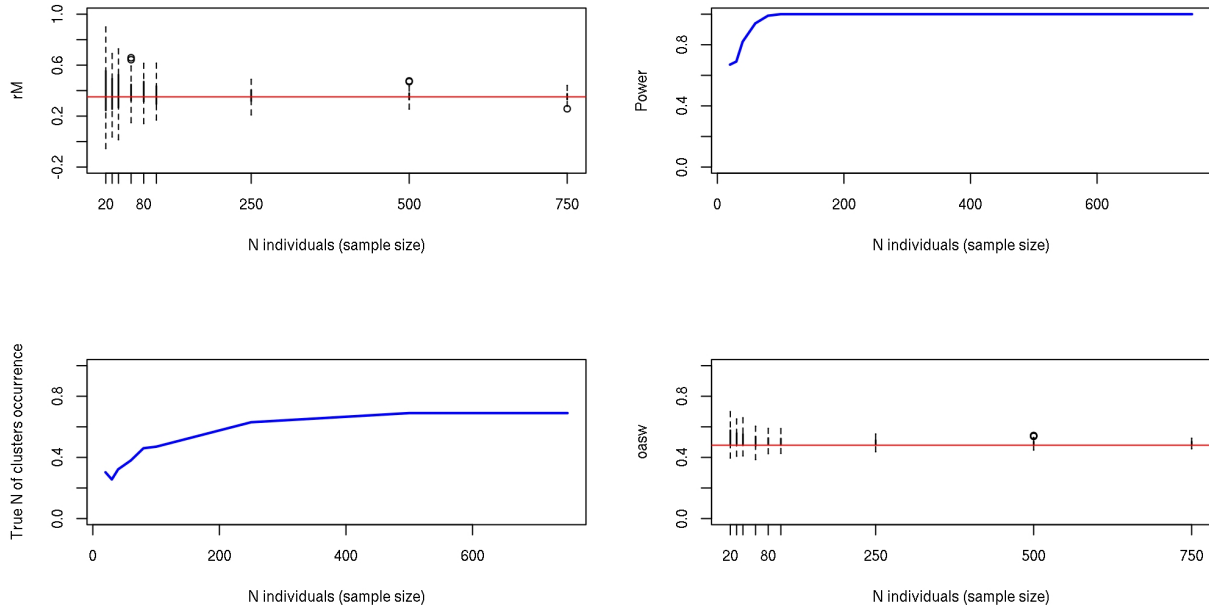


Figure 04500-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

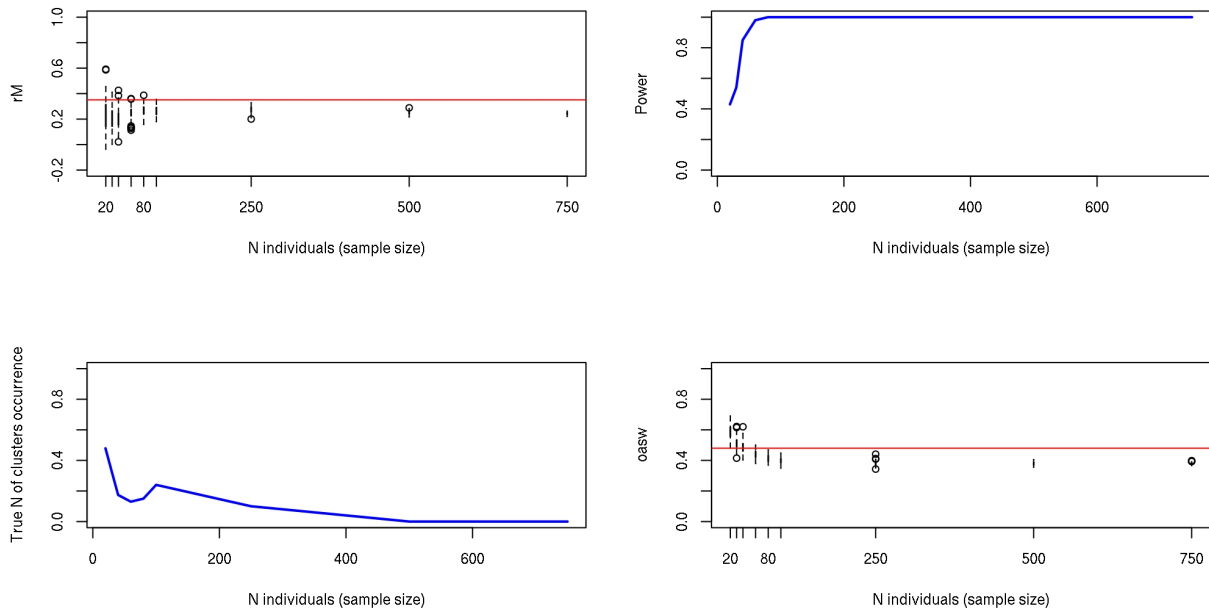


Figure 04500-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

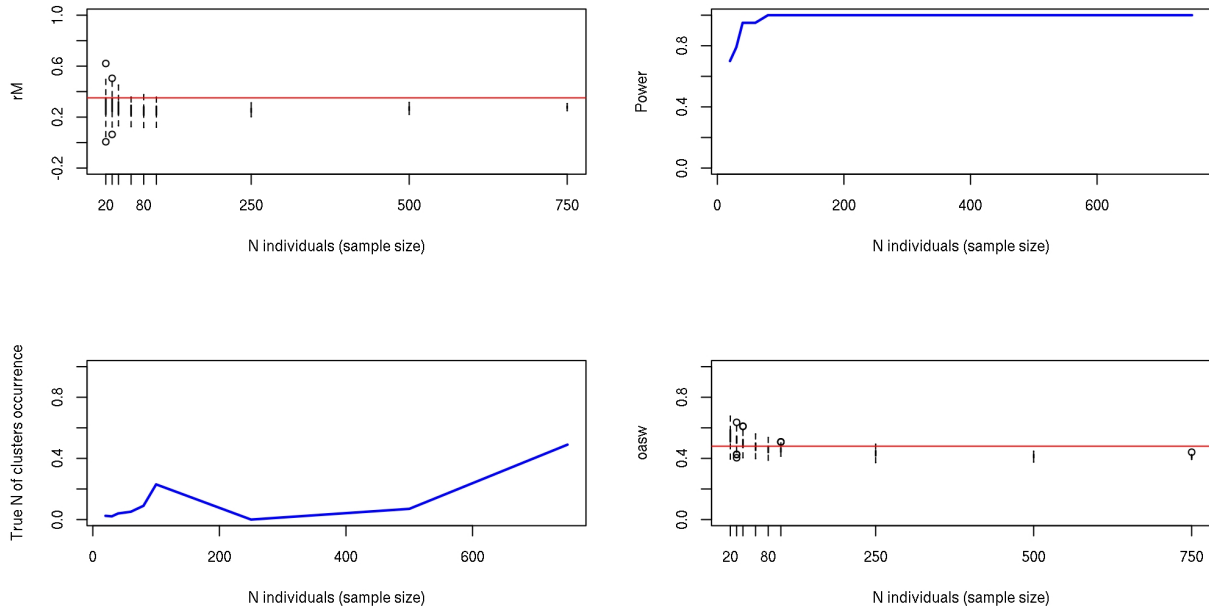


Figure 04500-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 04500-5).

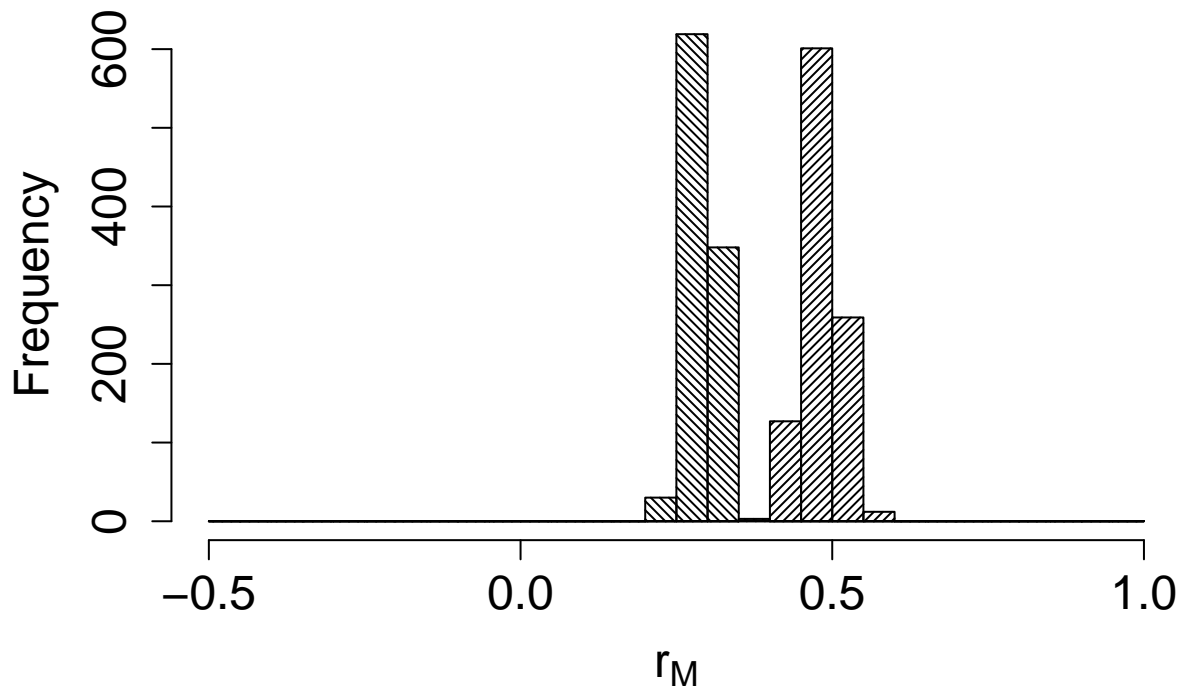


Figure 04500-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity (MC = 0.3; MC = 0.3 when adjusted for absolute abundance) between 6 breeding regions and 7 non breeding regions (Table 04500-2; Figure 04500-6).

Table 04500-2. 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	58040	Central Europe	0.313
Central Europe	58040	South-west Europe	0.017
Central Europe	58040	West Europe	0.670
East Europe	30367	Central Europe	0.188
East Europe	30367	North-west Europe	0.062
East Europe	30367	West Europe	0.750
North Europe	134300	Central Europe	0.100
North Europe	134300	North Europe	0.022
North Europe	134300	North-west Europe	0.435
North Europe	134300	South-west Europe	0.009
North Europe	134300	West Europe	0.435
North-west Europe	255403	Central Europe	0.001
North-west Europe	255403	North-west Europe	0.935

