

Migratory connectivity analysis

by EURING Migration Atlas

Ardea cinerea (EURING code 01220)

1.1 Connectivity between individuals

The analysis evaluated 2131 individuals (4262 encounters) filtered from a total of 47242 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 01220-1; Figure 01220-1).

Table 01220-1. 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	2131	0.374	0.001	0.333	0.421	2	0.474

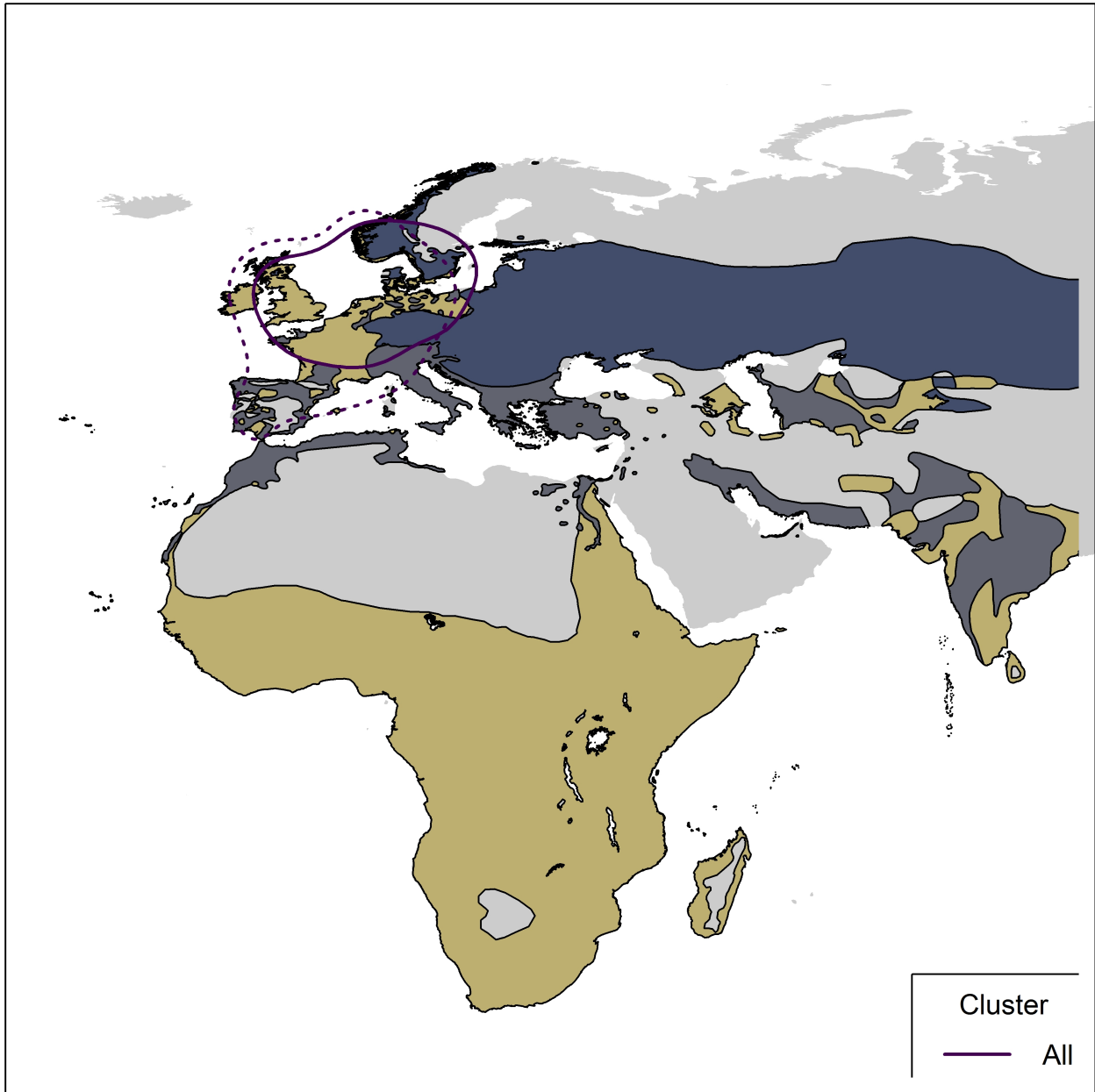


Figure 01220-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 01220-2) and stratified sampling of individuals within the breeding range (Figure 01220-3) and the non breeding range (Figure 01220-4). 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.

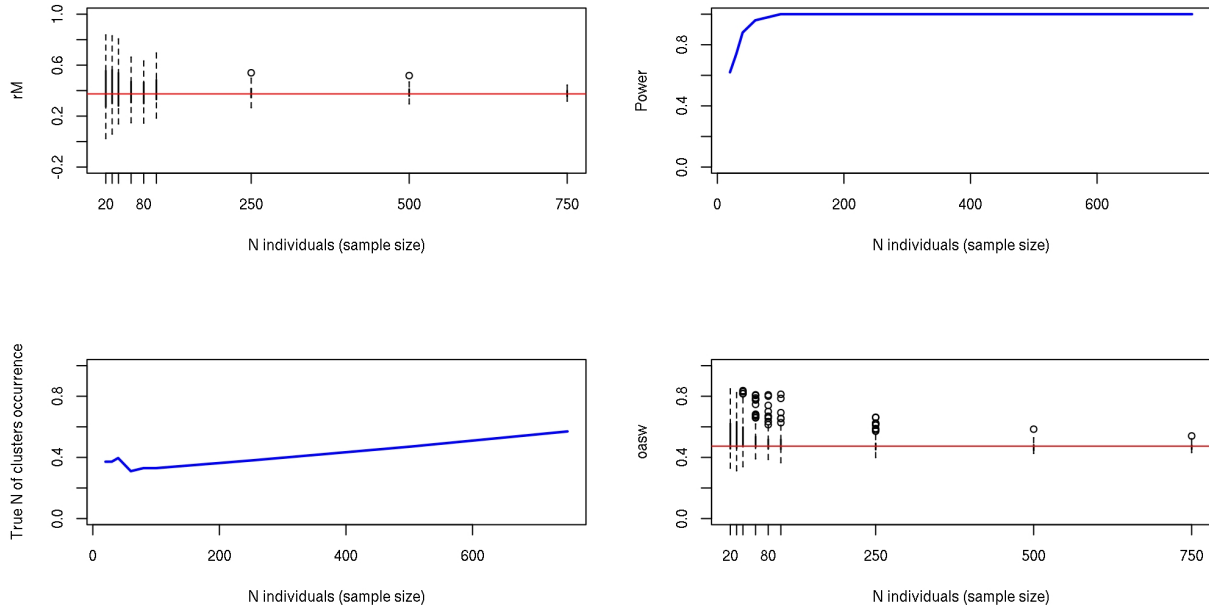


Figure 01220-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

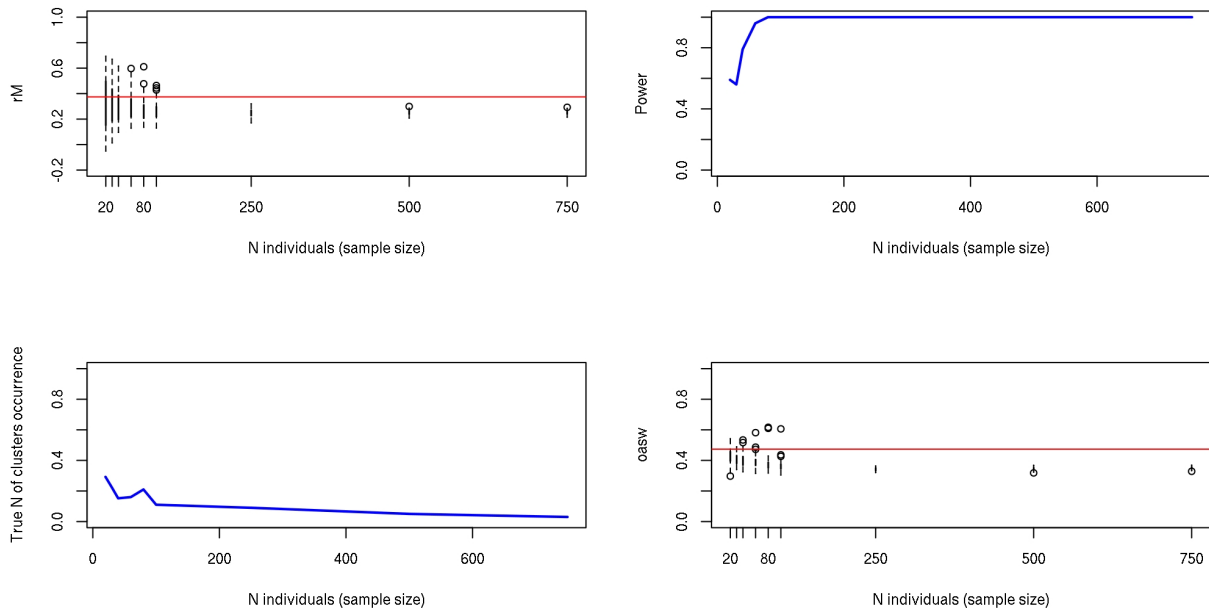


Figure 01220-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

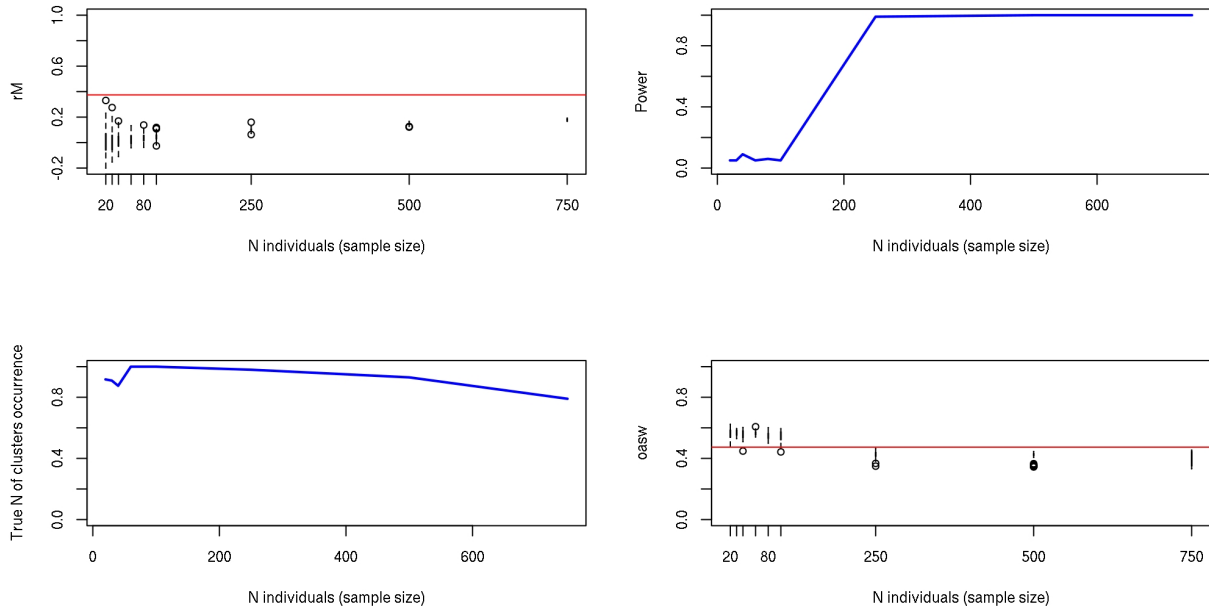


Figure 01220-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.33$); Figure 01220-5).

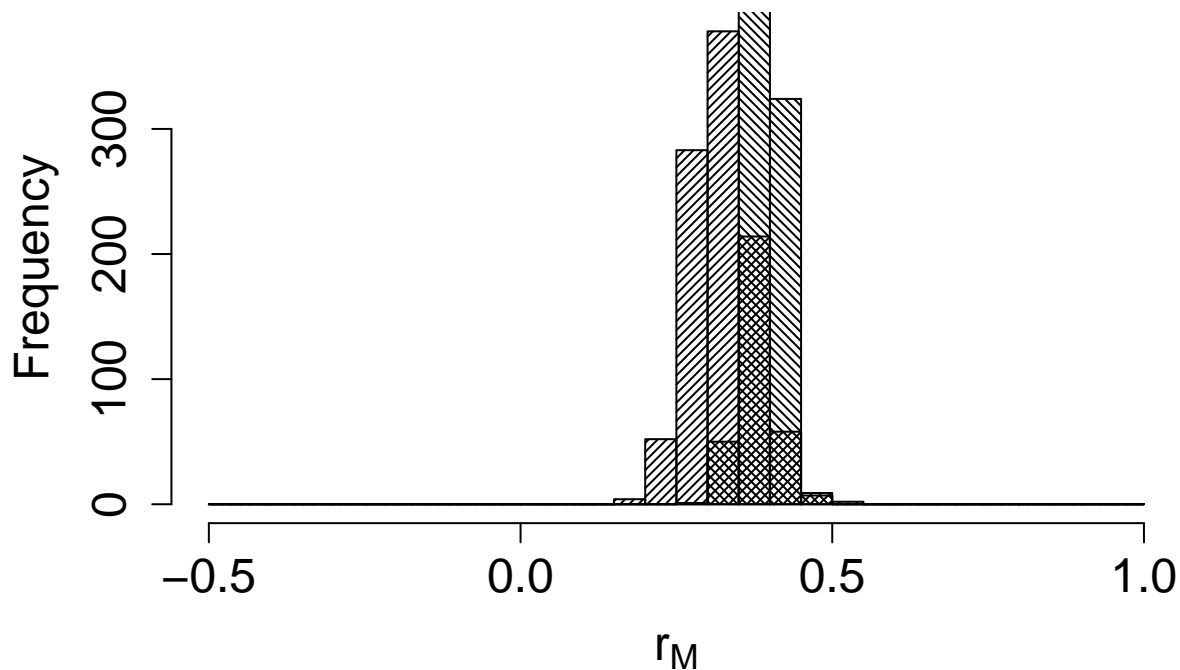


Figure 01220-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity ($MC = 0.27$; $MC = 0.269$ when adjusted for absolute abundance) between 6 breeding regions and 9 non breeding regions (Table 01220-2; Figure 01220-6).

Table 01220-2. 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	93475	Central Europe	0.281
Central Europe	93475	North Africa	0.038
Central Europe	93475	North Europe	0.004
Central Europe	93475	South-central Europe	0.094
Central Europe	93475	South-east Europe	0.004
Central Europe	93475	South-west Europe	0.209
Central Europe	93475	West Africa	0.038
Central Europe	93475	West Europe	0.332
East Europe	181182	Central Europe	0.206
East Europe	181182	North Africa	0.029
East Europe	181182	North Europe	0.029
East Europe	181182	South-central Europe	0.382
East Europe	181182	South-east Europe	0.059

Breeding region	Abundance	Non breeding region	Transition probability
East Europe	181182	South-west Europe	0.176
East Europe	181182	West Africa	0.029
East Europe	181182	West Europe	0.088
North Europe	33800	Central Europe	0.177
North Europe	33800	North Africa	0.019
North Europe	33800	North Europe	0.325
North Europe	33800	North-west Europe	0.107
North Europe	33800	South-central Europe	0.012
North Europe	33800	South-west Europe	0.078
North Europe	33800	West Africa	0.010
North Europe	33800	West Europe	0.271
North-west Europe	32174	North Africa	0.003
North-west Europe	32174	North-west Europe	0.943
North-west Europe	32174	South-west Europe	0.011
North-west Europe	32174	West Europe	0.044
South-west Europe	27587	North Africa	0.400
South-west Europe	27587	South-west Europe	0.600
West Europe	182464	Central Europe	0.017
West Europe	182464	North Africa	0.008
West Europe	182464	North-west Europe	0.018
West Europe	182464	South-west Europe	0.030
West Europe	182464	West Africa	0.002
West Europe	182464	West Europe	0.925

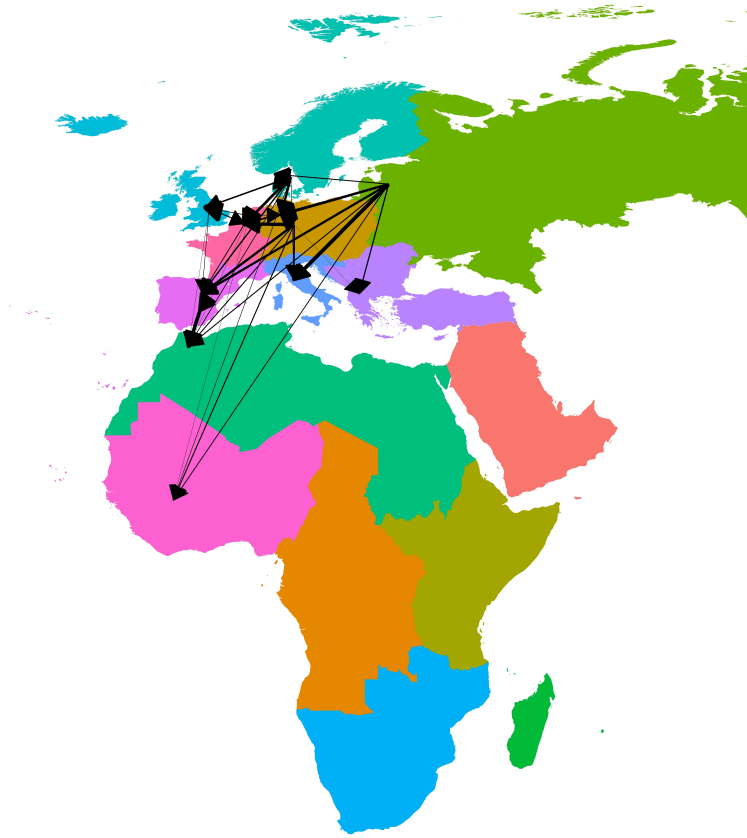


Figure 01220-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.